

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:28:41 ; Search time 168.02 Seconds

(without alignments)  
611.388 Million cell updates/sec

Title: US-09-771-382-4

Perfect score: 3019  
Sequence: 1 MNKIRYIMNSALNMAVAVS.....TASGNSHGCGASAVCYQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL\_19:\*  
1: sp.archaea:\*  
2: sp.bacteria:\*  
3: sp.fungi:\*  
4: sp.human:\*  
5: sp.invertebrate:\*  
6: sp.mammal:\*  
7: sp.mhc:\*  
8: sp.organelle:\*  
9: sp.phage:\*  
10: sp.plant:\*  
11: sp.todent:\*  
12: sp.virus:\*  
13: sp.vertebrate:\*  
14: sp.unclassified:\*  
15: sp.virus:\*  
16: sp.bacteriap:\*  
17: sp.archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3019	100.0	594	2	Q93QY4
2	2931	97.1	594	2	Q9JPI3
3	2927	97.0	594	2	Q9JPS2
4	2874	95.2	594	2	Q9JPH7
5	2863	94.8	598	2	Q9JPR9
6	2861	94.8	598	2	Q9JPT0
7	2855	94.6	598	2	Q9JPS0
8	2852	94.5	598	2	Q9JPS5
9	2806	92.9	600	2	Q9JPS6
10	2790	92.4	590	2	Q9JPS3
11	2762.5	91.5	599	2	Q9JPS8
12	2758.5	91.4	591	2	Q9JPS7
13	2758.5	91.4	591	16	Q9JRI8
14	2751	91.1	592	2	Q9AOF0
15	2739.5	90.7	591	2	Q9JQY3
16	2736.5	90.6	599	2	Q9JPS8

17	2718	90.0	598	2	Q9JPR7	Q9JPR7 neisseria m
18	2678	88.7	592	2	Q9JPS9	Q9JPS9 neisseria m
19	2655.5	88.0	595	2	Q9JPH0	Q9JPH0 neisseria m
20	2636	87.3	592	2	Q9JQY2	Q9JQY2 neisseria m
21	2606	86.3	600	2	Q9JPS5	Q9JPS5 neisseria m
22	2533	83.9	592	16	Q9JQW4	Q9JQW4 neisseria m
23	2527.5	83.7	589	2	Q9JPI0	Q9JPI0 neisseria m
24	2516.5	83.4	589	2	Q9JQY1	Q9JQY1 neisseria m
25	2444.5	81.0	526	2	Q9JPS4	Q9JPS4 neisseria m
26	2442.5	80.9	530	2	Q9JPS1	Q9JPS1 neisseria m
27	1328.5	44.0	2353	2	P71401	P71401 haemophilus
28	1030	34.1	1098	2	Q48152	Q48152 haemophilus
29	423	14.0	1299	16	Q9F3X6	Q9F3X6 pasteurrella
30	398.5	13.2	2059	16	Q9PD50	Q9PD50 xyella fas
31	384.5	12.7	1190	16	Q9PC04	Q9PC04 xyella fas
32	384.5	12.7	2712	16	Q9F3X5	Q9F3X5 pasteurrella
33	375.5	12.4	1107	2	Q9F2D8	Q9F2D8 salmoneilla
34	263	8.7	1291	16	Q92K07	Q92K07 rhizobium m
35	257.5	8.5	1953	16	Q98HJ2	Q98HJ2 rhizobium l
36	244	8.1	1039	2	Q9L6T7	Q9L6T7 escherichia
37	243	8.0	2276	2	Q93T16	Q93T16 staphylococ
38	239	7.9	1004	16	Q9PD53	Q9PD53 xyella fas
39	236	7.8	1039	2	Q9L6T8	Q9L6T8 escherichia
40	230	7.6	1040	2	Q9AL50	Q9AL50 shigella fl
41	228.5	7.6	1265	2	Q9RDA0	Q9RDA0 xanthomonas
42	228.5	7.6	1557	2	Q9RNI2	Q9RNI2 haemophilus
43	224.5	7.4	989	2	Q9XD84	Q9XD84 escherichia
44	223	7.4	1213	16	Q98JH8	Q98JH8 rhizobium l
45	222	7.4	1018	16	Q9HW06	Q9HW06 pseudomonas

## ALIGNMENTS

RESULT 1  
Q93QY4 PRELIMINARY: PRT: 594 AA.  
ID Q93QY4  
AC Q93QY4:  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxId=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG327;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157605; AAK68866.1; -  
SQ SEQUENCE 594 AA: 62297 MW: 9DD48B043A8BA2 CRC64:

Query Match 100.0%; Score 3019; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.2e-118;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKIRYIMNSALNMAVAVSELTRNHTKRASATVATVATLTLFAVQASTDDDDLYLE 60  
DB 1 MNKIRYIMNSALNMAVAVSELTRNHTKRASATVATVATLTLFAVQASTDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKEGTEKEVTEEDSNMGVYEDKKGVLTAGTITTKAGDNLIKONTNE 120  
DB 61 PVORTAVVLSFRSDKEGTEKEVTEEDSNMGVYEDKKGVLTAGTITTKAGDNLIKONTNE 120  
QY 121 NTNASSFTYSLKKDLTDLTSVGTETKLSFSANSKNKVNITSDTKGLNPAKKTAEFTNGDTYVH 180  
DB 121 NTNASSFTYSLKKDLTDLTSVGTETKLSFSANSKNKVNITSDTKGLNPAKKTAEFTNGDTYVH 180

QY	181	LNNGSGSTLTDTLTLWTFGATTTNTNDNNVDDDKKRAASVQDVLNKGNNIKGVPQGTTSADNV	240
Db	181	LNNGSGSTLTDTLTLWTFGATTTNTNDNVDTDEKKRAASVQDVLNKGNNIKGVKPGGTTSADNV	240
QY	241	DFVATYDTVEFLSADTKTTTVTVNVEBSKDKNGRTEVYKIGAKTSVJKEKGGKLVYTRKDGEND	3000
Db	241	DFVATYDTVEFLSADTKTTTVTVNVEBSKDKNGRTEVYKIGAKTSVJKEKGGKLVYTRKDGEND	3000
QY	301	SSTGKBGELVYAKVEYIDAVNKAAGKRRMKTTTTANGOTGADKFEYVYSTNTVTFASGKGTTA	3600
Db	301	SSTGKBGELVYAKVEYIDAVNKAAGKRRMKTTTTANGOTGADKFEYVYSTNTVTFASGKGTTA	3600
QY	361	TVSKDDOGCNITVMTDVNVNGDALNTNOLONGSGNNLDSKAAVAGSSGSKVYISGAVSPSKGKMD	4200
Db	361	TVSKDDOGCNITVMTDVNVNGDALNTNOLONGSGNNLDSKAAVAGSSGSKVYISGAVSPSKGKMD	4200
QY	421	TVTNINAGNNIEITFRNGKNNIIDATSMTPQSFSSVLSGAADAPLTVLSVDEGALNNGSKDKANK	4800
Db	421	TVTNINAGNNIEITFRNGKNNIIDATSMTPQSFSSVLSGAADAPLTVLSVDEGALNNGSKDKANK	4800
QY	481	PVRITNVAAPGVKEBQDVTNVVAOLKQVAAONLNHNDVNDGNAIRAGIAQAIAATAGLVQAVLP	5400
Db	481	PVRITNVAAPGVKEBQDVTNVVAOLKQVAAONLNHNDVNDGNAIRAGIAQAIAATAGLVQAVLP	5400
QY	541	KSMMAIGGGTTRGEGAGVAILGSSISDSDGNNIITKCTAAGNSRGRHFGASASVGYQW	594
Db	541	KSMMAIGGGTTRGEGAGVAILGSSISDSDGNNIITKCTAAGNSRGRHFGASASVGYQW	594

RESULT	2
Q9JPI3	
ID	Q9JPI3
PRELIMINARY;	
PRT;	594 AA.

DT 01-OCT-2000 (TReMBLrel\_15, Created)  
DT 01-OCT-2000 (TReMBLrel\_15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel\_16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC *Neisseria*, Proteobacteria; beta subdivision; *Neisseriaceae*; *Neisseria*  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, AND B2332;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlito V., Masingani V., Giuliani M.M., Arico' B.,  
RA Comanducci C.M., Jennings G.T., Baldi L., Bartolotti E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,  
RA Ratti G., Santilli L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappunli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226376; AAF42525.1; -  
DR EMBL: AF226369; AAF42518.1; -  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D004B46 CRC64;

Query Match	97.1%;	Score 2931;	DB 2;	Length 594;
Best Local Similarity	97.1%;	Pred. No. 5.6e-115;		
Matches 577;	Conservative 5;	Mismatches 12;	Indels 0;	Gaps 0;

[illegible]

Dd	121	NTMASSFFIYSLKROLDITDILSVETKESLSFGANGKRVNITTSOTKGLNFKKETAFTAGINDOTTVAH	180
Qy	181	LNIGIGSTLTDLTLLNTGATFTVNTVNDNVTDDEKKRAASVYDVLNMGWNIKGVPGTASDNY	240
Dd	181	LNIGIGSTLTDLTLLNTGATFTVNTVNDNVTDDEKKRAASVYDVLNMGWNIKGVPGTASDNY	240
Qy	241	DFVRTYDVEFLSADDTTYYVNTVSKDKNGKRTVEYIAKTSYVIEKEDGKLYTGDKDGEN	300
Dd	241	DFVRTYDVEFLSADDTTYYVNTVSKDKNGKRTVEYIAKTSYVIEKEDGKLYTGDKDGEN	300
Qy	301	SSTPKGEBELVAKFVIAVAVNAGKRMKMTTANCGOTGADKFEVYTSCTNTYPPASGKTTA	360
Dd	301	SSTDEGBELVAKFVIAVAVNAGKRMKMTTANCGOTGADKFEVYTSCTNTYPPASGKTTA	360
Qy	361	TVSKDDQGNITVAMDVVNVGDALANTNOLNONGSMWNLDSKAVAGSSGKTVISGVNVPSPKGMDE	420
Dd	361	TVSKDDQGNITVAMDVVNVGDALANTNOLNONGSMWNLDSKAVAGSSGKTVISGVNVPSPKGMDE	420
Qy	421	TVINAGANNIEITRNGKNIDIAITSMTPOFSSVSLGAGADAPTILSVDEDEGALNVGSKDANK	480
Dd	421	TVINAGANNIEITRNGKNIDIAITSMTPOFSSVSLGAGADAPTILSVDEDEGALNVGSKDANK	480
Qy	481	PVRTTNVAPGVKEDDVYNVAOLKQVAAONLNHHIDNVGNARAGIAQAIAIATAGLYQAYLPB	540
Dd	481	PVRTTNVAPGVKEDDVYNVAOLKQVAAONLNHHIDNVGNARAGIAQAIAIATAGLYQAYLPB	540
Qy	541	KSMMAIGGGYTRGEGAGVAILGSSISDGGNNMTIKETASGNSRGHFGASASVGYOM	594
Dd	541	KSMMAIGGGYTRGEGAGVAILGSSISDGGNNMTIKETASGNSRGHFGASASVGYOM	594

RESULT	3	
Q9JPS2		
ID	Q9JPS2	PRELIMINARY;
		PRT; 594 AA

DT 01-OCT-2000 (TReMBLrel\_15, Created)  
DT 01-OCT-2000 (TReMBLrel\_15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel\_16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC  
RC STRAIN=NEE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Ntli S.,  
RA Ratteli G., Sartelli L., Savino S., Scarselli M., Scorn E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blar E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT *Meningococcus* by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
SR EMBL; AF226379; AAF42528.1;  
SO SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match	97.0%	Score 2927	DB 2	Length 594
Best Local Similarly	97.0%	Pred. No. 8.2e-115		
Matches 576; Conservative	5;	Mismatches 13;	Indels 0;	Gaps 0;

Qy	1	MNKYIRIIINWLSLAAMWAVSELTPTNHRKRSAPATATVLTMTLLPAFQAOSTDDDDLLYLE	60
Db	1	MNKYIRIIINWLSLAAMWAVSELTPTNHRKRSAPATATVLTMTLLPAFQAOSTDDDDLLYLE	60
Qy	61	PVGRTAVVLSFRSDKEGTGEKEVEDSNMGVYEDFKRGVLATGTTTLKAGDNLIKONTNE	120
Db	61	PVGRTAVVLSFRSDKEGTGEKEVEDSNMGVYEDFKRGVLATGTTTLKAGDNLIKONTNE	120



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QY 121 NTNASSFTYSLKKDLTDLTSVGEKLSFNSANSKNVITSDTKLNFPAKKTAEFTNGDTYH 180
    |||||||
Db 121 NTNASSFTYSLKKDLTDLTSVGEKLSFNSANSKNVITSDTKLNFPAKKTAEFTNGDTYH 180
QY 181 LNCIGSTLTDLTLNTGATNTVNDVYDDEKKRAASVKDVLNAGWNIKGVKPGTASDVY 240
    |||||||
Db 181 LNCIGSTLTDLTLNTGATNTVNDVYDDEKKRAASVKDVLNAGWNIKGVKPGTASDVY 240
QY 241 DFRYTDYVEFLSADTKTTTVNVEKDKNGKRTVEKIGATSVYKEDEGLVYKDKGEND 300
    |||||||
Db 241 DFRYTDYVEFLSADTKTTTVNVEKDKNGKRTVEKIGATSVYKEDEGLVYKDKGEND 300
QY 301 SSTDKGEGLYTAAKEVIDAANKAGWRKTTTANGQTGADKFEFTVSGTNTVTFASGKTTA 360
    |||||||
Db 301 SSTDKGEGLYTAAKEVIDAANKAGWRKTTTANGQTGADKFEFTVSGTNTVTFASGKTTA 360
QY 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKKMD 420
    |||||||
Db 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKKMD 420
QY 421 TVNINAGNNIEITRNKNIDTATSMTPQSSVSLGAGADPTLSVDEGALNYSKDKANK 480
    |||||||
Db 421 TVNINAGNNIEITRNKNIDTATSMTPQSSVSLGAGADPTLSVDEGALNYSKDKANK 480
QY 481 PVRTTAVAPGKGDVNTVNAOLKGVANLNHNDVNGNARAGIAOAIATAGLYOAYLPG 540
    |||||||
Db 481 PVRTTAVAPGKGDVNTVNAOLKGVANLNHNDVNGNARAGIAOAIATAGLYOAYLPG 540
QY 541 KSMMAIGGTYRGEAGYAGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 594
    |||||||
Db 541 KSMMAIGGTYRGEAGYAGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 594

RESULT 4
09JPH7 PRELIMINARY: PRT: 594 AA.
AC 09JPH7:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-B2198, AND 297-0;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-B2198.
RA Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/Genbank/DBD databases.
DR EMBL: AF226336; AAF42517.1; -
DR EMBL: AF226358; AAF42507.1; -
DR EMBL: AF157604; AAK68865.1; -
SQ SEQUENCE 594 AA: 62361 MW: 436BDDDED68263C5C CRC64;
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Query Match 95.2%; Score 2874; DB 2; Length 594;
Best local Similarity 95.6%; Pred. No. 1.3e-112;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIRIIMNSALNAAVAVSELTNRHFKRASATVATATLLEFATVQASTDDDDLYLE 60
    |||||||
Db 1 MNKIRIIMNSALNAAVAVSELTNRHFKRASATVATATLLEFATVQASTDDDDLYLE 60
QY 61 PVQRTAVVLSFRSDKGTGTEKEDSNMGVYFDKKGVLTAGTITTKADNLIKQNTNPE 120
    |||||||
Db 61 PVQRTAVVLSFRSDKGTGTEKEDSNMGVYFDKKGVLTAGTITTKADNLIKQNTNPE 120
QY 121 NTNASSFTYSLKKDLTDLTSVGEKLSFNSANSKNVITSDTKLNFPAKKTAEFTNGDTYH 180
    |||||||
Db 121 NTNASSFTYSLKKDLTDLTSVGEKLSFNSANSKNVITSDTKLNFPAKKTAEFTNGDTYH 180
QY 181 LNCIGSTLTDLTLNTGATNTVNDVYDDEKKRAASVKDVLNAGWNIKGVKPGTASDVY 240
    |||||||
Db 181 LNCIGSTLTDLTLNTGATNTVNDVYDDEKKRAASVKDVLNAGWNIKGVKPGTASDVY 240
QY 241 DFRYTDYVEFLSADTKTTTVNVEKDKNGKRTVEKIGATSVYKEDEGLVYKDKGEND 300
    |||||||
Db 241 DFRYTDYVEFLSADTKTTTVNVEKDKNGKRTVEKIGATSVYKEDEGLVYKDKGEND 300
QY 301 SSTDKGEGLYTAAKEVIDAANKAGWRKTTTANGQTGADKFEFTVSGTNTVTFASGKTTA 360
    |||||||
Db 301 SSTDKGEGLYTAAKEVIDAANKAGWRKTTTANGQTGADKFEFTVSGTNTVTFASGKTTA 360
QY 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKKMD 420
    |||||||
Db 361 TVSKDQGNITVYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNVSPSKKMD 420
QY 421 TVNINAGNNIEITRNKNIDTATSMTPQSSVSLGAGADPTLSVDEGALNYSKDKANK 480
    |||||||
Db 421 TVNINAGNNIEITRNKNIDTATSMTPQSSVSLGAGADPTLSVDEGALNYSKDKANK 480
QY 481 PVRTTAVAPGKGDVNTVNAOLKGVANLNHNDVNGNARAGIAOAIATAGLYOAYLPG 540
    |||||||
Db 481 PVRTTAVAPGKGDVNTVNAOLKGVANLNHNDVNGNARAGIAOAIATAGLYOAYLPG 540
QY 541 KSMMAIGGTYRGEAGYAGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 594
    |||||||
Db 541 KSMMAIGGTYRGEAGYAGYSSISDGMWIIKGTASGNSRGHFGASASVGYOM 594

RESULT 5
09JPR9 PRELIMINARY: PRT: 598 AA.
AC 09JPR9:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brooker M., Hundi E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappelli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226382; AAF42531.1; -
SQ SEQUENCE 598 AA: 62718 MW: 9095F8E31AD7C76D CRC64;
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Query Match 94.8%; Score 2863; DB 2; Length 598;  
Best Local Similarity 95.0%; Pred. No. 3.8e-112;  
Matches 568; Conservative 5; Mismatches 21; Indels 4; Gaps 1;

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OY 1 MNKIRIIMNSALNMAVAVSELTNRNHTKRASATVATVATLLEFATVOASTTDDDDLYLE 60
    1 MNKIRIIMNSALNMAVAVSELTNRNHTKRASATVATVATLLEFATVOANATDDDDLYLE 60
DB 1 MNKIRIIMNSALNMAVAVSELTNRNHTKRASATVATVATLLEFATVOANATDDDDLYLE 60
OY 61 PVQRTAVAVLSRPSDEKGEKGEVTEDSNMWGYFDEKGVLAGTTLKAGDMLIKQNTNE 120
    61 PVQRTAVAVLSRPSDEKGEKGEVTEDSNMWGYFDEKRVLKAGATTLKAGDMLIKQNTNE 120
DB 61 PVQRTAVAVLSRPSDEKGEKGEVTEDSNMWGYFDEKRVLKAGATTLKAGDMLIKQNTNE 120
OY 121 NTNA-----SFTYSLKRLDTLTSVGTETKLSFSANSKNVNTSPTKGLNFAKKAETNGD 176
    121 NTNETNDSFTYSLKRLDTLTSVETKLSFGANGKNVNTSPTKGLNFAKKAETNGD 180
DB 121 NTNETNDSFTYSLKRLDTLTSVETKLSFGANGKNVNTSPTKGLNFAKKAETNGD 180
OY 177 TTVHLNGIGSTLTDTLLNTGATTVNTNDVTDDEKKRAASVADVLNAGMNIKGVKPGTTA 236
    177 TTVHLNGIGSTLTDTLLNTGATTVNTNDVTDDEKKRAASVADVLNAGMNIKGVKPGTTA 240
DB 177 TTVHLNGIGSTLTDTLLNTGATTVNTNDVTDDEKKRAASVADVLNAGMNIKGVKPGTTA 240
OY 237 SDNDFEVTYDTVEFLSADTKTTTVNVESSKDKGRTEYKIGAKTSVIEKDGKLVTKGDK 296
    241 SDNDFEVTYDTVEFLSADTKTTTVNVESSKDKGRTEYKIGAKTSVIEKDGKLVTKGDK 300
DB 241 SDNDFEVTYDTVEFLSADTKTTTVNVESSKDKGRTEYKIGAKTSVIEKDGKLVTKGDK 300
OY 297 GENDSTDKGGLVYAKFVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTNTTFFASGK 356
    301 DENGSSTDEGEGVYAKFVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTNTTFFASGK 360
DB 301 DENGSSTDEGEGVYAKFVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTNTTFFASGK 360
OY 357 GTTATVSKDDGNGNTVMYDVNVDALNVNOLNSGMNLSKRAVAGSSKRVISGNVSPSKG 416
    361 GTTATVSKDDGNGNTVYKDVNVDGALNVNOLNSGMNLSKRAVAGSSKRVISGNVSPSKG 420
DB 361 GTTATVSKDDGNGNTVYKDVNVDGALNVNOLNSGMNLSKRAVAGSSKRVISGNVSPSKG 420
OY 417 KMDFTVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDVDEGALNVGSK 476
    421 KMDFTVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDVDEGALNVGSK 480
DB 421 KMDFTVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDVDEGALNVGSK 480
OY 477 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHIDNVGNARAGIAQAIATAGLVQA 536
    481 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHIDNVGNARAGIAQAIATAGLVQA 540
DB 481 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHIDNVGNARAGIAQAIATAGLVQA 540
OY 537 YLPKGSMAIGGTYRGAGYAGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 594
    541 YLPKGSMAIGGTYRGAGYAGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 598
DB 541 YLPKGSMAIGGTYRGAGYAGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 598
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RESULT 6  
O9JPT0 PRELIMINARY; PRT; 598 AA.

AC O9JPT0;  
DB 01-OCT-2000 (TREMblrel. 15, Created)  
DB 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DB 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=2996;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piazza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hündt E., Knapp B., Blair E., Mason T., Tetteilin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).

DR EMBL; AF226359; AAF42508.1; -.  
S0 SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EB3 CRC64;

Query Match 94.8%; Score 2861; DB 2; Length 598;  
Best Local Similarity 94.8%; Pred. No. 4.6e-112;  
Matches 567; Conservative 5; Mismatches 22; Indels 4; Gaps 1;

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OY 1 MNKIRIIMNSALNMAVAVSELTNRNHTKRASATVATVATLLEFATVOASTTDDDDLYLE 60
    1 MNKIRIIMNSALNMAVAVSELTNRNHTKRASATVATVATLLEFATVOANATDDDDLYLE 60
DB 1 MNKIRIIMNSALNMAVAVSELTNRNHTKRASATVATVATLLEFATVOANATDDDDLYLE 60
OY 61 PVQRTAVAVLSRPSDEKGEKGEVTEDSNMWGYFDEKGVLAGTTLKAGDMLIKQNTNE 120
    61 PVQRTAVAVLSRPSDEKGEKGEVTEDSNMWGYFDEKRVLKAGATTLKAGDMLIKQNTNE 120
DB 61 PVQRTAVAVLSRPSDEKGEKGEVTEDSNMWGYFDEKRVLKAGATTLKAGDMLIKQNTNE 120
OY 121 NTNA-----SFTYSLKRLDTLTSVGTETKLSFSANSKNVNTSPTKGLNFAKKAETNGD 176
    121 NTNETNDSFTYSLKRLDTLTSVETKLSFGANGKNVNTSPTKGLNFAKKAETNGD 180
DB 121 NTNETNDSFTYSLKRLDTLTSVETKLSFGANGKNVNTSPTKGLNFAKKAETNGD 180
OY 177 TTVHLNGIGSTLTDTLLNTGATTVNTNDVTDDEKKRAASVADVLNAGMNIKGVKPGTTA 236
    177 TTVHLNGIGSTLTDTLLNTGATTVNTNDVTDDEKKRAASVADVLNAGMNIKGVKPGTTA 240
DB 177 TTVHLNGIGSTLTDTLLNTGATTVNTNDVTDDEKKRAASVADVLNAGMNIKGVKPGTTA 240
OY 237 SDNDFEVTYDTVEFLSADTKTTTVNVESSKDKGRTEYKIGAKTSVIEKDGKLVTKGDK 296
    241 SDNDFEVTYDTVEFLSADTKTTTVNVESSKDKGRTEYKIGAKTSVIEKDGKLVTKGDK 300
DB 241 SDNDFEVTYDTVEFLSADTKTTTVNVESSKDKGRTEYKIGAKTSVIEKDGKLVTKGDK 300
OY 297 GENDSTDKGGLVYAKFVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTNTTFFASGK 356
    301 GENDSTDEGEGVYAKFVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTNTTFFASGK 360
DB 301 GENDSTDEGEGVYAKFVIDAVNKAQRMKTTTANGOTGADKFEYVTSCTNTTFFASGK 360
OY 357 GTTATVSKDDGNGNTVMYDVNVDALNVNOLNSGMNLSKRAVAGSSKRVISGNVSPSKG 416
    361 GTTATVSKDDGNGNTVYKDVNVDGALNVNOLNSGMNLSKRAVAGSSKRVISGNVSPSKG 420
DB 361 GTTATVSKDDGNGNTVYKDVNVDGALNVNOLNSGMNLSKRAVAGSSKRVISGNVSPSKG 420
OY 417 KMDFTVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDVDEGALNVGSK 476
    421 KMDFTVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDVDEGALNVGSK 480
DB 421 KMDFTVNNAGNNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLTSDVDEGALNVGSK 480
OY 477 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHIDNVGNARAGIAQAIATAGLVQA 536
    481 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHIDNVGNARAGIAQAIATAGLVQA 540
DB 481 DANKPVRTTNVAPGVKEDVTNNVQKGAONLNHIDNVGNARAGIAQAIATAGLVQA 540
OY 537 YLPKGSMAIGGTYRGAGYAGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 594
    541 YLPKGSMAIGGTYRGAGYAGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 598
DB 541 YLPKGSMAIGGTYRGAGYAGYSSISDGNMIIKGTASGNSRGHGASASVGYQW 598
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RESULT 7  
O9JPS0 PRELIMINARY; PRT; 598 AA.

AC O9JPS0;  
DB 01-OCT-2000 (TREMblrel. 15, Created)  
DB 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DB 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_Taxid=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH15;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piazza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hündt E., Knapp B., Blair E., Mason T., Tetteilin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-H15.  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226381; AAF42530.1; -  
DR EMBL: AF157607; AAK68868.1; -  
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B8A63CB CRC64;

Query Match 94.6%; Score 2855; DB 2; Length 598;  
Best Local Similarity 94.6%; Pred. No. 8.2e-112;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIRIINMSALNANWAVSELTRNHTKRASATVATVATLTLFAVVOASTDDDDLYLE 60  
DB 1 MNKIRIINMSALNANWAVSELTRNHTKRASATVATVATLTLFAVVOANATDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKSGTGEKEVEDSNMGVYFDKKGVLTAGTTTLKAGDNLIKONTNE 120  
DB 61 PVORTAVVLSFRSDKSGTGEKEVEDSNMAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120  
QY 121 NTNENTNDSSEFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTGLNFAKETAAGTNGD 180  
DB 121 NTNENTNDSSEFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTGLNFAKETAAGTNGD 180  
QY 177 TTVHLNGISGTLDTLNTGATNTVNDVTDDEKKRAASVKOVLANGMNKGKPGTTA 236  
DB 181 PTVHLNGISGTLDTLNTGATNTVNDVTDDEKKRAASVKOVLANGMNKGKPGTTA 240  
QY 237 SDNVDVFRITDYEFSLADTKTTTVNESKDNKRTEVKIGATSVYIKEDGKLVYTGDKR 296  
DB 241 SDNVDVFRITDYEFSLADTKTTTVNESKDNKRTEVKIGATSVYIKEDGKLVYTGDKR 300  
QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFEVTSVGTVTFASGN 356  
DB 301 GENDSSTDKGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFEVTSVGTVTFASGN 360  
QY 357 GTTATVSKDDQGNITVYVNDVNDALNVNOLQNSGMNLSKAVAGSSGKVISGNVSPSG 416  
DB 361 GTTATVSKDDQGNITVYVNDVNDALNVNOLQNSGMNLSKAVAGSSGKVISGNVSPSG 420  
QY 417 KMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDEGALVNGSK 476  
DB 421 KMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDEGALVNGSK 480  
QY 477 DANKPVRTINVAAGVEGDTNVAOLKGAQONLNHIDVNGNARAGIAQAIATAGLVQA 536  
DB 481 DANKPVRTINVAAGVEGDTNVAOLKGAQONLNHIDVNGNARAGIAQAIATAGLVQA 540  
QY 537 YLPKGSMAIAGGTYRGEAGYAGYSSISDGMWIIKGTASGNSRGHFGASASVGYOW 594  
DB 541 YLPKGSMAIAGGTYRGEAGYAGYSSISDGMWIIKGTASGNSRGHFGASASVGYOW 598

RESULT 8  
ID 0930Y5 PRELIMINARY; PRT: 598 AA.  
AC 0930Y5;  
DT 01-DEC-2001 (Tremblrel. 19, Created)  
DT 01-DEC-2001 (Tremblrel. 19, last sequence update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN-B210;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157603; AAK68864.1; -  
SQ SEQUENCE 598 AA; 62687 MW; 18CEFF6410A15DF CRC64;

Query Match 94.5%; Score 2852; DB 2; Length 598;  
Best Local Similarity 94.6%; Pred. No. 1.1e-111;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKIRIINMSALNANWAVSELTRNHTKRASATVATVATLTLFAVVOASTDDDDLYLE 60  
DB 1 MNKIRIINMSALNANWAVSELTRNHTKRASATVATVATLTLFAVVOANATDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKSGTGEKEVEDSNMGVYFDKKGVLTAGTTTLKAGDNLIKONTNE 120  
DB 61 PVORTAVVLSFRSDKSGTGEKEVEDSNMAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120  
QY 121 NTNENTNDSSEFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTGLNFAKETAAGTNGD 180  
DB 121 NTNENTNDSSEFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTGLNFAKETAAGTNGD 180  
QY 177 TTVHLNGISGTLDTLNTGATNTVNDVTDDEKKRAASVKOVLANGMNKGKPGTTA 236  
DB 181 PTVHLNGISGTLDTLNTGATNTVNDVTDDEKKRAASVKOVLANGMNKGKPGTTA 240  
QY 237 SDNVDVFRITDYEFSLADTKTTTVNESKDNKRTEVKIGATSVYIKEDGKLVYTGDKR 296  
DB 241 SDNVDVFRITDYEFSLADTKTTTVNESKDNKRTEVKIGATSVYIKEDGKLVYTGDKR 300  
QY 297 GENDSSTDKGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFEVTSVGTVTFASGN 356  
DB 301 GENDSSTDKGEGLVTAKEVIDAVNKAQWRRKTTTANGQTQADKFEVTSVGTVTFASGN 360  
QY 357 GTTATVSKDDQGNITVYVNDVNDALNVNOLQNSGMNLSKAVAGSSGKVISGNVSPSG 416  
DB 361 GTTATVSKDDQGNITVYVNDVNDALNVNOLQNSGMNLSKAVAGSSGKVISGNVSPSG 420  
QY 417 KMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDEGALVNGSK 476  
DB 421 KMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDVDEGALVNGSK 480  
QY 477 DANKPVRTINVAAGVEGDTNVAOLKGAQONLNHIDVNGNARAGIAQAIATAGLVQA 536  
DB 481 DANKPVRTINVAAGVEGDTNVAOLKGAQONLNHIDVNGNARAGIAQAIATAGLVQA 540  
QY 537 YLPKGSMAIAGGTYRGEAGYAGYSSISDGMWIIKGTASGNSRGHFGASASVGYOW 594  
DB 541 YLPKGSMAIAGGTYRGEAGYAGYSSISDGMWIIKGTASGNSRGHFGASASVGYOW 598

RESULT 9  
ID 09JPS6 PRELIMINARY; PRT: 600 AA.  
AC 09JPS6;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, last sequence update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-E26;  
RX MEDLINE=20175756; Pubmed=10710308;  
RA Pizze M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capocchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226371; AAF42520.1; -  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 92.9%; Score 2806; DB 2; Length 600;  
Best Local Similarity 92.7%; Pred. No. 9.1e-110;  
Matches 557; Conservative 14; Mismatches 22; Indels 8; Gaps 2;

OY 1 MKKIRIIINSLNLMVAVSELTNRHTRKASATVATLTLFAT-----VOASTTD 53  
DB 1 MKKIRIIINSLNLMVAVSELTNRHTRKASATVATLTLFATVOASADNVOASADN 60  
OY 54 DDLELEPOTAVVLSFSDKEGTEKEVEDSDNMGVFDDKGVLTAGTITLKAGDNLK 113  
DB 61 EEEELPEPVRTAPVLSFSDAEDEGEKEVENTNMGITFDKNGVIKAGTITLKAGDNLK 120  
OY 114 IKONTNEMTASFTYSLKKDLTDLTSVTEKLSFSANSKNVITSDTKGLNFAKTAET 173  
DB 121 IKONTNEMTASFTYSLKKDLTDLTSVTEKLSFGANGKNVITSDTKGLNFAKTAET 180  
OY 174 NGDTVHLNGIGSTLDTLNTGATNTVNDVTDDEKRAASVMDVNLNAGNIGVPRG 233  
DB 181 NGDTVHLNGIGSTLDTLNTGATNTVNDVTDDEKRAASVMDVNLNAGNIGVPRG 240  
OY 234 TTASDNVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTVEKIGAKTSVYKEKDKLVYG 293  
DB 241 TTASDNVDFVHTDYVEFLSADTKTTTVNVESEKDNKRTVEKIGAKTSVYKEKDKLVYG 300  
OY 294 KKGENDSTDKGEGVLTAKEVIDAVNKAQWPAKTTTANGOTGOADKFEFTVSGTNVTA 353  
DB 301 KKGENDSTDKGEGVLTAKEVIDAVNKAQWPAKTTTANGOTGOADKFEFTVSGTNVTA 360  
OY 354 SKGKTATVSKDDGNITVYVNGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSP 413  
DB 361 SKGKTATVSKDDGNITVYVNGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSP 420  
OY 414 SKGKDETVNINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSDGALNV 473  
DB 421 SKGKDETVNINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSDGALNV 479  
OY 474 GSKDANKPRTITNVAAPGKEGDTVNAQLKGYAQNLNHIDVNDGNARAGIAQAIATAGL 533  
DB 480 GSKDANKPRTITNVAAPGKEGDTVNAQLKGYAQNLNHIDVNDGNARAGIAQAIATAGL 539  
OY 534 VOAYLPKGSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGO 593  
DB 540 VOAYLPKGSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGO 599  
OY 594 W 594  
DB 600 W 600

RESULT 10  
O9JPS3 PRELIMINARY: PRT: 590 AA.  
AC O9JPS3:  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-NCE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Battolini E., Capocchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 92.4%; Score 2790; DB 2; Length 590;  
Best Local Similarity 93.5%; Pred. No. 4.1e-109;  
Matches 557; Conservative 12; Mismatches 19; Indels 8; Gaps 3;

OY 1 MKKIRIIINSLNLMVAVSELTNRHTRKASATVATLTLFATVOASTDDDDLY-L 59  
DB 1 MKKIRIIINSLNLMVAVSELTNRHTRKASATVATLTLFATVOANATDEDEEDL 60  
OY 60 EPVOTAVVLSFSDKEGTEKE-VTEDSNMGVFDKGVLTAGTITLKAGDNLKIKONT 118  
DB 61 EPVOTAVVLIYNSRKEGTEKEKEVENSMAVYRNEKGVLTAGTITLKAGDNLKIKO-- 118  
OY 119 NENTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNVITSDTKGLNFAKTAETNGDTT 178  
DB 119 ---NGTNETYSLKKDLTDLTSVTEKLSFSANGKNVITSDTKGLNFAKTAETNGDTT 174  
OY 179 VHLNGIGSTLDTLNTGATNTVNDVTDDEKRAASVMDVNLNAGNIGKVPETASD 238  
DB 175 VHLNGIGSTLDTLNTGATNTVNDVTDDEKRAASVMDVNLNAGNIGKVPETASD 234  
OY 239 NVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTVEKIGAKTSVYKEKDKLVYKGE 298  
DB 235 NVDFVRTDYVEFLSADTKTTTVNVESEKDNKRTVEKIGAKTSVYKEKDKLVYKGE 294  
OY 299 NDSSTDKGEGVLTAKEVIDAVNKAQWPAKTTTANGOTGOADKFEFTVSGTNVTA 358  
DB 295 NDSSTDKGEGVLTAKEVIDAVNKAQWPAKTTTANGOTGOADKFEFTVSGTNVTA 354  
OY 359 TATVSKDDGNITVYVNGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSP 418  
DB 365 TATVSKDDGNITVYVNGDALNVNQLNSGNLDSKAVAGSSGKVIISGNVSP 414  
OY 419 DETVINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSDGALNVSKDA 478  
DB 415 DETVINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSDGALNVSKDA 474  
OY 479 NKPVRTITNVAAPGKEGDTVNAQLKGYAQNLNHIDVNDGNARAGIAQAIATAGLYL 538  
DB 475 NKPVRTITNVAAPGKEGDTVNAQLKGYAQNLNHIDVNDGNARAGIAQAIATAGLYL 534  
OY 539 PKGSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGO 594  
DB 535 PKGSMAAIGGTYRGEAGYAIIGYSSISDGNMIIKGTASGNSRGHFGASASVGO 590

RESULT 11  
O9JPR8 PRELIMINARY: PRT: 599 AA.  
AC O9JPR8:  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]

NCBI\_TaxID=487;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN-NGH38;  
 RX MEDLINE=20175756; PubMed-10710308;  
 RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
 RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappelli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-H38;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 RT membrane protein of *Neisseria meningitidis*.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF226383; AAF42532.1; -  
 DR EMBL: AF157608; AAK68869.1; -  
 SQ SEQUENCE 599 AA: 62844 MW: BBA16BFB53C1970C CRC64;

Query Match 91.5%; Score 2762.5; DB 2; Length 599;  
 Best Local Similarity 91.7%; Pred. No. 5.9e-108;  
 Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

1 MKKIYRIIINNSALNANVAVSELTNRNHTKRASATVATVATLTLFAVQASTTD-DDDLYL 59  
 1 MNKIYRIIINNSALNANVAVSELTNRNHTKRASATVATVATLTLFAVQANADEDEEEL 60  
 60 EPYQRTAVVLSFRSDKEGTEKEVEDSDSNMGVYFDKKGVLTAGTITLKAGDNLIKQ--- 116  
 61 EPYRSALVLOFMDIKDEGENENSTNGIMSYIDHNHNLHGATVTLKAGDNLIKQNN 120  
 117 -NTNENTNASSFTYSLKRDLDLTLSVTEKLSFNSANSKNVITSDTKGLNFAKTAETNG 175  
 121 KNTNENTNASSFTYSLKRDLDLTLSVTEKLSFGANGKNVITSDTKGLNFAKTAETNG 180  
 176 DTTVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVADVNLNAGNNIKGVKPTT 235  
 181 DTTVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVADVNLNAGNNIKGVKPTT 240  
 236 ASDNVDVRYTDVEPLSADTKTTTVNVESSKDNKRTVEKIGAKTSVIREKDKLVTGKD 295  
 241 ASDNVDVRYTDVEPLSADTKTTTVNVESSKDNKRTVEKIGAKTSVIREKDKLVTGKG 300  
 296 KGENSDSTKDEGLVTAKEVIDAVNKAQWRMKTTTANGQTGAQDKFETVTSCTNVTFAAG 355  
 301 KGENSDSTKDEGLVTAKEVIDAVNKAQWRMKTTTANGQTGAQDKFETVTSCTNVTFAAG 360  
 356 KGTATVSKDDOGNITVMTDVNVDALNVLNOLNSGMNLSKRAVSSGKVISGNVSPSK 415  
 361 KGTATVSKDDOGNITVMTDVNVDALNVLNOLNSGMNLSKRAVSSGKVISGNVSPSK 420  
 416 GKDEVTNINAGNNIEITRNKNIDITATSMTPQSSVSLGAGADAPTLSTVDEGALNVGS 475  
 421 GKDEVTNINAGNNIEITRNKNIDITATSMTPQSSVSLGAGADAPTLSTVDEGALNVGS 480  
 476 KDANKPVRTITNVAQVKEGDTNVAOLKVAQNLNHNDVNDGNARAGIAQAIAATAGLVQ 535  
 481 KDANKPVRTITNVAQVKEGDTNVAOLKVAQNLNHNDVNDGNARAGIAQAIAATAGLVQ 540  
 536 AYLPGKSMAAIGGGTYRGEGAGTAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594  
 541 AYLPGKSMAAIGGGTYRGEGAGTAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 599

RESULT 12

09JPS7  
 ID 09JPS7 PRELIMINARY; PRT: 591 AA.  
 AC 09JPS7;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS *Neisseria meningitidis*.  
 OC Bacteria; Proteobacteria; beta subdivision; *Neisseriaceae*; *Neisseria*.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-B2147;  
 RX MEDLINE=20175756; PubMed-10710308;  
 RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capocchi B.,  
 RA Galeotti C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappelli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226366; AAF42515.1; -  
 SQ SEQUENCE 591 AA: 62113 MW: 533453CAE5A91E1F CRC64;

Query Match 91.4%; Score 2758.5; DB 2; Length 591;  
 Best Local Similarity 92.3%; Pred. No. 8.5e-108;  
 Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;

1 MKKIYRIIINNSALNANVAVSELTNRNHTKRASATVATVATLTLFAVQASTTD---DDLY 57  
 1 MNKIYRIIINNSALNANVAVSELTNRNHTKRASATVATVATLTLFAVQANADEDEEEL 60  
 58 YLEPYQRTAVVLSFRSDKEGTEKEVEDSDSNMGVYFDKKGVLTAGTITLKAGDNLIKQ 116  
 61 YLEPYQRTAVVLSFRSDKEGTEKEVEDSDSNMGVYFDKKGVLTAGTITLKAGDNLIKQ 120  
 117 -NTNENTNASSFTYSLKRDLDLTLSVTEKLSFNSANSKNVITSDTKGLNFAKTAETNGD 176  
 121 -NTNENTNASSFTYSLKRDLDLTLSVTEKLSFNSANSKNVITSDTKGLNFAKTAETNGD 174  
 177 TTVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVADVNLNAGNNIKGVKPTT 236  
 175 TTVHLNGIGSTLTDTLLNTGATTNTVNDVDEKKRAASVADVNLNAGNNIKGVKPTT 234  
 237 SDNVDVRYTDVEPLSADTKTTTVNVESSKDNKRTVEKIGAKTSVIREKDKLVTGKD 296  
 235 SDNVDVRYTDVEPLSADTKTTTVNVESSKDNKRTVEKIGAKTSVIREKDKLVTGKD 294  
 297 GENDSDSTKDEGLVTAKEVIDAVNKAQWRMKTTTANGQTGAQDKFETVTSCTNVTFAAG 356  
 295 GENDSDSTKDEGLVTAKEVIDAVNKAQWRMKTTTANGQTGAQDKFETVTSCTNVTFAAG 354  
 357 GTTATVSKDDOGNITVMTDVNVDALNVLNOLNSGMNLSKRAVSSGKVISGNVSPSK 416  
 355 GTTATVSKDDOGNITVMTDVNVDALNVLNOLNSGMNLSKRAVSSGKVISGNVSPSK 414  
 417 KMDVTNINAGNNIEITRNKNIDITATSMTPQSSVSLGAGADAPTLSTVDEGALNVGS 476  
 415 KMDVTNINAGNNIEITRNKNIDITATSMTPQSSVSLGAGADAPTLSTVDEGALNVGS 473  
 477 DANKPVRTITNVAQVKEGDTNVAOLKVAQNLNHNDVNDGNARAGIAQAIAATAGLVQ 536  
 474 DANKPVRTITNVAQVKEGDTNVAOLKVAQNLNHNDVNDGNARAGIAQAIAATAGLVQ 533  
 537 YLPGKSMAAIGGGTYRGEGAGTAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 594  
 534 YLPGKSMAAIGGGTYRGEGAGTAIGYSSISDGGNMIKGTASGNSRGHFGASASVGYOW 591

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RESULT 13
O9JRI8 PRELIMINARY: PRT; 591 AA.
AC O9JRI8:
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE
  PROTEIN).
GN GNA992 OR NMB0992 OR NHHA.
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487, 491;
RN 11
  SEQUENCE FROM N.A.
RC STRAIN-MC58 / SEROGROUP B, BZ169, BZ83, AND H44/76;
RX MEDLINE=20175756; PubMed-10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
  Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,
  Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
  Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
  Broeker M., Hundt E., Knapp B., Blair E., Mason F., Tettelin H.,
  RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
  RT "Identification of Vaccine Candidates Against Serogroup B
  meningococcus by Whole-Genome Sequencing."
  Science 287:1816-1820(2000).
  [2]
RN SEQUENCE FROM N.A.
RC STRAIN-MC58 / SEROGROUP B;
RX MEDLINE=20175755; PubMed-10710307;
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,
  Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,
  Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,
  Halt D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,
  Mason T., Ciecko A., Parksey D.S., Blair E., Clifton H., Clark E.B.,
  RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Yamathavan J.,
  Gill J., Scarlato V., Masignani V., Piza M., Grandi G., Sun L.,
  RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;
  RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
  MC58."
  Science 287:1809-1815(2000).
  [3]
RN SEQUENCE FROM N.A.
RC SPECIES=N.meningitidis; STRAIN=PMC21;
  Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;
  RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis."
  Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
  DR EMBL: AF226375; AAF42524.1; -
  DR EMBL: AE002450; AAF41395.1; -
  DR EMBL: AE226367; AAF42516.1; -
  DR EMBL: AF226370; AAF42519.1; -
  DR EMBL: AF226374; AAF42523.1; -
  DR EMBL: AF157611; AAK68872.1; -
  DR TIGR: NMB0992; -
  KW Complete proteome.
  SO SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;
  Query Match 91.4%; Score 2758.5; DB 16; Length 591;
  Best Local Similarity 92.3%; Pred. No. 8.5e-108;
  Matches 552; Conservative 14; Mismatches 21; Indels 11; Gaps 4;
  OY 1 MNKIRIITNSALNMAVAVSELTRNNHTRKASATVATATLTLFATVQASTDD---DDDL 57
  DB 1 MNKIRIITNSALNMAVAVSELTRNNHTRKASATVATATLTLFATVQASANNEDQEDL 60
  OY 58 YLEPQRTAVVLSFRSDEGTEGEKE-VTEDSMWGVYFPDKGVLTAGTTTLKAGDNLIKIQ 116
  DB 61 YLDPQRTAVVAVLIVNSDKETGEKEVEENSDMAVYFNKGVLTARETTTLKAGDNLIKIQ 120

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OY 117 NTNENTNASSFTYSLKLDLDTLSVGTETKLSFSANSKKNVITSDPKGLNFAKKTAEITNGD 176
DB 121 -----NQTNTTYSLKLDLDTLSVGTETKLSFSANSKKNVITSDPKGLNFAKKTAEITNGD 174
OY 177 TTVHLNIGSGTLDPTLNTGATNTVNDNTDDEKRRASVADVLANGMWIKGVKPGTTA 236
DB 175 TTVHLNIGSGTLDPTLNTGATNTVNDNTDDEKRRASVADVLANGMWIKGVKPGTTA 234
OY 237 SDNVDFRTYDTVEFLSADTKTTTVNVESSKDKNGKRTVEKIGAKTSVIEKDKGLVTGDK 296
DB 235 SDNVDFRTYDTVEFLSADTKTTTVNVESSKDKNGKRTVEKIGAKTSVIEKDKGLVTGDK 294
OY 297 GENDSSTDKGGLVTAKEVIDAVKAKGRKTTTANGOTGADKFEVYTSNTNTFASGK 356
DB 295 GENGSSSTDEGEGLVTAKEVIDAVKAKGRKTTTANGOTGADKFEVYTSNTNTFASGK 354
OY 357 GTTATVSKDDGQNTVWADVAVGALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKG 416
DB 355 GTTATVSKDDGQNTVWADVAVGALNVNOLONGMNLDSKAVAGSSGKVTSGNVSPSKG 414
OY 417 KMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVDEGALNVGSK 476
DB 415 KMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVDEGALNVGSK 473
OY 477 DANKPVRTNVAPEGKESDVTNVAQLKGVQNLNHNIDVNGNARAGTAQAIAIAGLVQA 536
DB 474 KDNKPVRTTNVAPGVKEGDDVTNVAQLKGVQNLNHNIDVNGNARAGTAQAIAIAGLVQA 533
OY 537 YLPGKSMVAIGGGYRGRAGVAGYSSISDGGNNITIKTASGNSRGHGCASAGVGYOM 594
DB 534 YLPGKSMVAIGGGYRGRAGVAGYSSISDGGNNITIKTASGNSRGHGCASAGVGYOM 591

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RESULT 14
O9AOF0 PRELIMINARY: PRT; 592 AA.
AC O9AOF0:
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN 11
  SEQUENCE FROM N.A.
RC STRAIN-MC58;
  Peak I.R., Strikhanova Y., Dieckelman M., Moxon E.R., Jennings M.P.;
  RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis."
  Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
  DR EMBL: AF125375; AAK09243.1; -
  SO SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
  Query Match 91.1%; Score 2751; DB 2; Length 592;
  Best Local Similarity 92.0%; Pred. No. 1.7e-107;
  Matches 551; Conservative 13; Mismatches 23; Indels 12; Gaps 4;
  OY 1 MNKIRIITNSALNMAVAVSELTRNNHTRKASATVATATLTLFATVQASTDD---DD 56
  DB 1 MNKIRIITNSALNMAVAVSELTRNNHTRKASATVATATLTLFATVQASANNRPKRD 60
  OY 57 YLEPQRTAVVLSFRSDEGTEGEKE-VTEDSNMGVYFPDKGVLTAGTTTLKAGDNLIKIR 115
  DB 61 YLDPQRTAVVAVLIVNSDKETGEKEVEENSDMAVYFNKGVLTARETTTLKAGDNLIKIR 120
  OY 116 QNTNENTNASSFTYSLKLDLDTLSVGTETKLSFSANSKKNVITSDPKGLNFAKKTAEITNG 175
  DB 121 Q-----NQTNTTYSLKLDLDTLSVGTETKLSFSANSKKNVITSDPKGLNFAKKTAEITNG 174

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OY 176 DTFVHLNGIGSTLDTLLNTGATNTVNDVDEDEKKRAASVKDVLNAGNIGVKPGTT 235
DB 175 DTFVHLNGIGSTLDTLLNTGATNTVNDVDEDEKKRAASVKDVLNAGNIGVKPGTT 234
OY 236 ASDNDFVRTYDVEFLSADFTKTTVNVESKDNKGRTEVKIGAKTSVIREKDKLVTGKD 295
DB 235 ASDNDFVRTYDVEFLSADFTKTTVNVESKDNKGRTEVKIGAKTSVIREKDKLVTGKD 294
OY 296 KGENSSTDKGEGLVTAKEVIDAVNKAQWRMKTNTANGOTGQADKFEYTSNGNTVTFASG 355
DB 295 KGENSSTDKGEGLVTAKEVIDAVNKAQWRMKTNTANGOTGQADKFEYTSNGNTVTFASG 354
OY 356 KGTATVSKDDOGNITVMTDVNVGDALNVNOLNSGNNLDSKAVAGSSGKVISGNVSPSK 415
DB 355 KGTATVSKDDOGNITVMTDVNVGDALNVNOLNSGNNLDSKAVAGSSGKVISGNVSPSK 414
OY 416 KMDFTVNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLVSDEGALNVGS 475
DB 415 KMDFTVNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLVSDEGALNVGS 473
OY 476 KQANKPVRTTNVAPGVEGDDVTNVAOLKGYAQNINHNIDVNGNARAGIAQAIATAGLVQ 535
DB 474 KQANKPVRTTNVAPGVEGDDVTNVAOLKGYAQNINHNIDVNGNARAGIAQAIATAGLVQ 533
OY 536 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
DB 534 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 592

RESULT 15
OY3OY3 PRELIMINARY: PRT: 591 AA.
AC O93OY3:
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxId=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EG329;
RA Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.;
RT Identification and characterization of a gene encoding a novel outer
RL membrane protein of Neisseria meningitidis.*;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF157606; AAK68867.1; -.
SQ SEQUENCE 591 AA: 62048 MW: CDDC600798859C65 CRC64;

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Query Match 90.7%; Score 2739.5; DB 2; Length 591;  
 Best Local Similarity 91.8%; Pred. No. 5.3e-107;  
 Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;

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OY 1 MKKIYIINNSALNNAVAVSELTNRNHTKRASATVATVATLTLFATVQASTTD---DDDL 57
DB 1 MNEILRIINNSALNNAVAVSELTNRNHTKRASATVATVATLTLFATVQASANNEQEDDL 60
OY 58 YLEPVORTAVVLSFRSDKGTGEGKE-VTEDSNMNGVYFEDKGVLTACTITLLKAGDNLKIKO 116
DB 61 YLDPVLTAVVLSVNDKGTGEGKEVEKESDVAVFNEKGVLTAREITLLKAGDNLKIKO 120
OY 117 NTNENTNASSFTYSLKKDLTDLTSVTEKLSFSANSKNVNTSDTKGLNFAKTAFTNGD 176
DB 121 -----NGTNFTYSLKKDLTDLTSVTEKLSFSANGKNVNTSDTKGLNFAKTAFTNGD 174
OY 177 TTYVHLNGIGSTLDTLLNTGATNTVNDVDEDEKKRAASVKDVLNAGNIGVKPGTTA 236
DB 175 TTYVHLNGIGSTLDTLLNTGATNTVNDVDEDEKKRAASVKDVLNAGNIGVKPGTTA 234
OY 237 SDNVDVVRTYDVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIREKDKLVTGKDK 296

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DB 235 SDNVDVVRTYDVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIREKDKLVTGKDK 294
OY 297 GENDSSTDKGEGLVTAKEVIDAVNKAQWRMKTNTANGOTGQADKFEYTSNGNTVTFASG 356
DB 295 GENDSSTDKGEGLVTAKEVIDAVNKAQWRMKTNTANGOTGQADKFEYTSNGNTVTFASG 354
OY 357 GTTATVSKDDOGNITVMTDVNVGDALNVNOLNSGNNLDSKAVAGSSGKVISGNVSPSK 416
DB 355 GTTATVSKDDOGNITVMTDVNVGDALNVNOLNSGNNLDSKAVAGSSGKVISGNVSPSK 414
OY 417 KMDFTVNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLVSDEGALNVGS 476
DB 415 KMDFTVNINAGNNIEITRNKNIDTATSMTPQFSSVSLGAGADAPTLVSDEGALNVGS 473
OY 477 DANKPVRTTNVAPGVEGDDVTNVAOLKGYAQNINHNIDVNGNARAGIAQAIATAGLVQ 536
DB 474 DANKPVRTTNVAPGVEGDDVTNVAOLKGYAQNINHNIDVNGNARAGIAQAIATAGLVQ 533
OY 537 YLPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594
DB 534 YLPGKSMMAIGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 591

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Search completed: July 3, 2002, 08:28:43  
 Job time: 1164 sec





GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model  
Run on: July 3, 2002, 08:12:18 ; Search time 95.27 Seconds  
(without alignments)  
596.083 Million cell updates/sec

Title: US-09-771-382-5  
Perfect score: 2999  
Sequence: 1 MNEILRIIWSALNAWVVS.....TASGNSRGHFGASASVGYQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2984	99.5	591	2 G81133	adhesin NMB0992 [i
2	2445.5	81.5	592	2 A81888	probable surface f
3	600	20.0	298	2 I64138	adhesin homolog Hi
4	393	13.1	2059	2 D82671	surface protein XF
5	375	12.5	1107	2 AC0976	probable autotrans
6	372.5	12.4	1190	2 A82615	surface protein XF
7	368	12.3	1588	2 A86036	probable adhesin Z
8	368	12.3	1588	2 H91188	probable adhesin E
9	332.5	11.1	658	2 AH0110	probable surface p
10	239.5	8.0	1004	2 C82672	surface-exposed ou
11	230.5	7.7	1536	2 A43855	high-molecular-wei
12	228.5	7.6	1091	2 G64964	hypothetical prote
13	225	7.5	1477	2 B43855	high-molecular-wei
14	219	7.3	1910	2 AF0394	probable adhesin h
15	216.5	7.2	2020	2 C48399	ABC-type transport
16	213.5	7.1	5291	2 F90696	hypothetical prote
17	212.5	7.1	4152	2 T31102	filamentous hemagg
18	212	7.1	1635	2 AI0452	hemolysin [importe
19	211.5	7.1	4919	2 T31105	hypothetical prote
20	209	7.0	949	2 D90803	Aida-I adhesin-lik
21	209	7.0	1005	2 H85611	probable adhesin z
22	209	7.0	2273	2 T09083	hemagglutinin/hemo
23	208.5	7.0	936	2 I40711	sapB protein - Cam
24	207.5	6.9	1109	2 A56143	surface-array prot
25	207.5	6.9	1577	2 A35140	hemolysin A precu
26	207	6.9	5188	2 B85547	probable RTX faml
27	203.5	6.8	1286	2 S28634	adhesin AIDA-I pre
28	202.5	6.8	1018	2 H83135	probable adhesin P
29	199	6.6	1325	2 A64905	ydek protein - Esc

30 199 6.6 1461 2 E90696 hypothetical prote  
31 197 6.6 585 2 F90961 flagellin [importe  
32 197 6.6 585 2 F85809 hypothetical prote  
33 196.5 6.6 1487 2 AG2560 hypothetical prote  
34 196.5 6.6 3013 2 AB0480 probable invasiv Y  
35 196 6.5 3705 2 AD0123 probable autotrans  
36 195 6.5 1461 2 A85547 hypothetical prote  
37 194.5 6.5 1428 2 AC2224 hypothetical prote  
38 193.5 6.5 4936 2 AH2515 hypothetical prote  
39 192.5 6.4 3029 2 S76109 hypothetical prote  
40 191.5 6.4 1343 2 D85724 hemolysin A - Serr  
41 191.5 6.4 1608 2 A28182 190K surface anti  
42 191 6.4 2249 2 A41477 autotransporter pr  
43 190.5 6.4 1035 2 AD3203 outer membrane pro  
44 190 6.3 1651 2 JC1340 probable autotrans  
45 189.5 6.3 1430 2 AF0351

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81133  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlata, V.; Maignani, V.; Pizzia, M. Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.  
A:Reference number: A81000; MUID:20175755  
A:Accession: G81133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-591 <TET>  
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722  
A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0992

Query Match 99.5%; Score 2984; DB 2; Length 591;  
Best Local Similarity 99.5%; Pred. No. 3.9e-143;  
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIIWSALNAWVVSSELTRNHTKRASATVKAVLATLTLFATVQASANNEEQEDL 60  
||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVKAVLATLTLFATVQASANNEEQEDL 60  
||:||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 61 YLDPVLRVAVLVNSDKEGTGEKVEKVEENSDNAVTFNEKGVLTAREITLKAGDNLKIKQ 120  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 61 YLDPVQRTVAVLVNSDKEGTGEKVEKVEENSDNAVTFNEKGVLTAREITLKAGDNLKIKQ 120  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 121 NGNFYISLKKDLTSLTSGTEKLSFANGKNYITSDTKGLNFAKETAGTGGTTVHLN 180  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 121 NGNFYISLKKDLTSLTSGTEKLSFANGKNYITSDTKGLNFAKETAGTGGTTVHLN 180  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 181 GIGSTLTDLTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKVKPGTTASDNVDF 240  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 181 GIGSTLTDLTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNIKVKPGTTASDNVDF 240  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 241 VRTYDVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDGKLVTKGDKGENGSS 300  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 241 VRTYDVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSVIKEKDGKLVTKGDKGENGSS 300  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 301 TDEGEGLVTAKEVIDAVNKAGWEMKTTTANGOTQADKFEFTVSGTNTVFASGKGTTATV 360  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
Db 301 TDEGEGLVTAKEVIDAVNKAGWEMKTTTANGOTQADKFEFTVSGTNTVFASGKGTTATV 360  
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

QY 361 SKDDQGNITVMYDVNVGDALNVNLQNSGWNLDKAVAGSSGKVISGNSPKGKMDETV 420

Db 361 SKDDGNTMYDYNVGDALNVLQNSGWNLDKAVAGSSGKVISGNSPFSKMDQTV 420  
Qy 421 NINAGNNIETRNKNDIATSWTPQSSVSLGAGADAPTLSDVDGALNVGSKDKNKPVR 480  
Db 421 NINAGNNIETRNKNDIATSWTPQSSVSLGAGADAPTLSDVDGALNVGSKDKNKPVR 480  
Qy 481 ITNVPAGVKEGDTNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAYLPKSM 540  
Db 481 ITNVPAGVKEGDTNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGLVQAYLPKSM 540  
Qy 541 MAIGGGTYRGEAGYAIGYSSISDGGNNIIGKTASGNSRGRHFGASASVGYOW 591  
Db 541 MAIGGGTYRGEAGYAIGYSSISDGGNNIIGKTASGNSRGRHFGASASVGYOW 591

RESULT 2  
A:1888  
probable surface fibril protein NMAL200 [imported] - Neisseria meningitidis (strain 2249  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jørgensen, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1200

Query Match 81.5%; Score 2445.5; DB 2; Length 592;  
Best Local Similarity 83.7%; Pred. No. 5.2e-116;  
Matches 503; Conservative 31; Mismatches 48; Indels 19; Gaps 8;

Qy 1 MNEILRIWNSALNAWVVSSELTRNHTKRASATVKTAVLATLFLFATVQASANNEEQEDL 60  
Db 1 MNKIFKIWNVVTQVWVVSSELTRNHTKRASATVKTAVLATLFLFATVQANATDEDEEE- 59  
Qy 61 YLDPVLTAVAVLIIVNSDKETGEKEVE-ENSDWAVFNEKGVLTAREITLKGADNLKIK 119  
Db 60 -LESVQKRSV-VGSIQASMEGSGELETISLMTNDSKEFVDPIV----VTLKAGDNLKIK 113  
Qy 120 Q-----NGTNFTYSLKKDLTDLTSVGTETKLSFSGANGKVNITSDTKGLNFAKETAGTNG 173  
Db 114 QNTWENTNASSFTYSLKKDLTGLINVTETKLSFGANGKVNITSDTKGLNFAKETAGTNG 173  
Qy 174 DTTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKRAASVKDVLNAGNINIKVKGTT 233  
Db 174 DTTVHLNGIGSTLTDLLAGSSASVHDAGNOST--HYTRAASIKDVLNAGNINIKVKGTT 231  
Qy 234 A--SDNVDFRTYDTVEFLSADTTTNNVNSKONGKKTVEKIGAKTSVKEKDKGLVTG 291  
Db 232 TGQSENVDFRTYDTVEFLSADTTTNNVNSKONGKKTVEKIGAKTSVKEKDKGLVTG 291  
Qy 292 KDKGSSSTDEGELVTAKEVIDAVNKGWRMKTITTTANGQTQADKFEVTSCTNVTFA 351  
Db 292 KDKGSSSTDEGELVTAKEVIDAVNKGWRMKTITTTANGQTQADKFEVTSCTNVTFA 351  
Qy 352 SGKGTATVSKDDGNTVMTVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNSVP 411  
Db 352 SGKGTATVSKDDGNTVMTVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNSVP 411  
Qy 412 SKGKMDVTNINAGNNIETRNKNDIATSWTPQSSVSLGAGADAPTLSDVDGALNV 470  
Db 412 SKGKMDVTNINAGNNIETRNKNDIATSWTPQSSVSLGAGADAPTLSDVDGALNV 471

Qy 471 GSKDKNKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGL 530  
Db 472 GSKDKNKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNDVGNARAGIAQAIAATAGL 531  
Qy 531 VQAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNNIIGKTASGNSRGRHFGASASVGYQ 590  
Db 532 VQAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNNIIGKTASGNSRGRHFGASASVGYQ 591  
Qy 591 W 591  
Db 592 W 592

RESULT 3  
I64138  
adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: I64138  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:L42023; NID:gl574589; PID:gl574589; TIGR:H11732

Query Match 20.0%; Score 600; DB 2; Length 298;  
Best Local Similarity 44.7%; Pred. No. 1.8e-23;  
Matches 144; Conservative 39; Mismatches 91; Indels 48; Gaps 8;

Qy 1 MNEILRIWNSALNAWVVSSELTRNHTKRASATVKTAVLATLFLFATVQASANNEEQEDL 54  
Db 1 MNKIFKIWNVVTQVWVVSSELTRNHTKRASATVKTAVLATLFLFATVQAINDACTEVKQV 60  
Qy 55 EQEDLYLDPVLTAVAVLIIVNSDKETGEKEVE-ENSDWAVFNEKGVLTAREITLKGAD 114  
Db 61 STEDDI-----EDSAATKDDNK-----NQALKAGDTTLTLKAGK 93  
Qy 115 NLKTK--QNGTNFTYSLKKDLTDLTSVGTETKLSFSGANGKVNITSDTKGLNFA 165  
Db 94 NLKAKLDQGGKSVTFLAKDLVDKTKVSDFLITGGNTPPAGGATPKVSTISTADGLKLA 153  
Qy 166 KETAGTNGDTTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKRAASVKDVLNAGNIN 225  
Db 154 K--GTNGDTAVHLNGLASTLPDVTNTGASTSVT-FSPSDIEKTRAATIKDVLNAGNIN 209  
Qy 226 KGVKPGTTASDNVDFRTYDTVEFLSADTTTNNVNSKONGKKTVEKIGAKTSVKEKD 285  
Db 210 KGKAVAGNTENVDVAGYDNVEFTGDKNTDLVLTAKENGKTTVEKFTPTKTSVINDNN 269  
Qy 286 GKLVTGKD--KGENGSTDEGE 305  
Db 270 GKLLTGKQLKDANTGTATNATE 291

RESULT 4  
D82671  
surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below

A:Accession: D82671

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-2059 <STM>

A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001

A:Experimental source: strain 9a5c

R:Simpon, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Cartaro, D.M.; Carrer, F. as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigz

chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;

, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; Palmieri, D.A.

Rodrigues, V.; Rosa, A.C. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir

M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z

A:Reference number: A59328

A:Contents: annotation

A:Status: preliminary

A:Accession: AC0976

A:Molecule type: DNA

A:Residues: 1-1107 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176

C:Genetics:

A:Gene: XFL529

Query Match 13.1%; Score 393; DB 2; Length 2059;

Best Local Similarity 24.3%; Pred. No. 5.9e-12;

Matches 173; Conservative 93; Mismatches 216; Indels 230; Gaps 31;

QY 72 LIVNSDKECTGKEKEVEENSDWAVFNE-KGVLTAARE-----ITLKAGDNLKIKONGT--- 123

DB 1386 VVINGGKISGVTAGTEETD---AVFSQLKSISTAVDQGWTLTASGANGSKVASGGTVDL 1443

QY 124 -----NFYSLKDLTDL-----TSVGTKEKLSFSA-----GNKVNTS 157

DB 1444 KWTDCNLTISKSGDNDVFNLSDELKEKSIYGVNTQDKGVKSSNVLLDSNELVITS 1503

QY 158 DT-----KGLNFAKETA-----GTNGDTPTVHLNGI-----GSTLTDTLLNTGA--T 196

DB 1504 HSSTSVKTLANGSVNRTVNGDGNIDVVVYNDLGLSVGASLTSLGINAGSHKI 1563

QY 197 TNYT-----NDNVTDEKRAASVDVLNAGNI-----KGVPKGTASDNVD----- 239

DB 1564 TNYTAGTEETDVAVNFSQLK-----SVSEAVDKGWTLTASGANGSKVYSGGTVDLKNTDGNLA 1620

QY 240 ---FVRTDVTVEFLSADTK-----TTTVNVESKDNKGKTEVKIGAKTSVKEKDGKIV 289

DB 1621 ISKSGSDNDVFNLSKDFKVDVTAAGNTVVNTDGVKVG---SDVSLGMLFTANGPSVTA 1678

QY 290 TGKDRKEN-----GSSTDEGEGLVTAKEVIDAYNKAGWRMKTIT-----ANGQ 332

DB 1679 SGFNAGDKVISHVAVGMADTDVAVNSQLKQAVQSVTVKATRYYSTNDGGTGGNVDGGA 1738

QY 333 TCQ---ADKFEVTSGTNV-----TFASGKGTTA----- 358

DB 1739 TGSKAIAAGVGTQASGEAAAAGVSGAAASGKSTAGRNAIASADGVALGDCAKDGGRG 1798

QY 359 -----TVS-----KDOGNITVVDVNVG--DALNVNOL-----QNSGN 391

DB 1799 AESYTGKSGVQNNVTGTVSGDAAKGETRSISNVADAKEAMDVNLKQLDVAQKSNLQ 1858

QY 392 LDS-----KAVAGSGKVISGNVSPSKGMDVTNIN 423

DB 1859 TDDMRHEINNIEDVFKITGDSASSVKGKGVNMAIGTNAAVSGTESVALGK---NTNVS 1915

QY 424 AGNNTEITRNKNIDIASTMTPOFSSVSLGAGADPTLSVGDALNVGSKDKNPKVRITN 483

DB 1916 ADNVAI--GNG-----SVADRANSVSVSGS-----GSER-----QVTN 1947

QY 484 VAPVGKGDVTVNAOLKGAQVNLNRRINVDGNAR-----AGTAAIATAGLVQAYLPCKS 539

DB 1948 VAAGTADTADVNSQLNOGLITAKQYTDGQVGNLRRSETSGGVAAAIATANLPQAYVQGRG 2007

QY 540 MMAIGGGTYRGEAGYAGYSSISDGNWLIKGTASGNSRGHFGASASVGYQW 591

DB 2008 MTSVGVSSYQGSATAVGVSAVSESCHWVFKFSGSANTRSHVGVGAGVGYQW 2059

RESULT 5

AC0976

probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serova

C:Species: Salmonella enterica subsp. enterica serovar Typhi

A:Note: this species has also been called Salmonella typhi

C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001

C:Accession: AC0976

R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Church

th, T.; Cronin, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr

, S.; Moule, S.; O'Gaora, P.

Nature 413, 848-852, 2001

A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,

A>Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A:Reference number: AB0502; PMID:11677608

A:Accession: AC0976

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1107 <PAR>

A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176

C:Genetics:

A:Gene: sapB

Query Match 12.5%; Score 375; DB 2; Length 1107;

Best Local Similarity 21.1%; Pred. No. 2.1e-11;

Matches 176; Conservative 106; Mismatches 238; Indels 314; Gaps 31;

QY 9 WNSALNAWVVVSELTRNRHTKRASATVKTAVLATLLFATVQASANNBEEQEDLYLDPVLT 68

DB 337 WNETNSF-----SASHGSSST-----TNKTNVAAGELSEESTDAVNGSOLFET 380

QY 69 VAVLIVNSDKETGKEKEVEENSDWAVFNEKGVLTAREITLKAGDNLKIKONGT---NF 125

DB 381 -----NEKVDQNT-----TDIAANTTITONSTAIENL 408

QY 126 TYSLKKDLTDLTSVTEKL-----SFSA--GNKVNTSDTKGLNFAKEFAGTNG--- 173

DB 409 NTSVSDINTSITGLTDNALLMDEDTGAFSANHGGSTSKITNVAAAGALSSEDSDAVNGSOL 468

QY 174 -DTTVHLNGIGSTLDTLLNTGATTNVTNDVNTDDEKRAASVKVNLNAGWIKGVKPGT 232

DB 469 YETNKQVDONTSAIAD--INT-SITNLGTDALSWDDEGAFSASHCTSGTNKTNVAAGE 525

QY 233 TASDNVDFV---RTYDT-----VEFLSADTKTITVN-----VESKDNKGKTE 271

DB 526 IASDSTDAINGSOLYETNMLISQYNESISQLAGDTSETVITENGTVKVIKRTNDNGLEQ 585

QY 272 VKIGAKTSVIKEDGKLVTGDKK-----GENGSSTDEG----- 304

DB 586 -----DAYATNGTAVGYDAVAGSAGCALGALGNSSSSIEGSLAGSGSTSNRAITTG 638

QY 305 -----EGLV-----TAKEVIDAVNKA---GNRMKTTTANGTGO----- 335

DB 639 IRETSAISDGVVIGVNTDRELLGALSGLTGDGSTRQITNVADGSEAQAQDAVTVRQLQNAI 598

QY 336 -----ADKFETVTSCTNVTFASGKGTTA---TVSKDDQG-----NITVMYDVNVGDAL 380

DB 699 GAVTTPTPKYKHANSTEEDSLAVGTDLSLAMGAKTIVNADAGIGLNTLVMDAINGIAI 758

QY 381 NVN-----QLNSGWNLDK-----AVAGSSGKVISGNVSPS 412

DB 759 GSNARANHANSIANGMSQTTTGAQTDYATYNNMDTPQNSVGEFSVSGEDGQRQITNVAAG 818

QY 413 KCKMDETIVNAG---NNIEITRNKNTI-----DIATSMTPQ 446

DB 819 SADTDA---VNVGQLKVTDQAQVSRNFTQSTNLNTQVSNLDTRVTNIENGIGDIVITGSKT 875

QY 447 F-----SSVSLGAGADAP-----TSLVDGDLNVGSKKDNKPVRI 481



Db 1154 YRQIIN-----VADGSEAHDAVT--VROLNAIGAVALTPPTKYFPHANSTEEDSLAVGTD 1205  
QY 271 EVKIGAKTSVIREK-----DGKLVTKGDKGE-----NGSSTDGEGL 307  
Db 1206 SLAMGAKTTVNGDKGIGIGYGAYVDANALNGAIGSNAQVIVHNSTAIGNGSTTTTGAOT 1265  
QY 308 VTAKEVIDAVNAGWRMKTITANGQ-----TGQADKEFTVTSCTNVTTFASGKGTTATV 360  
Db 1266 NVTAYNMDAPQNSVGEFSVGSADGQROIITNVAAGSAD-----TDAVNV--GOLKVTDAQV 1318  
QY 361 SKDDQGNITVM-----YDVNVGDAL-----NVNQLNSGNWLDKAV 397  
Db 1319 SONTQ--SITNLDNRVTNLDSTRTNIENGICDITVTGSKYFKTNTDGVDSAAQKDSVAI 1377  
QY 398 AGSSGKVISGNSPSKGM---DETVINAGNNIEITRN---GKN-----IDIATSTMTPOF 447  
Db 1378 GSGSIAAANDNSVALGTGVSATEENTISVGSSTNQRITNVAAGKNATDAVNVAAQLKSSA 1437  
QY 448 SSVSLGAGADAPTSLVDGDLNVGSKDNKPVRIITNVAPVKEGDVTNVAQLKGVAQ---- 504  
Db 1438 GGVRYDTKADG---SIDYSNITLGG--GNGGTRISNVSAVNNNDVVNVAQLKQSVQETK 1493  
QY 505 -----NLNKRIDNVGDNARAGIAQAATAGLVQAYLPGKSMMAIGGTYRGEAGYAI 556  
Db 1494 QYTDQRMVEMDNKLSKTESKLSGGIASAMAMTGLPQAYTPGASMASIGGTYNGESAVAL 1553  
QY 557 GYSSISDGGNWIITKTASGNSRGHFCASASVGYQW 591  
Db 1554 GVSWSANGRWYKLOGSTNSQGEYSAAALGAGIQW 1588

RESULT 8  
H91188  
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain R1MD  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: H91188  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA37903.1; PID:gl3363955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain R1MD 0509952  
C:Genetics:  
A:Gene: ECs4480

Query Match 12.3%; Score 368; DB 2; Length 1588;  
Best Local Similarity 23.3%; Pred. No. 7.6e-11;  
Matches 162; Conservative 99; Mismatches 280; Indels 154; Gaps 25;  
QY 31 SATVKTAVLATLLFATVQASANNEQEEDLYLDPVLTAVVLVNSDKEGTGEK-EKVVEE 89  
Db 914 SAASDAINGSOLYTNKYIADALGDAEVNADGTTAPTPTIANAEYNNVGDALDLD 973  
QY 90 N-----SDWAVYNEKGLVTAREITLKAGDNLK-----IKONGTNTFTYSLKKD 132  
Db 974 NALLWDETANGAGAYNASHDKGASITNVANGSISESTDVANGSQLNATNMIEQNTQ 1033  
QY 133 LDTLTSVGTKEKLSFANGKNV--ITSDTKGLNFAKETAGTNGDITVHLNGI----- 182  
Db 1034 IINQLAGNTDATYIOENGAGINVRTNDDGLAFNDASAQGVGATAIGYNSVAKGDDSSVAI 1093  
QY 183 -----GSTLTDLLNTGA--TTWVTNDV-----TDDEKKRAASVKD--- 217  
Db 1094 GOGYSVDVTGIALGSSSVSRVIAKGRSDTSITENGVIYDITTDGELLGALSIGDDGK 1153  
QY 218 ---VLNAGNINIKGVKPGTTASDNVDVFRITYDVEFLSADTKITTVNVESKDNGK----KT 270

RESULT 9  
AH0110  
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0902

Query Match 11.1%; Score 332.5; DB 2; Length 658;  
Best Local Similarity 24.3%; Pred. No. 1.5e-09;  
Matches 155; Conservative 86; Mismatches 241; Indels 155; Gaps 29;  
QY 27 TTRASATVVT-----AVLATLLFATVQAS-----ANNEQEEDLYLDPVLTAVV----LIV 74  
Db 105 TNLAPATISSTSDAVVGSQVLYLVQDGTRYFHANSVNPTDSLASG--LETIAVGPAVTV 162  
QY 75 NSDK-EGTGEKEKV--EENSDMWAVYNEK-----GVLTAR 106  
Db 163 SGDNVGVGINTALVGAATGGTAIGFGTQVTAAGATAIGSAAQQAQSLALGAGAVTSQ 222  
QY 107 EITLKAQDNKLKIQKQNTFTYSLKDLTDLTSVGTKEKLSFANGKNVNTSDFKGLNFAK 166  
Db 223 ANSIALG--AASINTVCAQSSYSAYALTAQASVGLGIG-TALGNR-KITGVAA----- 274  
QY 167 ETAGTNGDITVHLNGTSGTLTDTLLNGATNTVN--DNVTDEKKRAASVKDVLNAGWN 224  
Db 275 -SASSDAVNVAAQLTAVGQVQOQN-----TANITSLGRVTTIE---GSMASIANGG-G 322

QY 225 IKGVKPGCTTASNDVFRVYDVEFLSADTKTTTVNVESKDNCKKT-----EVKIGAKT 278  
Db 323 KYFHFANSTQPDV-----ASGTNSVAIGPASLAAALASGAGAVAIG--D 368  
QY 279 SVIKEDGKLVTKDKGKENGSSDEGEGLVTAKEVIDAVNKAQWKMKTITTTANGQTQADK 338  
Db 369 GAAASADGSAICGGSDNGRGVENIG-----KYSNASNTSSG----- 407  
QY 339 FETVTSCTNTVTFASGRGTTATVSKDQGNITVMYDNGDALNVNQLONGSMNLDSKAVA 398  
Db 408 --TVSGNTAT-----GETRTVSNVADG-----LQATDAVNRLQD-----I 443  
QY 399 GSGKVIQVNSVPSKMKMDTVNINAGNII-ETIRNGKNIDI--ATSMTPQFSSVSLGAG 455  
Db 444 AASIVVYNNVNSGLONGTDMFOVNNSSGLAKPSATGATGAGSVASGNNSTAFGSG 503  
QY 456 ADAP-----TSLVSDGALNVGSKDKNKPRTITNVAPGVKEGDVTVNAOLKQVAQN 505  
Db 504 AKATAANSALGANSVADRANSVSGVGNR--QITNVAPATQGTDAVNFDQLKSLSNQ 561  
QY 506 ----LNNRIDNVGNAR-----AGTAAATATAGLVQVLYLPGKSMMAIGGTYRGAGY 554  
Db 562 TNAYTNORYSELKQDLKQNSVLSAGTASAMSLTOPYTSSSMTTIGAASVYRGOSAL 621  
QY 555 AIGYSSISDGGNIIKGTASGNSRHFASASVGYOW 591  
Db 622 SLGVSSISDGRVYSLKQASSNTQDGFVGVGVGOW 658

## RESULT 10

C82672  
surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: G82672  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequen  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: C82672  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1004 <SIM>  
A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carter, H  
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Mencia, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1516

Query Match 8.0%; Score 239.5; DB 2; Length 1004;  
Best Local Similarity 22.3%; Pred. No. 0.00012;  
Matches 161; Conservative 97; Mismatches 277; Indels 193; Gaps 34;

QY 2 NEILRIIWNALNAWVVSSELTRNH-----TKRASATVKTAVLATLLFATVQASANNE 55  
Db 4 NQIYKFWNLISGWSVASHMTNDGGSDVVLRHSGVNRSLVLAIGLALTSVTHQSVK 63  
QY 56 QEDLDYLDPLVLTVA-VLIIVNSDKE-----GTGEKEKVEENSDWAV----- 95

Db 64 -----SPAWTASKVMVAHVDSQVNRADRIPTDGGSELMTMALKWKEFFPGHNST 116  
QY 96 --YFNEKGVLTAREITLKAGDNLKIKQNGTNYTSLKDLTDLTSVGTKEKLSANGKV 153  
Db 117 IGYFSKAFAPNA-----IALGYNSSVTQSANN-GVALGSNST-VSGYNSVALGAGSMASEL 170  
QY 154 NTSDFKGLNFAKETAGTNGDITVHLNGIGSLTDLTLLTGATTNTVNDVDEKKRAA 213  
Db 171 NVLSVGGG-----DGVTCPAVRRIINVNG-----DGIGNDAVNKSQLDGVTASVNDVAA 219  
QY 214 SVKDLV-----NAGWNIKGVKPGCTTA-SDNVDFVRTYDVEF----- 249  
Db 220 SVKTIALTNOVTGSSVASAGKKESTAIGSQAQAVDN-----TVAFGGRAIANAVGA 271  
QY 250 --LSADT-----KTTTVNVESKDNKKEKTEYKIGAKTSV-----IKEKDGKLVTKGD 293  
Db 272 SALGFDSHAKGINSTVGTQSVSLG--QGGVSLGYNFVGBGSLGALGSLVLLQGV 330  
QY 294 KGKGS-----STDEGBGL--VTAKEVI-----DAVNKAGWRMKTITTTANGQ 332  
Db 331 SVALGSGSMASEPNVSVSGDGLRGPVRRIRVNVGDIGNNDVAVNKSQLDGVTASVNDV 390  
QY 333 TGQADKFEIV--TSGTNTVTFASGKGTAT--YSKDDOGNITVMYDNGDALNVNQLONGS 399  
Db 391 VASVKNIAGAIQITGSGVASVSGDSTAGASQAAGDSSIA-----LGARSRAAIGSSA 446  
QY 390 WNLD-----SKAVAGSGKVIQVNSVPSKMKMDTVNINAGNIIETIRNGKNIDIAT 442  
Db 447 LGVDGHALGANSTALGGQSTAISEGGTSLG---YNSFVGQSATNGALGSN-----A 495  
QY 443 MTPQFSSVSLGAGADAPTLSV-----DGDALNVGSKDNKKEPRTITNVAPGVKEGDVTVNAQ 498  
Db 496 IVSGVNSVALGAGSVASELNVISVGGDGTGTPAVR-----RIVNVGDGIGNNDVAVNKSQ 550  
QY 499 LKQVAQNLLN---RIDNVGNAR---AGTAAQAI---ATAGLVQVLYLPGKSMMAIG----- 544  
Db 551 LDGVTASVNDVAAVSKKIVGTITGSGVASAIGKSTATGASQAQAVGDSVSLGTRATA 610  
QY 545 -----GGTYRGEAGYAIQYSSISDGGNIIK-----GTASGNSRHF 582  
Db 611 NATGSSVLGVDSRARGINSTALGRQSNALGDSVSLGSLFNSFVRSGBHVALGTDAVSG 670  
QY 583 A-SASVGY 589  
Db 671 KDSIALGY 678

## RESULT 11

A43855  
high-molecular-weight surface-exposed protein HMW1 - Haemophilus influenzae  
C:Species: Haemophilus influenzae  
C:Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 08-Oct-1999  
C:Accession: A43855  
R:Barenkamp, S.J.; Leininger, E.  
Infect. Immun. 60, 1302-1313, 1992  
A:Title: Cloning, expression, and DNA sequence analysis of genes encoding nontypeable  
detella pertussis.  
A:Reference number: A43855; MUID:92192797  
A:Accession: A43855  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1536 <BAR>  
A:Cross-references: GB:U08876; GB:M84616; NID:g475770; PIDN:AAA20527.1; PID:g475771  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBI:89235, NCBI:89239)

Query Match 7.7%; Score 230.5; DB 2; Length 1536;  
Best Local Similarity 22.3%; Pred. No. 0.00061;  
Matches 133; Conservative 86; Mismatches 228; Indels 149; Gaps 26;  
QY 40 ATLLFATVQASANNEDEEDLDPLVLTVAVLIVNSDKETGEKEKVEENSDWAVFNE 99

Db	778	SSLRFTSGSTYGTGFSIEKDLTLNATGNNILLQV-----ECTGMI-----G 820
Qy	100	KGVLTAIREITKAGDNLKIKQNGTNTFTYSLKLDLTSLVGTEKLSFSAANGKVNITSD- 158
Db	821	KGIVAKKNITFEFG-----NITEGSRKAVTEIEG---NVTINNANVTILGSD 866
Qy	159	---TKGLNFAKE-----TAGTN-----GDTVHLNGIGSTLDTLLNTGAT-TNVTN 201
Db	867	DNHQKPLTTTKDDVIINSGLTAGGNIVNAGNLVIESANAFKATFTFVNGGLFDNKG 926
Qy	202	DNYTDEKKRAASVKDVLNAGNNIKGVKPGGTASDNVDVFRTYDTVEFLSADTKTTTVN 261
Db	927	SNIS--IAKGGAREKDIONS---KNLSITTNSSS-----TYRTIISGNITNKGDNI 974
Qy	262	ESKDNGKTEVKIGAKTSVIKEOKGLVTGDKD-----GENGSTDGEGLVTA 310
Db	975	TNE--GSDTEMIGGDVS---QKEGNLTISSDKINIKQITIKAGVDGENSDS----- 1022
Qy	311	KEVIDAVNKGARMKMTTANGTGQADRFETVSGTNVTFASGKGTATVSKDDOGNITV 370
Db	1023	----DATNANLTIKT-----KELKITDQDNI---SGFNKAETAKD--GSDLT 1062
Qy	371	MYDVNVGDALNV-----NOLQSGWNLDKSAVAGSSGKVISGNSVPSKGMDEFVNINAG 425
Db	1063	IGNTNSADGNTAKKVTFNQVQSKISADGHKVTLHSKVETSGSNNTDSSD----- 1114
Qy	426	NNIEITRNKKNIDTATSMTPQSFSSVSLGAGADAPTLSDGDALNVGSKDKNPVRIITVA 485
Db	1115	NNAGLTIDAKNTVNNNIT-SHKAVSISATSEGITTKT-GPTINATTCNVEITAGTGSIL 1172
Qy	486	PGVK--EGDVTNVAQLKGVAQNLNRRIDNVGDNARAGIAQAIATAGVLQVAYLPCKSMMAI 543
Db	1173	GGIESSGSVTLTATEGALA-----VSNISGNTVTVTANSGLTTLTAGSTIKGESVTT 1226
Qy	544	G-----GGTYRGERAGYAIGVSSISDGGNWIK-----GTASGNS 577
Db	1227	SSQSGDIGTISGGTVEVKATESLTTQSNKIKATTGEANVTSATGTIGGTISGNT 1282
RESULT 12		
G64964		hypothetical protein b2000 - Escherichia coli
		C:Species: Escherichia coli
		C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2001
		C:Accession: G64964
		R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.;
		A.: Rose, D.J.; Mau, B.; Shao, Y.
		Science 277, 1453-1462, 1997
		A:Title: The complete genome sequence of Escherichia coli K-12.
		A:Reference number: A64720; MUID:97426617
		A:Accession: G64964
		A:Status: nucleic acid sequence not shown; translation not shown
		A:Molecule type: DNA
		A:Residues: 1-1091 <BLAT>
		A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:AACT5061.1;
		A:Experimental source: strain K-12, substrain MG1655
		C:Keywords: nucleotide binding; P-loop
		F:683-690/Region: nucleotide-binding motif A (P-loop)

**Qy** 119 KONGTFTYSLKKDLTLDSVTEKLSANSNGKNVNITSDFGKLNFAPETAGCTGTGVH 178  
|||:::||:::||:::||:::||:::||:  
**Dd** 131 TTTGMTISTGLPGPDNEANTGGWQQDGGTAATKTVTSG--GLQ-RVPGGSVSYDVIS 187  
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Qy** 179 LNIIGSTL-----TDLLNTG-----ATTNVNDNVTDEKKRAASVKVDVLNAGWNI 225  
|||:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Dd** 188 AGG-GGSLOGRAVVNTTLNGEOWMHGAIAITGVINDK-----GWQV 228  
|||:::||:|:|:|:|:~::~||:|:|:|:|:|:|:|:|  
**Qy** 226 KGVPPTTASDNDFVRT-----YDTVEFLSADTKTTTVNESKONGKKTEVKIG 275  
|||:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Dd** 229 --VKPQTVAIDTV- VNTCAEGSPDAENGCDTGQFVRGDARTTN----KNGRQIVRAEG 280  
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Qy** 276 -AKTSVIKEKGKLVTKDGKGENGSTDB---GGELY---TAKEIVIDAVNKAGRWN-- 324  
|||:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Dd** 281 TANTTV-----YAGGDOTVHGHALDRTLNGGYQYYHHGGTASDTV-VNSDDWGQIIVK 331  
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Qy** 325 -----KITTTANGOTCGADRFEIVTSCTNNVTFASG---KGTATNVSKDDQG-NITVMYDV 374  
|||:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Dd** 332 NGVGAGNTTVN-QGRRL-QVDAGGATAINTVLKQGGALVSTAATVT---GINLRGAFSV 385  
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Qy** 375 NVGDALNVNLQGNWLNSDKAVAGSSGKVITSGNYSPSKMDETVINAGNNIEIRNRG 434  
|||:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Dd** 386 VEGKADV-VLENGG-RLD-----VLTHGTATN-----TRVDDGGTLDVD-RNG 425  
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Qy** 435 KNIDIATSMTPOFSVSYSLGAGADAPTLSVDGDALNVGSKKONKPVRITINVAPGVKEGDVT 494  
|||:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Dd** 426 ----GTATT-----VSMNGG---VLLADSAAVSGTRSDBG-----AFIGGGQAD 465  
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Qy** 495 NVALQLKGVQNLANRNIRDVNGARNAGIAQAATAGLVQAOYLPGKSMMAIAGGTTVRGEAGY 554  
|||:::||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Dd** 466 ALMLEXGSSFTLN-----AGDATATDTT-----VNGGLEFARGGT 499  
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|  
**Qy** 555 AIGYSSISDGNWIIKGTASN 576  
||:||||:|:|:|:|:|:|  
**Dd** 500 LAGTTLLNNGAILTLSGKTVNN 521  
||||:|:|:|:|:|:|:|:|:|:|:|:|:|:|

**RESULT 13**

B43855  
high-molecular-weight surface-exposed protein - Haemophilus influenzae  
C:Species: Haemophilus influenzae  
C>Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 18-Nov-1994  
C:Accession: B43855  
R:Barenkamp, S.J.; Leininger, E.  
Infect. Immun. 60; 1302-1313, 1992  
A>Title: Cloning, expression, and DNA sequence analysis of genes encoding n detella pertussis.  
A:Reference number: A43855; MUID:92192797  
A:Accession: B43855  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1477 <BAR>  
A>Note: sequence inconsistent with the nucleotide translation  
A>Note: sequence extracted from NCBI backbone (NCBIN:89237, NCBIIP:89240)

Query Match 7.6%; Score 228.5; DB 2; Length 1091;  
Best Local Similarity 23.6%; Pred. NO. 0.0005;  
Matches 147; Conservative 69; Mismatches 203; Indels 203; Gaps 36;



Db 977 TDSNDAEIQGNGISQKEGNLTSSDKINITKQITIKKIDGEDSSDSDATSNANLT-1K 1035  
Qy 209 KRAASVKQDLNAGWNTKVKPGTASDNVDFVRYDTVEFLGADTKTTVNVESKDNKG 268  
Db 1036 TKEKLTEDLSISGFN---KAEITAKDGRDLTIGNSDNGSNGAEAKTVTFN-----NVK 1086  
Qy 269 KTEVKIGAKTSVKEKDKGLVTKDKGSGSSTDEGEL-VTAKEVIDAYNKAQWRMKT 327  
Db 1087 DSKISADGHNWTL---NSKVKTSSNGRESNDSNDTGLTITAKNV---EVNKDITSUKTV 1141  
Qy 328 TANGQTOAQKPFETVSGTNVTFASGKGTATVSKDDQGNITVYDVNVDGALNVNQLN 387  
Db 1142 NIT-----ASEKVTTAGTINATNGRASITTKTGDISGTIS-----GNTVSVSA--- 1186  
Qy 388 SGWNLDSKAVAGSGKVIYS- NVSPSKGKMDETVNNAGNIEITRNGKNIDTATSWTP 445  
Db 1187 ---TVDLTTSGSKIEAKSGEANVTATGTIGGTI---SGNTVNVATANAGDLTVG----- 1235  
Qy 446 QFSSVSLGAGADAPTLSDVDGDL--NVGSKDNKPVKITVAPGVKEDVTNVAQLKGVA 503  
Db 1236 --NGAEINATEGAATLATNTLTTEAGSS-----ITST-----KGQVDLLAQNGSIA 1281  
Qy 504 QNLNRRIDNVGDNARAGIAQAIATAGLVQAYLPCKSMMAIGGGTYRGEAGYAIYSISD 563  
Db 1282 GSIN--AANVTLN-----TTG-----TLTTVAGSDIKATSG-----TLVIN 1315  
Qy 564 GGNWIKGTASGNS 577  
Db 1316 AKDAKNGDASGDS 1329

## RESULT 14

AF0394  
Probable adhesin hmwA [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AF0394  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; Ill, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0394  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1910 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175  
C:Genetics:  
A:Gene: hmwA

Query Match 7.3%; Score 219; DB 2; Length 1910;

Best Local Similarity 20.5%; Pred. No. 0.0031;

Matches 146; Conservative 92; Mismatches 255; Indels 228; Gaps 28;

Qy 14 NAWVVSELTEHHTKRASATVKTAVLTLFPATVQ-----ASA 51  
Db 998 NATITANNISMN-----GNITANDAVLMTNTFLTAKGDIKTDLTSPTKGLFRNGGMTAA 953  
Qy 52 NNEEQEEDLYDPLVRLTVAVLIVNSDEGTGEKEVEENSDWVYFNEKGVLTAREITLK 111  
Db 954 NN-----ILLVANS--TSSGETVKINASS-----NKNMTAGKDISII 990  
Qy 112 AG-----DNLIKONGNFYSLKKDLDTSVGTTEKLSFSAKNGKNIYISDT 159  
Db 991 AGNSKTATGPNINIERNIETNNGFT-----TNGTSTWLSGVNVSANG--VDITSNS 1042  
Qy 160 KGLNFAKETACTGDTTVHLNGIGSTLTDTLTNGATTNTVNDVNDDEKKRAASVDV- 218  
Db 1043 TG-----TGGIVLDNTNLTTVGD-----INT-IVTNSSGKGIWIKSNSTLNSNKDIT 1089

Qy 219 ---LNAGWNKGV--KPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVK 273  
Db 1090 LVGVSAQN-EGVIOGSSDASN-----NISAQGNITLIGKMGNGSGQSHLIN 1137  
Qy 274 IG--AKTSVKEKDKGLVTKDKGSGSSTDEGELVTAKEVIDAVNKAQWRMKTITA-- 329  
Db 1138 LGNVSLTS-----SORNIDINGSSAGTGDVFTVVELNATAGNVSIIAETKTALS 1187  
Qy 330 -----NGOTGQADKPFETVSGTNVTFASGKGTATVSKDDQGNITV----- 370  
Db 1188 TSLNAVLSLGGNNSIKRAQNGWLICKAFNTTQAGIGFRANSSLSVDGNIILKGETEGVGA 1247  
Qy 371 -----MYDVNVGDALNVNQLNSGNWNLDSKAVAG----- 399  
Db 1248 TRKGIDFYGANTLNIILKGSQSLGKGAQDTAGGNGISYTSIAKLTVNNGSLKMEGR 1307  
Qy 400 -----SSGKVISGNVSPSKGKMD----- 417  
Db 1308 STSGTGINFPPSSNNTLVFNGDGLIKGSSVAGTGAAGVNVNNSGTPMTIEGISTDGAG 1367  
Qy 418 -----ETVINAGN---NIEITRNGKNIDIA-TSMTPOFSSVSLGA--GADAPT 460  
Db 1368 VHLESAEHRIDRINVTCSSSTHAEGLRISGNAIVDTTLTCKSINGSGVKIDSLPGSSVVT 1427  
Qy 461 LSVGDALNVGSKDNKPVKITVAPGVKEDVTNVAQLKGVAQNLNRRIDNVGDNARAG 520  
Db 1428 RSVLDNATLNGSSSGKGVETISDINGIHSSINGTTGTGTGIGIDIGEN-SNVTGTSEAD 1486  
Qy 521 --TAQATATAGL-VQAYLPCKSMMAIGGGTYRGEAGYAIYSS-ISPQGNWIKGTASGN 576  
Db 1487 LLILQGVATTGTGTGKIKNNGNNDLSNTSLNSSAVDGIALDITGLANQGNVILNGTASGS 1546  
Qy 577 SRG 579  
Db 1547 GIG 1549

## RESULT 15

C48399  
ABC-type transport protein ydBA.2 - Escherichia coli  
C:Species: Escherichia coli  
C:Date: 19-Nov-1993 #sequence\_revision 16-Oct-1998 #text\_change 08-Oct-1999  
C:Accession: C48399; D64891; H64891  
R:Moszer, I.; Glaser, P.; Danchin, A.  
Biochimie 73, 1361-1374, 1991  
A:Title: Multiple IS insertion sequences near the replication terminus in Escherichia coli  
A:Reference number: A48399; MUID:92190338  
A:Accession: C48399  
A:Molecule type: DNA  
A:Residues: 464-2020 <MOS>  
A:Cross-references: GB:D85081; NID:g3041754  
A:Experimental source: strain K-12  
A:Note: sequence inconsistent with the nucleotide translation  
A:Note: sequence extracted from NCBI backbone (NCBIN:88089, NCBTP:88090)  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; .A.; Rose, D.J.; Mau, B.; Sha, Y.  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: D64891  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-839, <LDPLYFOTSVIT', <BLA1>  
A:Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74483.1; PID:g17876  
A:Experimental source: strain K-12, substrain MGL655  
A:Accession: H64891  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 'M',915-2020 <BLA2>  
A:Cross-references: GB:AE000237; GB:U00096; NID:g1787665; PIDN:AAC74487.1; PID:g17876  
A:Experimental source: strain K-12, substrain MGL655  
C:Genetics:  
A:Gene: ydBA\_2



A:Start codon: GTG

Query Match 7.2%; Score 216.5; DB 2; Length 2020;  
Best Local Similarity 23.4%; Pred. No. 0.0044;  
Matches 165; Conservative 78; Mismatches 238; Indels 225; Gaps 38;

QY	33	TVKTAVALTLFPATQ-----ASANEEQEEDLY-LDPVLRVTAVLVNSDKEGTGE	83
Db	151	TEKTLIRSVFTYTENADGTISLQDSNGRKATINLWQIDEANNTVALEGVSDAG-----	206
QY	84	KEKVEENSQWAVYFNEKGVLTAREITLKAGDNLKIKONGTNFTYSLKKOLTDLTSGTE-	142
Db	207	-----TKWQYNHGELVIT-----GDNATVNNNG-----KTTVDGKDSGTGTEI	244
QY	143	-----KLSFSANGKNVITSDT-----KG-----LNFAK	166
Db	245	NGNNGKVIQDGDLDVSGGGHGIDITGDSATVDNKGTMVTDPESMGIOIDGDKAIVNNEG	304
QY	167	ETAGTNGDITVHLNG-----IGSTLTDTLNTGATNTVNDNVTDDKKRAASVKDVL	219
Db	305	ESTITNGGTGTQINGDDATANNNGKTTVDGKDSGTGEINGNCKVIOD-----GDLVDS	358
QY	220	NAGWNIGVKPGTASDNVDVRYDYVEF-LSADTKTTTVNVYESKD-----NG	267
Db	359	GGGHGI-DITGDSATVDNKGTMVTDPESIGIQVDGDAQVNNEGESAITNGGTGTQING	417
QY	268	KTEVKIGAKTSVIKEKDKLVTKGD-KGENG-----SSTDEG	304
Db	418	DDATANNGKTTV-----DGKDSGTGTAGNNGKVIQDGDLDVSGGGHGIDITGDSATVDN	473
QY	305	EGLVTAKE-----VIDA-----VNKAGWRMKTTTANGOTGOADKFEETVTSGTNVTFASGK	354
Db	474	KGTMTVTDPEIGIQIDGDAQIYNNEG---ESTITNGGTG-----TQINGNDAT-ANNS	523
QY	355	GTTATVSKDD-----QGNITVMYDVNVGDALNV-----NQLQNSGWN--LDSK-----AVA	398
Db	524	GKTTVDGKDSGTGKIAGNIGI---VNLDGSLVTGTGAHGVENIGDNGTVNNKGDIVVSDT	580
QY	399	GSSGKVISGNVSPSKGMDETVINAGNIEITRNKNIDTIATSM-TPQPS-----	448
Db	581	GSIGVLINGEGATVSNITGDVNVVS-NEATGFSITTSKGVSLAGSMQVGFSTGVDLNGNN	639
QY	449	-SVSLGA-----GADAPTLSDGDALNV---GSKKDNKPVRTNVA-----PGV-----	488
Db	640	NSVTLAAKDLKVVGQKATGINVSGDANTVNITGNVLVDKDKTADNAAEYFFDFPSGVINVY	699
QY	489	-KEGDVTNVAQLKGVQAN-LNNRIDNV-DGNARAGIAQAIATAGLV-----Q	532
Db	700	GSDNNVTLDGKLTWSDSEVTSRQSNLFDGSAE-----KTSGLVYIGDGNVNNMGG	752
QY	533	AYLPGSKMMAIGGTYRGEAGYAI-----GYSSISDGGNWIIG	571
Db	753	ELIGEKNALADGSQVTSRLTGYSTSVIVVSGESSVYLNGLDITISG	798

Search completed: July 3, 2002, 08:12:25  
Job time: 447 sec

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Db 364 KETDIDNRWFSYKDYDTEKEIOIGSOIDAKNNATLATKGDVTLDAAKINAGNNLA 423
Qy 118 IKQNGTNYFSLKDLTDLTSVG-TEKLSFSAANGKVNITS-----DTKGLNFA 165
Db 424 INAN-----KDIHNGLVEKSENGENRNRHTSRLESWSNSHQTETLKAS 471
Qy 166 KETAG-----TNGDTTVHLN-----GIGSTLTDLL---NT 193
Db 472 ELTAGDGLDLDAOGSITAQAKLHANENVLNKADINLNQKNTNDKTVTDHNVWGGI 531
Qy 194 GATTNYTNDN-----VTDDEKRAASVKDVLNAGWNIG-----VKPGTTASNDVD 239
Db 532 GGGONKNNNOQOVSHATQLTADQLLADNNVNITGSOVKGNQGAFFK--TTQGDVVI 589
Qy 240 FVRTYDVEFLSAD-----TKTTTVNVESKDKGKTEVKIGAKTSVIKEKD-----GKL 288
Db 590 DNALSETISKIDERTGTAFTNITKSSHKNETKOTSTGSELISDAQLTVVSGNDVNVIGSL 649
Qy 289 VTGDK-----GE-NGSST-----DEGEGLVT-----AKEVIDAVNKAGWRMKTITANG 331
Db 650 IKSADKLGISLGDINVKSAQVTKIDDEKTSLAITCHAKEVEDKQYSAGFHITHTKN 709
Qy 332 QTQADKFFETVSGTNYTFASGKGTATVS--KDDGNIITVYDVNVVGDALNQLONGS 389
Db 710 TSTETEQA NSTISGANVDLOANKDVTFAGSDLKTAGNASITGD-NVAFVSTENKKQTD- 767
Qy 390 WNLDSKAVAGSSGKVISGNVSPSKMDETVNINAGNNIETRN-GKNIDIATSMTPQFS 448
Db 768 -NTDTTISGGS---YTGGVYDKVGSRADFOYD-KQHTQTEVTNRSQTEVAGDLTITAN 822
Qy 449 SVSLGAGA-----DAPTLSDVDGDLNNGSKKD-----NKPV 479
Db 823 KDLLEHGAASHVBERVOEGENTIOHLAVNDSESKT--DSLNVGIDVGVNLDYSGVTKPV 880
Qy 480 R-----ITNVAPGVKEGDTNVNAQLKGVQNLNRRIDNVGDNARAGIAQAIATAGLVQA 533
Db 881 KKAIEDGVNTKPG-NNTDLTKKVTARDAIANLAN-LSNLE-TPNVGVEVGK-----930
Qy 534 YLPKSNMAATGGTYRGEAGYATGYSISDG 564
Db 931 -----GGGSQSQSTDSQAVSTISINAG 951
```

```
RESULT 4
AIDA_ECOLI
ID AIDA_ECOLI STANDARD; PRT; 1286 AA.
AC Q03155;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE Adhesin aidA-I precursor.
GN AIDA-I.
OS Escherichia coli.
OG plasmid pIB6.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OX Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 50-56.
RC STRAIN=2787 (O126:H27);
RX MEDLINE=92326638; PubMed=1625582;
RA Benz I., Schmidt M.A.;
RT "AIDA-I, the adhesin involved in diffuse adherence of the
RT diarrhoeagenic Escherichia coli strain 2787 (O126:H27), is
RT synthesized via a precursor molecule.";
RL Mol. Microbiol. 6:1539-1546(1992).
CC -I- FUNCTION: THIS IS AN ADHESIN PROTEIN NECESSARY FOR THE DIFFUSE
CC ADHERENCE OF DIARRHEA-CAUSING ENTEROPATHOGENIC ESCHERICHIA COLI
CC TO EPITHELIAL CELLS.
CC -I- SUBCELLULAR LOCATION: Outer membrane.
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; X65022; CAA46156.1; -  
KW PIR; S28634; S28634.  
DR Cell adhesion; Signal; Outer membrane; Plasmid.  
FT SIGNAL 1 49  
FT CHAIN 50 ? ADHESIN AIDA-I.  
FT PROPEP 5 ? 1286  
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match 6.8%; Score 203.5; DB 1; Length 1286;

Best Local Similarity 21.4%; Pred. No. 0.0065;

Matches 146; Conservative 92; Mismatches 274; Indels 171; Gaps 30;

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Qy 1 MNEILRIINLSALNAWVWVSELTRNH-----TKRASATVKTA--VLATLLFATVOASA 51
Db 1 MNKAYSIINSHSRQAMIVASELARGHGFVLAKNTLLVLAVVSTIGNAFVNIISTVSSGG 60
Qy 52 NNEEQEEDLYL-----DPVLRVAVLIIV-----SDKEGT-GEKEKVEEN 90
Db 61 TVSSGETQIIVSGRGSNATVNSGGTQIVNNGKTTATTVNSSGSQNVGTSGATISTIVN 120
Qy 91 SDNAVYFNEKGLVTAREIT-----LKAGDNLKIKQNGTNYFSLK-KDLTDLTSVGT 141
Db 121 SGGIQRVSSGGVASATNLSCGAQNIYNLGHASNTVIFSGGNQTIIFSGITDSTNISSGG 180
Qy 142 EKLFSFANGKVNITSDTKGLNFAKETAGTNGDTTVHLN-----GIGSTLTDLLNTG 194
Db 181 QRV--SSGGVASTNTINSSG---AONILSEGAISTHISGGNOYISAGANATETIVNSG 235
Qy 195 ATTNVTNDVNTDEKKRAASVKDVLNAGNIKGVKPTTASDNDVDFRTDVTVEFLSADT 254
Db 236 GFQRVNSG-----AVATGTVLSGG--TQNVSSGSAISTSVYNSGVQTV-FAGATV 283
Qy 255 KTTVNVESKDN---CKKTEVKIGAKTSVIKEKDKGLVTGKDKGNGSGSTDEGEGLVTA 310
Db 284 TDTTVNSGGNONISSGGIVSETTVNVSQNTIYSGGSALSANIKGS-----329
Qy 311 KEVIDAVNKAGWRMKTITANG-----QTQADKFFETVSGTNTVTFASG-----KGT 356
Db 330 ----QIVNSEGTALNTLVSDGGYQHIRNGGLASCTIVNQSGYVNISSGGYAEASTIINSG 385
Qy 357 TATVSKDDQGNITVMD--VNVGD-ALNVNQLONSQNL-----DSKAVAGSSG--K 403
Db 386 TLRVLSGYARGTILNNSGRNVSNGGVSYNAMINTGQNIYISDGEATAAIVNTSGFOR 445
Qy 404 VISGNVSPSKKMDETVNIAGN--NIETIRNGKN-----IDIATSMTPQF 447
Db 446 INSGGTAPVNSVVVTVRTVSSAAKPFDAEVYSGGQTVYLMRWIYNSNFLTAVWSMPTGT 505
Qy 448 SS---VSLGAGADAPTLSDVDGDLN-----VGSKKDNKPKVRIITNVAPGV 488
Db 506 ASGANVNLGRLNFAFAGNVGVTILNQEGRYQYVSGATATSTVGNNEGREV---LSGGI 561
Qy 489 KEGDVTNVAOLKGVQNLNRRIDNVGDNARA-----GIAQAIATAGLVQALPKSMAI 543
Db 562 TDGTVLNSGGIQAQVSSG-----GKASATVINEGAQFVYDGGV---TGTNIK--606
Qy 544 GGTYRGEAGYATGYSISDGGN 566
Db 607 NGGTIRVDSGASALNIALSSGN 629
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RESULT 5  
YDEK\_ECOLI  
ID YDEK\_ECOLI STANDARD; PRT; 1325 AA.  
AC P32051; P76140; P77168;

01-OCT-1993 (Rel. 27, Created)  
01-NOV-1997 (Rel. 35, Last sequence update)  
16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical lipoprotein ydek precursor (ORF1).  
GN YDEK OR ORF1 OR B1510.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=K12 / MG1655;  
RX MEDLINE=97251357; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.,  
RA "The complete genome sequence of Escherichia coli K-12";  
RT Science 277:1453-1474(1997).  
RL [2]  
RN SEQUENCE FROM N.A.  
RX STRAIN=K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
RA Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 570-Kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 28.0-40.1 min region on the linkage map";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 595-1325 FROM N.A.  
RX MEDLINE=94100243; PubMed=8274505;  
RA Cartwright P.J., Timms M.W., Lithgow T., Hoeg P.B., Hoogenraad N.J.;  
RT "An Escherichia coli gene showing a potential ancestral relationship  
to the genes for the mitochondrial import site proteins ISP42 and  
MOM38";  
RT Blochim. Biophys. Acta 1153:345-347(1993).  
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor  
(Potential).  
CC -1- SIMILARITY: TO E. COLI YFAL.  
CC -1- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS  
ISP42 AND MOM38.  
CC -1- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
FRAMESHIFT IN POSITION 653.  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL: AE000248; AAC74583.1; --  
CC EMBL: D90793; BAA15190.1; ALT\_INIT.  
CC EMBL: D90794; BAA15197.1; ALT\_INIT.  
CC EMBL: X73295; CAA51730.1; ALT\_FRAME.  
CC FIR; S34315; S34315.  
CC EcoGene; EG11780; ydek.  
CC PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.  
CC Hypothetical protein; Membrane; Lipoprotein; Signal;  
KW Complete proteome.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.  
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).  
FT CONFLICT 884 884 N -> K (IN REF. 3).  
FT CONFLICT 1317 1317 M -> S (IN REF. 3).  
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 6.6%; Score 199; DB 1; Length 1325;  
Best Local Similarity 21.0%; Pred. No. 0.011;  
Matches 158; Conservative 91; Mismatches 244; Indels 260; Gaps 34;  
QY 1 MNEILRIIWNALNANVVSSELTR-----NHTKRASATVKTA--VLATLLFATVOAS 50  
DB 1 MNRIYRIVWNCITLOVFOACSELTRRAGKTSTVNLKRKSGSLTTRFSLTLGLVLLALSAS 60  
QY 51 ANNEEED-----LYLDPVLR-----TVAVLIVNSDKET 81  
DB 61 GASLEVDNDQITNIDTDVAYDAYLVGWYTCVNLNLAGNASLTTITTSVIGANEDSEGT 120  
QY 82 GEKEKVEENSDWAVYFNEKGVLTAREITLKAGDN---LKIQKQNTNFTYSLKKDLTDLTS 138  
DB 121 VN-----VLGCTWRLY-----DSGNNARPLNVGQSGTG-TLNIKQ----- 154  
QY 139 VCTEKLFSFANGKNVITSDTKLGNFAKTAGTNDTIVHLNGIGSTLTDTLLNTGA--- 195  
DB 155 -----KGVDGGYLRGSGTGGV-----TVNVEGDSVLTITTELFEGSYGT 196  
QY 196 -TTNVTNDNVTDDEKRAASVKDVLNAGWNKGVKPGTASDNVDVFTVDTVEFLSADT 254  
DB 197 GSNIT-----DKGYVTSSIVAIL-----GYQAGSNGQ----- 224  
QY 255 KTTTVNVES-----KDNKKTEYKIGAK-TSVIKERDKGLVTGCKDGENSGSTDEG--- 304  
DB 225 ---VVVEKGEWLKKNDSIEFQIGNQGTGEATIREGLVTAENTIIGGNATGICTLN 280  
QY 305 -----EGLVTAKE-----VIDAVNKAGWRMK 325  
DB 281 VQDQSVITVRLRYGFGNGTVNISNGLNNKKEYSLVGVQDGSNGVNVNVDKGHWNFL 340  
QY 326 TTTANGOTGQADKFETV-TSGTNTVFASGK-----TTATVSKDDOGNTIVMYDVNVGD 378  
DB 341 -----GTGAFRIYICDAGDELNVSSSEKGVDSGLIITACMKETGNTVTKDKNSVIT 394  
QY 379 ALNVN-----QLONGWNLDKAVAGSSKGVISGNVSPSKGKMD-----TVNI 422  
DB 395 NLGTNLGYDGHGEMNISNOGLVSVNGSSSLGYGETGVGVNSITTTGGMWENKKNVYTTIGV 454  
QY 423 NAGNNITENGK-----NIDATSWTPQFSVSLGACADAPTLSVDGDALNVGSKDKNP 478  
DB 455 AGVGNLISDGGKRFVSNITFLGDKASGIGTLNL---MDA-TSFDFTVGVNG---NFG 506  
QY 479 VRITNVAPGVK-----EGDVTNVAQLGVAQNLNRRDNDV-DGNARAGIAQA----- 524  
DB 507 SGIVNSNGATLNTSGYGFIGNASGKGIYINISTDSLWNKTSSTNAQLQVGLGTGEL 566  
QY 525 -IATAGLVQA-----YLPKSMMAIGGGTYRGEAGYAIYSSISDGGNWI 568  
DB 567 NITGGIVKARDTQIALNDKSKGVDVRVDGQNSLLETENMYVGTSG--TGTILTNNGTLN 624  
QY 569 IKG-----TASGN---SRHFGASASGVY 589  
DB 625 VEGGEVLYVFEPVAVGTGLNIGAAHGAADAGF 657  
RESULT 6  
OMPB\_RICRI  
ID OMPB\_RICRI STANDARD; PRT; 1654 AA.  
AC Q53047;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scd5) (rOmpB)  
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
GN OMPB  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=783;





Best Local Similarity 21.5%; Pred. No. 0.033;

Matches 157; Conservative 83; Mismatches 266; Indels 223; Gaps 31;

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QY 24 RNHTKRASTVTKAVLATILFATVQASANNNEQEDLYLDPVLTAVAVLVNSDK-----79
Db 396 RELOQAGSTVAASAKLI-----STQEDVKLGANVSADRAVSUKAARDVHLA 445
QY 80 GTCSEKVEE-----NSDWAYFNEKGVLTAREITLTKAGDNLKIKQNG 122
Db 446 GLVEKDKSERGYORNHTSSLRGTGRWSNDESELSKASELSRSEGLTLKAGRVNSTQAG 505
QY 123 TNYTSLKDLTDLTSVGTSEKLS-----FSANGKNVNTSDTKGLNFAKET 168
Db 506 VHAQRLDITDADNQIGVQVKTANAKAVRDKTSGWIGGGDNKN--SNRREISHASEL 563
QY 169 AGTNGDTVHLNG-IGSTLTDTL--NTGATTNTVNDVTDDEKKRAASVKVDLNA---221
Db 564 --TSGG-TLRLNGQQGVITGSKARQKQGEVATHGGLRID--NALSTTVDKIDATGT 618
QY 222 GWNKGVKPGTASDNVDVFTYDTVEFLSADTKTTTVNVESKD-NCKKT-----EVKIGA 276
Db 619 AFNI-----TSSHKADNSYQSSTASELSKSDTNLTLSHKDADVIGSQVASSGELSVE 672
QY 277 KTSVKEKDKGLVTKDKKENGSGSTDEGELVT-----AKEVIDAVNKAGWRM-----K 325
Db 673 KTGNIINV-----AAEROQNIDEQKTALTVPNGYAKEAGDKQYRAGLRIEHTRDSEK 723
QY 326 TT-----TANGOTGOADKPFETVTSNTVTFASGKGTTA-----358
Db 724 TTRTENSASSLGGSVKLKAEKDVTSFGSKLVADKGDASVSGNKKVFLAADDKTASNTEQ 783
QY 359 -----TVSKDDQGNITVMYDYNVGDALN 381
Db 784 TKIGGGFYVTGGIDKLGSGVEAGYENKTKAQSSKAITSGSDVKGNLT-----INARDKLT 839
QY 382 VNQLONGNHLDSKAVAGSGKVISGNVSPSKGMDETVNNAGNNIETRNKNIDDIAT 441
Db 840 QQGAQHSVGGAYQENAAAGVDHLLAAADTASTTTTKTDVGVI-----GANVDYSA 888
QY 442 SMTPOFSSVSLGA-----CADAPTLSDVDALNVGSK--DNKPVRTNVAPG 487
Db 889 VTRPVRVAVGKAAKLDATGVINDIGIGAPNVGLDIGAOGGSEKSSSSQAVVSSVQAG 948
QY 488 V-----KEGDV---TNVAQLKGVAQNLN-----NRIDNVGDNARAGTAAATAG 529
Db 949 SIDINAKGEVROGTOYQASKG-AVLTADSHSEAAANRQDSRDTR-----GSAG 1000
QY 530 LVQAYLPKGSMAIG-----GGYRGAGYAIGYSSISDGGNW-----IKGTASGN 576
Db 1001 -VRVYTTGSDLTVDKAGGEGGTORSNSASQAVTGSIDAANGINNVNKKDAIYQGTALNG 1059
QY 577 SRGHFCASA 585
Db 1060 GRGKTAVNA 1068
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RESULT 8  
OMPA\_RICRI  
ID OMPA\_RICRI STANDARD; PRT: 2249 AA.  
AC P15921;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmpA).  
GN OMPA.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiaseae; Rickettsia.  
OX NCBI\_TaxID=783;  
RN [1]  
RC SEQUENCE FROM N.A.  
RP STRAIN=R;

```
RX MEDLINE=90354033; PubMed=2117568;  
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
RT "A protective protein antigen of Rickettsia rickettsii has tandemly  
RL repeated, near-identical sequences.";  
RL Infect. Immun. 58:2760-2769(1990).  
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -!- PTM: GLYCOSYLATED (PROBABLE).  
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC  
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CC  
CC EMBL; M31227; AAA26380.1; -  
DR PIR; A41477; A41477.  
DR InterPro; IPR003858; rOmpA_rOmpB.  
DR Pfam; PF02708; rOmpA_rOmpB; 1.  
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
FT SIGNAL 1 28 POTENTIAL.  
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.  
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.  
FT REPEAT 212 286 A (TYPE I).  
FT REPEAT 287 358 B (TYPE II).  
FT REPEAT 359 430 C (TYPE II).  
FT REPEAT 431 505 D (TYPE I).  
FT REPEAT 506 577 E (TYPE II).  
FT REPEAT 578 652 F (TYPE I).  
FT REPEAT 653 724 G (TYPE II).  
FT REPEAT 725 799 H (TYPE I).  
FT REPEAT 800 874 I (TYPE I).  
FT REPEAT 875 949 J (TYPE I).  
FT REPEAT 1022 1093 K (TYPE II).  
FT REPEAT 1094 1165 L (TYPE II).  
FT REPEAT 1166 1180 M (TYPE II).  
FT REPEAT TYPE I (INCOMPLETE).  
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;
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Query Match 6.4%; Score 191; DB 1; Length 2249;

Best Local Similarity 24.4%; Pred. No. 0.051;

Matches 142; Conservative 56; Mismatches 212; Indels 172; Gaps 30;

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QY 98 NEKGVLTAREITLTKAGDNLKIKQNGTFTYSLKK-----DLTDLTSVGTSEKLSFSAN-----G 150
Db 766 NANAVLTGAIDNTTGDNVGV-----LNLNGALSOVTDGIGNTNSLAT--ISVGAGTATLG 819
QY 151 NKVNITSDTKGLNFAKETAGTN-----GDT--TVHLNGIGSTLDTLLNT- 193
Db 820 GAVIKATTTKLTNAASVLTLTANAVLTGAVDNTTGGDNGVNLNGLNGALSOVTDGIGNT 879
QY 194 -----GATTNVNDNVTDDEKKRAASVKDVLNAGNVIKVKPOTTFASDNV 238
Db 880 SLATISVGAGTATLGAVIKATTTKLTN-----AASVLTLTANAVLTGAIDNTTGDNV 934
QY 239 DFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIAGKTSVIKEDKGLVTGKDKGENG 298
Db 935 GVNLNGLNGALSOVTDGIGNT-----NSLAT-ISVGAGTATL-----968
QY 299 SSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGOTGOADKFEFTVSGTNVTFASGKGTTA 358
Db 969 -----GGAVIKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGI-VTFGTGNTVGT 1020
QY 359 TVSKDDQGNITVMYDYNVGDALNVQLONGNLSKAVAGSSGKVISGNVSPSKGMD 418
Db 1021 NV-----GNTNALATVNVGAGL--LQVQGVVKKANTINLTNDNASAVTFTNPVVVTGAIDN 1073
QY 419 TVNINAG-----NNIEITRNGKNIDIATSMTPQFSSVSLGADAPTLSVDGDAL--NVG 471
```

Db 1074 TGNANNGIVTFTGNTVGN-----TNALATVNVGAG-----LLQVQGVVVKANTI 1122  
Qy 472 SKDN-KPVRTNVPAGVKEGVDVNVQALKGVAQNLRNIDVGNARA-----GIAQAIA 526  
Db 1123 NLTDNASAVFTN-PVVVTGAIDNTG-----NANNGIVTFTGNTVGTGIGNTALA 1173  
Qy 527 T-----AGL-VQAYLPKGSMA-----IGGGTYRGEAGYAIY-----SSIS 562  
Db 1174 TVNVGAGITLQA---GGSLAANNIDFGARSTLEFNGPLDGG-----GKAIPYFKGAIA 1224  
Qy 563 DGGNMIK-----GTASGNSRGRH-----FGASASVSG 588  
Db 1225 NGNNAILNVNTKLLTASHLTICTVAEINAGNGLFTIDASVG 1266

## RESULT 9

BIGA\_SALTY STANDARD; PRT; 1953 AA.  
ID BIGA\_SALTY STANDARD; PRT; 1953 AA.  
AC P25927; P25928; Q9XCQ3;  
DT 01-MAY-1992 (Rel. 22, Created)  
DT 01-MAR-2002 (Rel. 41, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Putative surface-exposed virulence protein biga precursor.  
GN BIGA OR STM3478.  
OS Salmonella typhimurium.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Salmonella.  
OX NCBI\_TaxID=602;  
RN [1]  
RN SEQUENCE FROM N.A.  
RC STRAIN=14028;  
RA Stojiljkovic I., Valentine P., Heffron F.;  
RT "Salmonella typhimurium rhs homolog.";  
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=LT2 / SGSC1412 / ATCC 700720;  
RX MEDLINE=21534948; PubMed=11677609;  
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,  
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,  
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,  
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,  
RA Waterston R., Wilson R.K.;  
RT "Complete genome sequence of Salmonella enterica serovar Typhimurium  
LT2.";  
RL Nature 413:852-856(2001).  
RN [3]  
RN SEQUENCE OF 1-765 FROM N.A.  
RC STRAIN=LT2;  
RX MEDLINE=911100301; PubMed=1987123;  
RA Wu J.Y., Siegel L.M., Kredich N.M.;  
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:  
requirement for a cloned *ysg* plasmid to overcome limiting shiroheme  
cofactor.";  
RL J. Bacteriol. 173:325-333(1991).  
CC -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts  
CC in positions 414 and 732.  
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CC -----  
DR EMBL; AF133696; AAD39458.1; -  
DR EMBL; AE008859; AAL22340.1; -  
DR EMBL; M64506; AAA27042.1; ALT\_FRAME.  
DR EMBL; M64506; AAA27043.1; ALT\_FRAME.  
DR PIR; C39200; C39200.  
DR PIR; D39200; D39200.

DR StyGene; SG10437; bigA.  
KW Virulence; Repeat; Signal; Complete proteome.  
FT SIGNAL 1 27  
FT CHAIN 28 1953  
FT PUTATIVE SURFACE-EXPOSED VIRULENCE  
FT PROTEIN BIGA.  
FT 15 X 11 AA TANDEM REPEATS.  
FT 1 (INCOMPLETE).  
FT 2 (INCOMPLETE).  
FT 3 (INCOMPLETE).  
FT 4.  
FT 5.  
FT 6.  
FT 7.  
FT 8.  
FT 9.  
FT 10.  
FT 11.  
FT 12.  
FT 13.  
FT 14.  
FT 15 (INCOMPLETE).  
FT D -> DRGDDVTPDD (IN REF. 1).  
FT A -> R (IN REF. 3).  
FT D -> N (IN REF. 1).  
FT QYLE -> ITLQ (IN REF. 1).  
FT SA -> T (IN REF. 1).  
FT CONFLICT 1836 1837  
SQ SEQUENCE 1953 AA; 200150 MW; 611B3FIC954D91AE CRC64;

Query Match 6.3%; Score 189.5; DB 1; Length 1953;

Best Local Similarity 23.1%; Pred. No. 0.051;

Matches 126; Conservative 64; Mismatches 194; Indels 161; Gaps 29;

Qy 113 GDNLIKIKONGNFYSLAKDLTSLVTEKLSFANGKNYNTSDTKGLNFAKETAGTN 172  
Db 447 GDNATIKNTGTS-----DISGAGSTGT-----VIDGNARVND----- 480  
Qy 173 GDTTVHLNGIGSTLT-DTLL--NTGATT-----NVTNDVTDDEKKRAASVKDLN 220  
Db 481 GDMITDGGTGGHITGNDVVDNAGSTTVSGADATALIEGDNAL-----VIN 528  
Qy 221 AG-WNIKVGKPGTTASNDVFRVYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTS 279  
Db 529 EGNQTISSGAVGTRIDGD-----DAHTTNTGDIADVAGAGAAV11----- 568  
Qy 280 VIKEDGKGLVTGKOKGNGSSSTDEGEGLVT--AKEVI--DAVNKAGWRMKTTTTANGQTQ 335  
Db 569 -----NGDNGSLTQAGDILLVTDGAMGLIITYGTGNEA-----KNTGNATVRD 609  
Qy 336 ADKFETVTSGTNVTF-----ASGKGTATVSKDDQGNITVYDVNVGDALNVNOLONS 388  
Db 610 ADSVGFVVGAKNTPKNGKGDIDVSLNGTGALVS-GDMSQVTLGDGINV---VSVQDSEGV 665  
Qy 389 GWNLDKAVASSGKV-ISGNVSPS-----KGMDETVMINAGNIEITRNGK-NI 437  
Db 666 FSSATGVSVSGDSNAVDITGNVNI SADYQDDDLAAGAPPLTGTVGVVGGNGTNTLALNI 725  
Qy 438 ---DIATSNTPQFSSVSLGACADAPTLSDGDLANVSGKKNKPVRTITNAPGVKEDVT 494  
Db 736 DNDLSATGGQYLDVVGSLVSGDDNDNDVEIDG-GINITISED--PLDGTG-----ADIT 775  
Qy 495 NYAQLKGAQVNLNNRDNVGNARAG-----TAQATATAGLV-----QAYLP----- 536  
Db 776 GISVSGNSTVTNLNGH-STIDTNTVGVGHVVLARVNVNGSLILGDDSVVDVNVSYIPTGY 834  
Qy 537 ---GKSMMAIGGTYRGEAG-----YAI-----GYSSISDGGNWIILKGTASNSRGHFA 583  
Db 835 TYNALLMADGEGTSTENKGDITSHGVYSYIRADNGSEVNSGDIILVYATSSNSSEDRAAI 894  
Qy 584 SASVG 588  
Db 895 TRASG 899





```

[2]
SEQUENCE OF 1-30 FROM N.A.
RC STRAIN-DL42 / SEROTYPE B;
MEDLINE=95270579; PubMed=7751272;
RA Cope L.D., Yorgev R., Mueller-Eberhard U., Hansen E.J.;
RX "A gene cluster involved in the utilization of both free heme and
RT heme:hemoexin by Haemophilus influenzae type b.";
RL J. Bacteriol. 177:2644-2653(1995).
CC CC -1- FUNCTION: BINDS HEME/HEMOEXIN COMPLEXES.
CC CC -1- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC -----
DR EMBL; U08348; AAA74138.1; -.
KW Transpos; Signal; Repeat.
FT SIGNAL 1 21
FT CHAIN 22 928 HEME/HEMOEXIN-BINDING PROTEIN.
FT DOMAIN 101 679 6 X 6 AA APPROXIMATE REPEATS.
FT REPEAT 101 106 1-1.
FT REPEAT 205 210 1-2.
FT REPEAT 279 284 1-3.
FT REPEAT 410 415 1-4.
FT REPEAT 635 640 1-5.
FT REPEAT 674 679 1-6.
FT DOMAIN 149 172 4 X 6 AA APPROXIMATE TANDEM REPEATS.
FT REPEAT 149 154 2-1.
FT REPEAT 155 160 2-2.
FT REPEAT 161 166 2-3.
FT REPEAT 167 172 2-4.
FT SEQUENCE 928 AA; 101228 MW; 67D454664B92390 CRC64;
CC -----
Query Match 6.1%; Score 183.5; DB 1; Length 928;
Best Local Similarity 20.6%; Pred. No. 0.042;
Matches 127; Conservative 92; Mismatches 253; Indels 145; Gaps 22;

QY 35 KTAVALTLFATVOASANNEEQEEDLYDPLVLRTVAVLVNSD-----KEGT----- 81
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 3 KLVNISLIILTCSGAAYASTPDFPQHKTTFVGFVTIEKTTADKMTIKQGSDKAQIDWKS 62

QY 82 --GEKEKV--EENSNDNAVYFNEKGVLTAREITLKAQGNLKI---KONGINFTYSLKKDL 133
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 63 FDIGQKKEVFEQPEQNEHAVAYNRVIGGNSAQIQGLKANGKVLNANPVIITOGAEIN 122

QY 134 TDLTSVGTKELSFSANGKNVNIISDTKGLNFAKTAGTNGDTTVH---LNGIGSLTD- 188
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 123 AGLLATTFKDLERISENSNSVQFTRTKDRQVLKGLVLDKGVVKEGVINEGNITAQDF 182

QY 189 TLLNTGATTNTDNDVDDDEKKRAASYKDVNLNAGWNIKGVKPGTTASDNDVFRTYDTVE 248
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 183 VVLNGDEVINKGNIN--EKNSTINGKVVYLLSGYNFTFTLPDGSIS----- 226

QY 249 FLSADTTTTPVNVESKONGKKEVKGICAK-----TSVTEKDGKLVTG 291
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 227 -VALEDNTVOGIVKEGSIKAGEITLAKGRKQALDSLVMNNGVLEATKVSNNKGVVLS 285

QY 292 KDKGE-NGSSTDECEGLVTAKEVIDANVAKGWRMKTITANGQTQADKFEVTSGTNVT 350
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 286 ADVLNLNESNIKE-IVTGCADVTSNKLKDNLIKTSKTSKVTSPKINFTGKSVING 344

QY 351 ASRGKGTATVSKDQGNITVMYDVGDALNVNOL---QNSGNWLDKAVAGSGKVI 407
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 345 NFGREDSTTHYKDEKFKLNTENVNDVDPNENIRIADIEDNTGTGTCG--TGTSSFQTG 401

QY 408 NVS---PSKQMD---ETVNI-----NAG-----NNIEITRNGK--- 435
   | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 402 ALSILLANNGKVNLUKGNVNIISGRHIDPSFGSDSLKLTNKGHIDNNADIHSGKGRUFF 461

```

Qy	436	-----NTDIATSWTPQPSVSSVSLGAGADAPTLTSDVGDALN-----VGSKKDNKPVRTIN	483
		: :	: :
Db	462	ITSLQNEEDFKSNITITDSKINLNGNAGMLGRSVDKDYDNRWKTEGQSQRKFKDVKMSN	521
		: :	: :
Qy	484	VAPGVKSGDVTNVAOLKGVAQNLANRIDNV---DGNARAGIAQAATATAGLTQVAYLPCKSM	540
		: :	: :
Db	522	VE-----FNOVDVIVLAGGFVKVNLDKIVAT-----GQTN	551
		: :	: :
Qy	541	MAIGGGTYRGEAGYAIG 557	
		: :	: :
Db	552	FYIDGGVSRNGRKYEG 568	
		: :	: :
RESULT 13			
Y741_CHLMU		STANDARD; PRT; 1007 AA.	
ID	Y741_CHLMU		
AC	Q9PJT6;		
DT	16-OCT-2001 (Rel. 40, Created)		
DT	16-OCT-2001 (Rel. 40, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Hypothetical protein TC0741 precursor.		
GN	TC0741		
OS	Chlamydia muridarum.		
OC	Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.		
OX	NCBI_TaxID=833560;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=MoPn / Nigg;		
RX	MEDLINE=20150255; PubMed=10684935;		
RA	Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,		
RA	White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,		
RA	Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,		
RA	Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,		
RA	Eisen J., Fraser C.M.;		
RT	"Genome sequences of Chlamydia trachomatis MoPn and Chlamydia		
RT	pneumoniae AR39.";		
RL	Nucleic Acids Res. 28:1397-1406(2000).		
CC	-!- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0572/CT456/TC0741		
CC	FAMILY.		
CC	-----		
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CC	or send an email to <a href="mailto:license@sib-sib.ch">license@sib-sib.ch</a> ).		
CC	-----		
DR	EMBL; AE002342; AAF39550.1; -.		
DR	TIGR; TC0741; -.		
KW	Hypothetical protein; Signal; Complete proteome.		
FT	SIGNAL 1 51		
FT	CHAIN 52 1007		
FT	SEQUENCE 1007 AA; 104006 MW; 842800C0871B1518 CRC64;		
Qy	31	SATVKTAVALTLATLFFATVQASANNBQEDLYLDPVLRTVAVLVNSD-----	77
		: :	: :
Db	227	SPTDKSSLLAFL--SNPTKAKMLEHSHLVFIDITRSFFIVPVGNDQVCSMKVQNGK	284
		: :	: :
Qy	78	-KEGTGEKEKVEE-----NSDWAVYFNEKGVLTAAREITLKAGDNL	116
		: :	: :
Db	265	TKEDLGLKD-LEDWCAKFCCTGYNKFSDDWG---NRVDPVLSVSKACIESGGHLPSSVIINN	340
		: :	: :
Qy	117	-----KIKONGNFTYSL--KKDLTDLTSV--GTEKLFSSANGKNV-----ITS	157
		: :	: :
Db	341	KPRTCVAYGPNWPKNGFNYPYSAWRGRHVDYFGKIFDGT-----APFNKINWSSPT	394
		: :	: :

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Query Match      6.1%; Score 183; DB 1; Length 1007;
Best Local Similarity 21.5%; Pred. No. 0.048;
Matches 156; Conservative 85; Mismatches 238; Indels 248; Gaps 38;

Qy 31 SATVKTAVLATLLFATVOASANNRQEEEDLYLDPVLRITVAVLVNSD----- 77
Db 227 SPTDKSSLLALF--SNPNTKAMLEHSHGLHFIDTTRSFIFVPNGNWDQVCMKVQNGK 284
Qy 78 -KEGTGEKEKVEE-----NSDWAVVFNEKGVLTAIREITLKAGDNL----- 116
Db 285 TKEDLGLKD-LEDWCAKECTGYNKSFSSDWG--NRVDPVLSKAGIESGGHLPSSVIINN 340
Qy 117 -----KIKONGNFNYSL--KKDLTDLTSLV--GTEKLFSGSANGKNV-----ITS 157
Db 341 KFTCVAYGPNWPKNGENYTPSAMWRGHRVDYFGKIFDGT-----APFNKINNGSSPT 394

```

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QY 158 DTGKLNFAKTAGTNGTTHVLNIGIGSTLDTLNTGAT-TNVNDNVDTDEKKRAASVK 216
Db 395 GDDGISFNETIGSEPTATPSPSPVNVNNGVNTVNGITNVVS-----443
QY 217 DVLNAGNIIKVRPGT-TASNDVDFVYTYDTVELSADTKT---TTNVNVEKONGKKEV 272
Db 444 -----KG-SGPTSSQSDVM--STDTSDLDTSIDTNTQNTGDIINTDNNVVDG 490
QY 273 KIGAKTSVIEKDG-----KLVTGDK-----GENG 298
Db 491 SLSDVDSRVEDDGVSTESTNGDSKTTSTENGDPSPDILAAVRKHLDTVYPGENG 550
QY 299 SSTDEGEGLTAKE-----VIDAVNAGWRMKTITANGQTGAADKFTVTSNTVTFASGK 354
Db 551 GST---EGPLPANQLGNVIHVEQNGSAKETIITPGDTGPTDSSSSVDADADVEDTS--605
QY 355 GTTATVSKDDQGNITVMYDVGALNVNQLONGSWNLDKAVAGSSGKVI-----405
Db 606 DTDSGIGGDD-----GVSDTESTNG--NNSGKTTSTENGDPSPDILAAVRKHL 654
QY 406 ----SGNVSPSKGMDETVINAGNNT-EITRNGKNIDIATSWP-----QFSSVSILGAG 455
Db 655 TVYPGENGSTEGPL--PANQNLGNVIHVEQNGAAQE--TIITPGDTSTDTSSSVNAN 710
QY 456 ADAPTL-----VDGALNVGSKDKNPV-----RITNVAP 486
Db 711 ADLEDVSDADSGFGDDGIDSTESTNGDSKNTPVGDTGTPSPDILAAVRKHLDTVYP 770
QY 487 GVRGEGDVTVAQLKGVAQNLNRRIDNVGNA-----RAGIAQAIATAGLVQAYLP 536
Db 771 GENGSTERLPAN--ONLGDIIHVEQNGSAKETVVSYPYRGGGNTSSPIGLA-SLLP 826
QY 537 -----GK-----SMAIGGCTYRGEAGYAGYSSYSDGNGWIIKGTAS---574
Db 827 ATPSTPLMTTPRTNGKAAASLMIKGETQA-----KLVKNGGN--IPGETTILAE 875
QY 575 -GNSRGH 580
Db 876 LPLRUGH 882
```

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RESULT 14
HX33_HAEIN STANDARD; PRT; 917 AA.
AC P45355;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Heme/hemopexin-binding protein precursor (Heme:hemopexin utilization
DE protein A).
GN HXUA.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NTHI N182;
RX MEDLINE=95115556; PubMed=7815944;
RA Cope L.D., Thomas S.E., Latimer J.L., Slaughter C.A.,
RA Mueller-Eberhard U., Hansen E.J.;
RT "The 100 kDa haem:haemopexin-binding protein of Haemophilus
RT influenzae: structure and localization.";
RL Mol. Microbiol. 13:863-873(1994).
CC -!- FUNCTION: BINDS HEME/HEMOPEXIN COMPLEXES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -----
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-----
DB EMBL; U08349; AAA74139.1; -.
KW Transport; Signal; Repeat.
FT SIGNAL 1 21
FT CHAIN 22 917
FT DOMAIN 24 38
FT REPEAT 24 28
FT REPEAT 29 33
FT REPEAT 34 38
FT DOMAIN 111 668
FT REPEAT 111 116
FT REPEAT 203 208
FT REPEAT 277 282
FT REPEAT 399 404
FT REPEAT 624 629
FT REPEAT 663 668
FT DOMAIN 159 170
FT REPEAT 159 164
FT REPEAT 165 170
SQ SEQUENCE 917 AA; 100148 MW; 7FF39BB8C046539D CRC64;

Query Match 6.0%; Score 181; DB 1; Length 917;
Best Local Similarity 21.6%; Pred. No. 0.054;
Matches 117; Conservative 88; Mismatches 212; Indels 124; Gaps 23;

QY 82 GEKEKVE--ENSQWVYFNEKGVLTAREITLKAGDNLKI---KONGTNFTYSLKKDLTDL 136
Db 76 GONKEFEKQSPENSAYNRVTGNSAQIOGKLTANGKLVYLANPVGVIITKGAENAVGL 135
QY 137 TSVGTEKLSFSANGKNVNIITSDTKGLNFAKETAGTN-----GDTTHLNGTSTLTTL 191
Db 136 LAITKLEQLSENSNSYQFTRKTKDROVKEGVINSEIKAKDFVLNG-----DEVI 189
QY 192 NTGATTNVNDVTDDEKKRAASVKQVNLNAGNITGVKPGTTASDNVDFVTDVTEFLS 251
Db 190 NKG-----NINV---EKNSTINGKVVYLSGYNFT-----FTLSDS-----GIS 224
QY 252 ADTKTTTVN--VESKONGKKTEVKIGAK-----TSVIEKDGKLVTKG 292
Db 225 VALEDNTVRGIVONEGSIKAGEITLSAKRKEALDSLVMNNGVLEATKVSNNRGKVVLSA 284
QY 293 DKGE-NGSSTDEGEGLVTAKEVIDAVNAGWRMKTITANGQTGAADKFTVTSNTVTF 351
Db 285 DNVLNNESNIKEIVNFGTEVTSNEDK---KLKITSKTGSKVTSKINFGKSVNNGN 341
QY 352 SGKGTATVSKDDQGNITVMYDVGALNVNQLON-SGNWLD-----KAVAGSSGK 403
Db 342 FGRENSTGYNEERKTLNTEVNDIVPGAEINRIADKDNTEFDSFIQTEALSSLLANNGK 401
QY 404 V-----ISGNVS-----PSKGKMD-ETVINA-GNNIETRNCKNIDIA 440
Db 402 VNLKGNVDNISGNINIDISFRGTSLLKLTNOGHINIDHADINSGRFLFVVTISLQNDVDFK 461
QY 441 TSMTPQFSSVSLGAGADAPTLTSLVDGALNVGSKDKNKPVRIT-NVAPGVKEGDVTNVAQL 499
Db 462 SNITITDSKINLNGAMGLGRSVNEDDYATRWKRAEKSQRKKNV-----DMRNV---511
QY 500 KGVAQNLNRRIDNV---DGNARAGIAQAIATAGLVQAYLPKSKMMAIGGTYRGEAGYAI 556
Db 512 -----VFNQVDEVILAGGFEKVNLDKIVAT-----GOTNFYIDGGVSRNRSRYEY 556
QY 557 G 557
Db 557 G 557

RESULT 15
YPUA_ECOLI
ID YPUA_ECOLI STANDARD; PRT; 1569 AA.
AC F52143; P76610; P77017; P77019;
DT 01-OCT-1996 (Rel. 34, Created)
```

01-NOV-1997 (Rel. 35, Last sequence update)  
16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical outer membrane protein ypjA.  
GN YJUA OR B2647.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae.  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97349980; PubMed=9205937;  
RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,  
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,  
RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,  
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
RA Yamagata S., Horiuchi T.;  
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli  
K-12 genome corresponding to 50.0-68.8 min on the linkage map and  
analysis of its sequence features";  
RL DNA Res. 4:91-113(1997).  
CC -!- SUBCELLULAR LOCATION: Outer membrane (Potential).  
CC -!- SIMILARITY: STRONG, TO BORDETTELLA PERTACTIN.  
CC  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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the European Bioinformatics Institute. There are no restrictions on its  
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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; U36840; AAA79815.1; ALT\_SEQ.  
DR EMBL; AE000350; AAC75695.1; -  
DR EMBL; D90889; BAAL6514.1; ALT\_INIT.  
DR EMBL; D90890; BAAL6518.1; ALT\_INIT.  
DR EcoGene; EG13213; YPJ\_A.  
KW Hypothetical protein; Outer membrane; Complete proteome.  
SQ SEQUENCE 1569 AA; 162774 MW; 0D006A9A32154596 CRC64;  
  
Query Match 6.0%; Score 180.5; DB 1; Length 1569;  
Best Local Similarity 19.7%; Pred. NO. 0.11;  
Matches 117; Conservative 102; Mismatches 277; Indels 97; Gaps 22;  
  
QY 25 NHTKRASATVKTAVLATLL-----FATVQASANNEEBEDLYDPVLRVAVLI VNS 76  
DB 322 NYQHDGALKTKNTGTVSGTNSGAFSIHNVADVLLLENGHLD-----INA 371  
  
QY 77 DKEGTGEKEKVEENSDWAVYFNEKGVLTAREITLKGONLKIQKQNTFTYSLKKDLTDL 136  
DB 372 --YGSANKTIIDKGTMSVLTNAKADAT----RIDGGVMDVAGNATN-----TI 415  
  
QY 137 TSVGTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVHLNG-----IGST 185  
DB 416 INGGTQNNINNYGIATGTNINSCTONIK-----SGKADTTIISGSRQVWEKDGTAIGN 470  
  
QY 186 LT--DTLLNTGATTNVNDYDDEKKRAASYKDVNLNAGWNKIG---VKPGTTASDNVD 239  
DB 471 ISAGGSLIVYTGGAHGVN-----QETGSALVANT-GAGTDIEGYNKLSHFTITGGEAN 523  
  
QY 240 FVRTYDVTVEFLSADTKTTTNNVNESKDNKGKTEVKIGAKTSVIEKDKGLVTCKDKGENS 299

DB 524 YVVLNTGE-LTWAKTSAKNT-TIDTGGKLIVQKEAKTDSRLNNGGVLEVQDGEAKH 581  
QY 300 STDEGEGLV-----TAKEVIDAVNKAG--WRMKTITANGOTGOADKFEETVTSCTNV--TFA 351  
DB 582 VEQQSGGALIASTTSGTLIEGTSYSDAFYIRNSEAKNVVLENAGSLTVVTVGSRAVDTTI 641  
QY 352 SGKGTATATVSKD-----DOGNITVMYDVNVGDALNVNQLNSGWNILDSKAVAGSSGKVIS 406  
DB 642 NANGKMDVYKDKVGVVLSAGTQTIYASATSDKANIKGKQTVYGLATEANIESGQIYD 701  
QY 407 GNVSPSKGKMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDGD 466  
DB 702 GGST-----EKTHINGGTQ-TVQNYGRAIN--TDIVSGLQIQIMANGTAEGSIINGGSG 751  
QY 467 ALNVGSKKDKPKVRITNVAPGVKEGDTVNAQLKGVAQNLNRRIDNVDCNARAGIAQAIA 526  
DB 752 VYNEGGLAENSVLNDGGTLDVREKGSATGIQSSOGALVATTRATRVGTGRADGVAFSIE 811  
QY 527 TAGLVQAVLPKGKSMMAIGGTYRGEAGYAIQYSSISDGGNWI--KGTASGNS 577  
DB 812 QGA-----ANNILLANGGVLTVESDTSDDKTQVNMGGREIVKTKATATGTT 857

Search completed: July 3, 2002, 08:30:09  
Job time: 1180 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:28:43 ; Search time 168.02 Seconds  
(without alignments)  
608.499 Million cell updates/sec

Title: US-09-771-382-5  
Perfect score: 2999  
Sequence: 1 MNEILRIIWSALNAWVVS.....TASGNSRGHGASASVGYQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5  
Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:  
1: sp\_archaea:  
2: sp\_bacteria:  
3: sp\_fungi:  
4: sp\_human:  
5: sp\_invertebrate:  
6: sp\_mammal:  
7: sp\_mhc:  
8: sp\_organelle:  
9: sp\_phase:  
10: sp\_plant:  
11: sp\_rodent:  
12: sp\_virus:  
13: sp\_vertebrate:  
14: sp\_unclassified:  
15: sp\_virus:  
16: sp\_bacteriaph:  
17: sp\_archaeap:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	2999	100.0	591	2	Q93QY3	Q93qy3 neisseria m
2	2984	99.5	591	16	Q9JRI8	Q9jri8 neisseria m
3	2980	99.4	591	2	Q9JPS7	Q9jps7 neisseria m
4	2952.5	98.4	592	2	Q9AQF0	Q9aqf0 neisseria m
5	2866.5	95.6	590	2	Q9JPS3	Q9jps3 neisseria m
6	2752.5	91.8	600	2	Q9JPS6	Q9jps6 neisseria m
7	2739.5	91.3	594	2	Q93QY4	Q93qy4 neisseria m
8	2732.5	91.1	594	2	Q9JPS2	Q9jps2 neisseria m
9	2728.5	91.0	594	2	Q9JPI3	Q9jpi3 neisseria m
10	2721.5	90.7	594	2	Q9JPH7	Q9jph7 neisseria m
11	2719.5	90.7	598	2	Q9JPR9	Q9jpr9 neisseria m
12	2706.5	90.2	598	2	Q9JPT0	Q9jpt0 neisseria m
13	2706.5	90.2	598	2	Q9JPS0	Q9jps0 neisseria m
14	2705.5	90.2	598	2	Q93QY5	Q93qy5 neisseria m
15	2676	89.2	599	2	Q9JPR8	Q9jpr8 neisseria m
16	2597.5	86.6	592	2	Q9JPS9	Q9jps9 neisseria m

17	2596	86.6	599	2	Q9JPS8	Q9jps8 neisseria m
18	2555.5	85.2	598	2	Q9JPR7	Q9jpr7 neisseria m
19	2554.5	85.2	592	2	Q93QY2	Q93qy2 neisseria m
20	2523	84.1	595	2	Q9JPH0	Q9jph0 neisseria m
21	2519.5	84.0	600	2	Q9JPS5	Q9jps5 neisseria m
22	2481	82.7	589	2	Q9JPI0	Q9jpi0 neisseria m
23	2467	82.3	589	2	Q93QY1	Q93qy1 neisseria m
24	2449.5	81.7	526	2	Q9JPS4	Q9jps4 neisseria m
25	2447.5	81.6	530	2	Q9JPS1	Q9jps1 neisseria m
26	2445.5	81.5	592	16	Q9JQW4	Q9jqw4 neisseria m
27	1243	41.4	2353	2	P71401	P71401 haemophilus
28	1054.5	35.2	1098	2	Q48152	Q48152 haemophilus
29	437.5	14.6	1299	16	Q9F3X6	Q9f3x6 pasteurella
30	393	13.1	2059	16	Q9PD50	Q9pd50 xylella fas
31	375	12.5	1107	2	Q9F2D8	Q9f2d8 salmonella
32	372.5	12.4	1190	16	Q9PC04	Q9pc04 xylella fas
33	368.5	12.3	2712	16	Q9F3X5	Q9f3x5 pasteurella
34	252.5	8.4	1291	16	Q92KQ7	Q92kq7 rhizobium m
35	243	8.1	1953	16	Q98HJ2	Q98hj2 rhizobium l
36	239.5	8.0	1004	16	Q9PD63	Q9pd63 xylella fas
37	233.5	7.8	2276	2	Q93TY6	Q93ty6 staphylococ
38	231.5	7.7	3930	16	Q98E20	Q98e20 rhizobium l
39	231	7.7	1265	2	Q9FDA0	Q9fda0 xanthomonas
40	230.5	7.7	1536	2	Q48031	Q48031 haemophilus
41	230	7.7	1557	2	Q9RN12	Q9rni2 haemophilus
42	228.5	7.6	1039	2	Q9L6T7	Q9l6t7 escherichia
43	226.5	7.6	1040	2	Q9AL50	Q9al50 shigella fl
44	222	7.4	1477	2	Q48028	Q48028 haemophilus
45	219.5	7.3	1039	2	Q9L6T8	Q9l6t8 escherichia

ALIGNMENTS

RESULT 1

Q93QY3 PRELIMINARY; PRT; 591 AA.  
AC Q93QY3;  
CT 01-DEC-2001 (TREMBlrel. 19, Created)  
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG329;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis.;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157606; AAK68867.1;  
SQ SEQUENCE 591 AA; 62048 MW; C0DC600798859C65 CRC64;

Query Match 100.0%; Score 2999; DB 2; Length 591;  
Best Local Similarity 100.0%; Pred. No. 6.8e-119;  
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNEILRIIWSALNAWVVSSELTRNHTKRASATVKAVLATLLFATVQASANNEQEEEDL 60  
Db 1 MNEILRIIWSALNAWVVSSELTRNHTKRASATVKAVLATLLFATVQASANNEQEEEDL 60  
QY 61 YLDPVLRTVAVLIVNSDKETGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
Db 61 YLDPVLRTVAVLIVNSDKETGEKEKVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
QY 121 NGTNFTYSLLKDLTDLTTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180  
Db 121 NGTNFTYSLLKDLTDLTTSVGTETKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180



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OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF26366; AAF42515.1; --
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 99.4%; Score 2980; DB 2; Length 591;
Best Local Similarity 99.3%; Pred. No. 4.3e-118;
Matches 587; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIIWNLSALNNAVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
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QY 1 MNEILRIIWNLSALNNAVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
Db [1]
QY 61 YLDPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
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QY 121 NGTNTFYSLKDLTDLTTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
Db [1]
QY 181 GIGSTLTDLTLLNTGATTTNVDNVTDEKKRAASVKDVLNAGNNIKGVKPGTTFASDNVDF 240
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QY 181 GIGSTLTDLTLLNTGATTTNVDNVTDEKKRAASVKDVLNAGNNIKGVKPGTTFASDNVDF 240
Db [1]
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Db [1]
QY 361 SKDDOGNITVMYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNSVSPSKGKMDIV 420
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QY 421 NINAGNNIEITRNKNIDATSMTPQFSSVSLGAGADAPTLSDVDGALNVGSKKNKPV 480
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QY 541 MAIGGTYRGEAGYAIYSSISDGGNWIIGTASGNSRHFAGASASVGYQW 591
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Db [1]

RESULT 4
Q9AQF0
ID Q9AQF0 PRELIMINARY; PRT; 592 AA.
AC Q9AQF0
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DE OUTER MEMBRANE PROTEIN.
GN NHHA.

OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF26366; AAF42515.1; --
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 99.4%; Score 2980; DB 2; Length 591;
Best Local Similarity 99.3%; Pred. No. 4.3e-118;
Matches 587; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db [1]
QY 1 MNEILRIIWNLSALNNAVYSELTRNHTKRASATVKTAVLATLLFATVQASANNEEQEEDL 60
Db [1]
QY 61 YLDPVLRVAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
Db [1]
QY 61 YLDPVQRTAVLIVNSDKEGTGEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIK 120
Db [1]
QY 121 NGTNTFYSLKDLTDLTTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAGTNGDTTVHLN 180
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QY 481 ITNVAPEGVDVTNVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVQAYLPKSM 540
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QY 541 MAIGGTYRGEAGYAIYSSISDGGNWIIGTASGNSRHFAGASASVGYQW 591
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Q9JPS3
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DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF26366; AAF42515.1; --
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;

Query Match 98.4%; Score 2952.5; DB 2; Length 592;
Best Local Similarity 98.5%; Pred. No. 6.1e-117;
Matches 583; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

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QY 241 FVRTYDFVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGDKGNGSS 300
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QY 480 RITNVAPEGVDVTNVAQLKGVAQNLRIDNVGNARAGIAQAATAGLVQAYLPKGS 539
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Db [1]
QY 540 MMAIGGTYRGEAGYAIYSSISDGGNWIIGTASGNSRHFAGASASVGYQW 591
Db [1]
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Db [1]

RESULT 5
Q9JPS3
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.
AC Q9JPS3;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF26366; AAF42515.1; --
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
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RC STRAIN=NGE28;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226378; AAF42527.1; -.
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 95.68; Score 2866.5; DB 2; Length 590;
Best Local Similarity 96.59; Pred. No. 2.5e-113;
Matches 571; Conservative 5; Mismatches 13; Indels 3; Gaps 2;

Qy 1 MNEILRIIWSALNAAVWVSELTRNHTRKASATVKTAVLATLLFATVOASANNEEQEDL 60
Db 1 MNKIYRIIWSALNAAVWVSELTRNHTRKASATVKTAVLATLLFATVOASATDEDED- 59
Qy 61 YLDPVLRFTAVLVNSDKEGTGEKEVEENSMDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
Db 60 -LDPVQRTAVLVNSDKEGTGEKEVEENSMDWAVYFNEKGVLTAGTITLKAGDNLKIQ 118
Qy 121 NGTFTYSLKDLTDLTSVGTKEKLSFSGANGKNVITSDTKGLNFAKETAGTNGDTHVHLN 180
Db 119 NGTFTYSLKDLTDLTSVGTKEKLSFSGANGKNVITSDTKGLNFAKETAGTNGDTHVHLN 178
Qy 181 GIGSTLDTLLTGATNTVNDVTDDEKRAASVKDVLNAGWNLKGVKPGTTASDNVDF 240
Db 179 GIGSTLDTLLTGATNTVNDVTDDEKRAASVKDVLNAGWNLKGVKPGTTASDNVDF 238
Qy 241 VRTYDTEVFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGKGENSS 300
Db 239 VRTYDTEVFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGKGENSS 298
Qy 301 TDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTTFASGKGTATV 360
Db 299 TDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTTFASGKGTATV 358
Qy 361 SKDDQGNITVYDVNVGDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKGMDET 420
Db 359 SKDDQGNITVYDVNVGDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKGMDET 418
Qy 421 NINAGNTEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLVSDGD-ALNVGSKDNKP 479
Db 419 NINAGNTEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLVSDGDALNVGSKDNKP 478
Qy 480 RITNVAPCKEGDVTNVAQLKGVAQNLRNDVNGNARAGIAQAIATAGLVQAYLPKGS 539
Db 479 RITNVAPCKEGDVTNVAQLKGVAQNLRNDVNGNARAGIAQAIATAGLVQAYLPKGS 538
Qy 540 MMAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 591
Db 539 MMAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQW 590

RESULT 6
Q9JPS6 PRELIMINARY; PRT; 600 AA.
AC Q9JPS6;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DR 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
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RN SEQUENCE FROM N.A.
RP STRAIN=E26;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226371; AAF42520.1; -.
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 91.8%; Score 2752.5; DB 2; Length 600;
Best Local Similarity 91.3%; Pred. No. 1.6e-108;
Matches 549; Conservative 16; Mismatches 25; Indels 11; Gaps 3;

Qy 1 MNEILRIIWSALNAAVWVSELTRNHTRKASATVKTAVLATLLFATVOASANN---EEQ 56
Db 1 MNKIYRIIWSALNAAVWVSELTRNHTRKASATVKTAVLATLLFATVOASADNVQASDN 60
Qy 57 EEDLYLDPVLRFTAVLVNSDKEGTGEKEVEENSMDWAVYFNEKGVLTAREITLKAGDNL 116
Db 61 EEEYLEPVPVTPAPLVYSFSDAEDTGEKE-VTENTNMGIIYFDKNGVTKAGTITLKAGDNL 119
Qy 117 KIKO-----NGTNFTYSLKDLTDLTSVGTKEKLSFSGANGKNVITSDTKGLNFAKETAG 170
Db 120 KIKQNTDENTNASSFTYSLKDLTDLTSVGTKEKLSFSGANGKNVITSDTKGLNFAKETAG 179
Qy 171 TNGDTTVHLNGIGSTLDTLLTGATNTVNDVTDDEKRAASVKDVLNAGWNLKGVK 230
Db 180 TNGDTTVHLNGIGSTLDTLLTGATNTVNDVTDDEKRAASVKDVLNAGWNLKGVK 239
Qy 231 GTTASDNVDFVRTYDTEVFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLV 290
Db 240 GTTASDNVDFVRTYDTEVFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLV 299
Qy 291 GKDKGENSSDDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVT 350
Db 300 GKDKGENSSDDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVT 359
Qy 351 ASGKGTATVSKDDQGNITVYDVNVGDALNVQNSGWNLDKAVAGSSGKVISGNVS 410
Db 360 ASGKGTATVSKDDQGNITVYDVNVGDALNVQNSGWNLDKAVAGSSGKVISGNVS 419
Qy 411 PSKGKMDETVNIAGNTEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLVSDGDALNV 470
Db 420 PSKGKMDETVNIAGNTEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLVSDGDALNV 479
Qy 471 GSKKDNKPVRTITNVAPGVKEGDTNVAQLKGVAQNLRNDVNGNARAGIAQAIATAGL 530
Db 480 GSKDANKPVRTITNVAPGVKEGDTNVAQLKGVAQNLRNDVNGNARAGIAQAIATAGL 539
Qy 531 VQAYLPKGSMAAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQ 590
Db 540 VQAYLPKGSMAAIGGGTYRGEAGYAGYSSISDGGNIIKGTASGNSRGHFGASASVGYQ 599
Qy 591 W 591
Db 600 W 600

RESULT 7
Q93QY4 PRELIMINARY; PRT; 594 AA.
AC Q93QY4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DR 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
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01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE NHHA OUTER MEMBRANE PROTEIN.  
 GN NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=EG327;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 membrane protein of Neisseria meningitidis."  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157605; AAK68866.1; -;  
 SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 91.3%; Score 2739.5; DB 2; Length 594;  
 Best Local Similarity 91.8%; Pred. No. 5.5e-108;  
 Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;

QY 1 MNEILRIIWSALNANWVVSSELTRNHTKRASATVKTAVLATLLFATVOASANNEEQEEDL 60  
 DB 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVKTAVLATLLFATVOASTTD---DDDL 57  
 QY 61 YLDPVLRITVAVLIVNSDKGTGEGEKEVEENSDWAVYNEKGVLTAREITLTKAGDNLKIK 120  
 DB 58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNMGVYFDKKGVLTAGTITLTKAGDNLKIK 116  
 QY 121 -----NGTFTVSLKKDLTDLTSVGTPEKLSFANGKNVNTSDTKGLNFAKETAGTNGD 174  
 DB 117 NTNENTNASSFTVSLKKDLTDLTSVGTPEKLSFANGKNVNTSDTKGLNFAKTAETNGD 176  
 QY 175 TTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 234  
 DB 177 TTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 236  
 QY 235 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDGKLVTKGDK 294  
 DB 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDGKLVTKGDK 296  
 QY 295 GENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFETVTSCTNVTFSAGK 354  
 DB 297 GENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFETVTSCTNVTFSAGK 356  
 QY 355 GTTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414  
 DB 357 GTTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
 QY 415 KMDETVMINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSK 473  
 DB 417 KMDETVMINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDGDEGALNVGSK 476  
 QY 474 KDNKPVRTITNVPAGVKEGDTNVAQLKGVAQNLRNIDNDVGNARAGIAQAIAIATAGLVQA 533  
 DB 477 DANKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNIDNDVGNARAGIAQAIAIATAGLVQA 536  
 QY 534 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKTASGNSRGRHFGASASVGYQW 591  
 DB 537 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKTASGNSRGRHFGASASVGYQW 594

RESULT 8  
 Q9JPS2 PRELIMINARY; PRT; 594 AA.  
 ID Q9JPS2  
 AC Q9JPS2  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OX NCBI\_TaxID=487;  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=EG31;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broecker M., Hurdtt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226379; AAF42528.1; -;  
 SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 91.1%; Score 2732.5; DB 2; Length 594;  
 Best Local Similarity 91.6%; Pred. No. 1.1e-107;  
 Matches 548; Conservative 14; Mismatches 25; Indels 11; Gaps 4;

QY 1 MNEILRIIWSALNANWVVSSELTRNHTKRASATVKTAVLATLLFATVOASANNEEQEEDL 60  
 DB 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVKTAVLATLLFATVOASTTD---DDDL 57  
 QY 61 YLDPVLRITVAVLIVNSDKGTGEGEKEVEENSDWAVYNEKGVLTAREITLTKAGDNLKIK 120  
 DB 58 YLEPVQRTAVVLSFRSDKEGTGEKE-VTEDSNMGVYFDKKGVLTAGTITLTKAGDNLKIK 116  
 QY 121 -----NGTFTVSLKKDLTDLTSVGTPEKLSFANGKNVNTSDTKGLNFAKETAGTNGD 174  
 DB 117 NTNENTNASSFTVSLKKDLTDLTSVGTPEKLSFANGKNVNTSDTKGLNFAKETAGTNGD 176  
 QY 175 TTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 234  
 DB 177 TTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 236  
 QY 235 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDGKLVTKGDK 294  
 DB 237 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDGKLVTKGDK 296  
 QY 295 GENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFETVTSCTNVTFSAGK 354  
 DB 297 GENGSSDDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFETVTSCTNVTFSAGK 356  
 QY 355 GTTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 414  
 DB 357 GTTATVSKDQGNITVMYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
 QY 415 KMDETVMINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDG-ALNVGSK 473  
 DB 417 KMDETVMINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLVSVDGDEGALNVGSK 476  
 QY 474 KDNKPVRTITNVPAGVKEGDTNVAQLKGVAQNLRNIDNDVGNARAGIAQAIAIATAGLVQA 533  
 DB 477 DANKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNIDNDVGNARAGIAQAIAIATAGLVQA 536  
 QY 534 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKTASGNSRGRHFGASASVGYQW 591  
 DB 537 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKTASGNSRGRHFGASASVGYQW 594

RESULT 9  
 Q9JPI3 PRELIMINARY; PRT; 594 AA.  
 ID Q9JPI3  
 AC Q9JPI3  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.



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QY 534 YLPKGSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASNSRGRHFGASASVGQW 591
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Db 537 YLPKGSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASNSRGRHFGASASVGQW 594
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RESULT 11
QJUPR9
ID QJUPR9 PRELIMINARY; PRT; 598 AA.
AC QJUPR9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226382; AAF42531.1; -.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 90.7%; Score 2719.5; DB 2; Length 598;
Best Local Similarity 91.0%; Pred. No. 3.8e-107;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

QY 1 MNEILRIIWSALNAWVVSSELTNRHTKRASATVATVATLTLFATVQASANNEOEEDL 60
|||:|||||
Db 1 MNKIRIIWSALNAWVVSSELTNRHTKRASATVATVATLTLFATVQANATD---DDDL 57
|||:|||||

QY 61 YLDPVLRVAVLIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
|||:|||||
Db 58 YLEPVQRTAVLVISFRSDKEGTEGEGED-SNWAYVFEKRVLKAGAITLKAGDNLKIQ 116
|||:|||||

QY 121 -----NCTNFTYSLKDLTDLTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAG 170
|||:|||||
Db 117 NTNENTNENTDSSEFTYSLKDLTDLTSVETSEKLSFGANGKNVNTSDTKGLNFAKETAG 176
|||:|||||

QY 171 TNGDPTVHLNGIGSTLTDPLLTGATTNTVNDVTDDEKKRAASVKDVLNAGNKGKVP 230
|||:|||||
Db 177 TNGDPTVHLNGIGSTLTDPLLTGATTNTVNDVTDDEKKRAASVKDVLNAGNKGKVP 236
|||:|||||

QY 231 GTTASNDVDFVRYDVEFLSADTKTTTVNVEKDKNGKTEVIGAKTSVIEKDGKLV 290
|||:|||||
Db 237 GTTASNDVDFVRYDVEFLSADTKTTTVNVEKDKNGKTEVIGAKTSVIEKDGKLV 296
|||:|||||

QY 291 GKDKGENSGSTDEGGLVTAKEVIDAVNKGWRMKTNTTANGOTQADKFTVTSGTNVTF 350
|||:|||||
Db 297 GKDKGENSGSTDEGGLVTAKEVIDAVNKGWRMKTNTTANGOTQADKFTVTSGTNVTF 356
|||:|||||

QY 351 ASGKGTATVSKDDQGNITVYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVS 410
|||:|||||
Db 357 ASGKGTATVSKDDQGNITVYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVS 416
|||:|||||

QY 411 PSKGMDETIVNAGNIIETRNKNIDTATSWTQFSSVSLGAGADAPTLSDG-D-ALN 469
|||||
Db 417 PSKGMDETIVNAGNIIETRNKNIDTATSWAQQFSSVSLGAGADAPTLSDVDEGALN 476
|||||

QY 470 VGSKDNKPKVRTITNVPAGYKGDVTNVAQLKGVAQNLNRRIDNVGNAAGIAQATAG 529
|||||
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Db 477 VGSKDNKPKVRTITNVPAGYKGDVTNVAQLKGVAQNLNRRIDNVGNAAGIAQATAG 536
QY 530 LYQAVLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASNSRGRHFGASASVG 589
|||||
Db 537 LYQAVLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASNSRGRHFGASASVG 596
|||||

QY 590 QW 591
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Db 597 QW 598
|||

RESULT 12
QJUPTO
ID QJUPTO PRELIMINARY; PRT; 598 AA.
AC QJUPTO;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226359; AAF42508.1; -.
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match 90.2%; Score 2706.5; DB 2; Length 598;
Best Local Similarity 90.4%; Pred. No. 1.3e-106;
Matches 544; Conservative 14; Mismatches 29; Indels 15; Gaps 4;

QY 1 MNEILRIIWSALNAWVVSSELTNRHTKRASATVATVATLTLFATVQASANNEOEEDL 60
|||:|||||
Db 1 MNKIRIIWSALNAWVVSSELTNRHTKRASATVATVATLTLFATVQANATD---DDDL 57
|||:|||||

QY 61 YLDPVLRVAVLIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIQ 120
|||:|||||
Db 58 YLEPVQRTAVLVISFRSDKEGTEGEGED-SNWAYVFEKRVLKAGAITLKAGDNLKIQ 116
|||:|||||

QY 121 -----NCTNFTYSLKDLTDLTSVGTSEKLSFANGKNVNTSDTKGLNFAKETAG 170
|||:|||||
Db 117 NTNENTNENTDSSEFTYSLKDLTDLTSVETSEKLSFGANGKNVNTSDTKGLNFAKETAG 176
|||:|||||

QY 171 TNGDPTVHLNGIGSTLTDPLLTGATTNTVNDVTDDEKKRAASVKDVLNAGNKGKVP 230
|||:|||||
Db 177 TNGDPTVHLNGIGSTLTDPLLTGATTNTVNDVTDDEKKRAASVKDVLNAGNKGKVP 236
|||:|||||

QY 231 GTTASNDVDFVRYDVEFLSADTKTTTVNVEKDKNGKTEVIGAKTSVIEKDGKLV 290
|||:|||||
Db 237 GTTASNDVDFVRYDVEFLSADTKTTTVNVEKDKNGKTEVIGAKTSVIEKDGKLV 296
|||:|||||

QY 291 GKDKGENSGSTDEGGLVTAKEVIDAVNKGWRMKTNTTANGOTQADKFTVTSGTNVTF 350
|||:|||||
Db 297 GKDKGENSGSTDEGGLVTAKEVIDAVNKGWRMKTNTTANGOTQADKFTVTSGTNVTF 356
|||:|||||

QY 351 ASGKGTATVSKDDQGNITVYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVS 410
|||:|||||
Db 357 ASGKGTATVSKDDQGNITVYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVS 416
|||:|||||
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	QY	411	PSGKWDVTVINAGNNIEITRNKKIDTATSMTPQFSSVSICAGADAPTLSDVDG-ALN 469 
	Db	417	PSGKWDVTVINAGNNIEITRNKKIDTATSMTPQFSSVSICAGADAPTLSDVDGALN 476 
	QY	470	VGSKDKNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRNRIDNVGNARAGIAQAATAG 529 
	Db	477	VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRNRIDNVGNARAGIAQAATAG 536 
	QY	530	LVOAYLPGRKSMAIGGGTYRGEAGYAIGYSISSDGCNWIIKTASNSRGHFCASAVGY 589 I
	Db	537	LAQAYLPGRKSMAIGGGTYRGEAGYAIGYSISDTGWNVIKGTASNSRGHGTSASVGY 596 I
	QY	590	QW 591 
	Db	597	QW 598 
		RESULT 13	
		Q9JPSO	
	ID	Q9JPSO PRELIMINARY; PRT;	598 AA.
	AC	Q9JPSO;	
	DC	01-OCT-2000 (TrEMBLrel. 15, Created)	
	DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)	
	DF	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)	
	DE	OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).	
	OS	GNA992 OR NHHA.	
	OX	Neisseria meningitidis.	
	OX	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.	
	OC	NCBI_TaxID=487;	
	RN	[1]	
	RP	SEQUENCE FROM N.A.	
	RC	STRAIN-NGH15;	
	RX	MEDLINE=20175756; PubMed=10710308;	
	RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,	
	RA	Camanducci M., Jennings G.T., Baldi L., Bartolini E., Capeccihi B.,	
	RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,	
	RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,	
	RA	Broecker H., Huudt E., Knapp B., Blair E., Mason T., Rettelin H.,	
	RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,	
	RA	Moxon E.R., Grandi G., Rappuoli R.;	
	RT	"Identification of Vaccine Candidates Against Serogroup B	
	RT	Meningococcus by Whole-Genome Sequencing.";	
	RM	Science 287:1816-1820(2000).	
	RN	[2]	
	RP	SEQUENCE FROM N.A.	
	RC	STRAIN=HI5;	
	RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;	
	RA	"Identification and characterization of a gene encoding a novel outer	
	RL	membrane protein of Neisseria meningitidis";	
	RT	Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.	
	DR	EMBL; AF26381; AAF42530.1; -.	
	DR	EMBL; AF157607; AAK68868.1; -.	
	SQ	SEQUENCE 598 AA; 62763 MW; EC67AE0FB8A63CB CRC64;	

	Query Match	90.2%	Score 2706.5;	DB 2;	Length 598;
	Best Local Similarity	90.5%;	Pred. No. 1.3e-106;		
	Matches 545; Conservative	13;	Mismatches 29;	Indels 15;	Gaps 4;
QY	1 MNEILRIWNSALNAAVVVSELTRNHHTKRASATVKVTAVLATLFLFATVOASANNEQEEDL	60			
	: :	:			
Dd	1 MNKIYRIIWNLSALNAAVVVSELTRNHHTKRASATVATAVLATLFLFATVOANATD--DDDL	57			
	:	:			
QY	61 YLDPLRTVAVLIVNSDKETGEKEKVEEVSNDWAAYNEKGVLTARETTLKAGDNLLTKQ	120			
	:	:			
Dd	58 YLEPVQTAVVLSPRSDEGTGEGECTED-SNAVVFDEKKVKAGAITLKAGDNLLTKQ	116			
	:	:			
QY	121 -----NGNTFTYSCLKDLTDLTSVGTEKLSPFSANGKNVNITSDTGKLNFAKETAG	170			
	:	:			
Dd	117 NTNETMNTENTNDSSFTYSLKKDLTDLTSVETEKLSPFGANGKNVNITSDTGKLNFAKETAG	176			
QY	171 TNGDTTVHLHIGISTGLTDTLTLCATGNVTNMNDNYTDDEKKRAASVKDVNLNAGWIINKGVP	230			

Db	177	TNGDPTVHLNGIGSTLTDFLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGWNKGVKP	236
Qy	231	GTTSADNVDFVRTYDVTVEFLSADTKTTTVNVEKDNKGKKTEVKIGAKTSVKEKDGKLVY	290
Db	237	GTTSADNVDFVRTYDVTVEFLSADTKTTTVNVEKDNKGKKTEVKIGAKTSVKEKDGKLVY	296
Qy	291	GKDKGENSSSTDEGEGLVTAKEVIDAVNKGAGWRMKTTTANGQTGQADKFETVTSGTNVTF	350
Db	297	GKDKGENSSSTDEGEGLVTAKEVIDAVNKGAGWRMKTTTANGQTGQADKFETVTSGTNVTF	356
Qy	351	ASGKGTATYTSKDDQGNITVWYDVNVGCDALNVNQLNSGNWLDKSAVGSSGKVISGNVS	410
Db	357	ASGKGTATYTSKDDQGNITVWYDVNVGCDALNVNQLNSGNWLDKSAVGSSGKVISGNVS	416
Qy	411	PSKGMDETNNIAGNNIEITRNGKNIDIAATMTPTQFSSVSLGAGADAPTLSVDGDP-ALN	469
Db	417	PSKGMDETNNIAGNNIEITRNGKNIDIAATMTPTQFSSVSLGAGADAPTLSVDGDEGALN	476
Qy	470	VGSKDKDKPVRIITNVAPGVKEGDVTNVQAQLGVAQLNNRINDVDCGNARAGIAQAIAATAG	529
Db	477	VGSKDANKPVRIITNVAPGVKEGDVTNVQAQLGVAQLNNRINDVDCGNARAGIAQAIAATAG	536
Qy	530	LVQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRGHFGASASVGY	589
Db	537	LAQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGTGNWVIKGTASGNSRGHFGASASVGY	596
Qy	590	QW 591	
Db	597	QW 598	
RESULT 14			
Q93QY5	PRELIMINARY; PRT; 598 AA.		
AC	Q93QY5; 598 AA.		
AD	Q93QY5; 598 AA.		
DT	01-DEC-2001 (TrEMBLrel. 19, Created)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last sequence update)		
DT	01-DEC-2001 (TrEMBLrel. 19, Last annotation update)		
DE	NHHA OUTER MEMBRANE PROTEIN.		
GN	NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=B210;		
RA	Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer		
RT	membrane protein of Neisseria meningitidis";		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
RQ	EMBL; AF157603; AAK68864.1; -		
SR	SEQUENCE 598 AA; 626167 MW; 18CFF66140A15DF CRC64;		

Query Match	90.2%	Score	2705.5	DB 2	Length	598			
Best Local Similarity	90.4%	Pred. No.	1.5e-106						
Matches	544	Conservative	14	Mismatches	29	Indels	15	Gaps	4
Qy	1	MNEILRIIWNALSALNAAVVVSELTNHHTKRASATVKTAVLATLLEATVQASANNEEQEDL	60						
Db	1								
	1	MNKLSRIIWNALSALNAAVVVSELTNHHTKRASATVATVATLLEATVQANATD	---	DDDL	57				
Qy	61	YLDPLVTRVAVLIWNSDKEGTGEKKEVENSDDWAVYNEKGVLTRAREITLKAGNLNLIKQ	120						
Db	58	YLEPQVTRAVVLSFRSDKEGTGEKGTED-SNWAVYFDEKRVLKAGATTLKAGNLNLIKQ	116						
Qy	121	-----NGTNTFVSLKKDLTDLTSVGTGKLSFGANGNKVNITSDTKGLNFAKETAG	170						
Db	117	NTNENTNNTNDSFTVSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAG	176						
Qy	171	TNGDPTVHLNGIGSTLTDTLTNTGATTNVTNDNTVDTDEKKRAASVKDVLNAGNWKGVKP	230						
Db	177	TNGDPTVHLNGIGSTLTDTLTNTGATTNVTNDNTVDTDEKKRAASVKDVLNAGNWKGVKP	236						



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QY 231 GTTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDGKLT 290
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Db 237 GTTASDNVDFVRYDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDGKLT 296
|||||
QY 291 GKDKGSGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFPETVTSGTNVT 350
|||||
Db 297 GKDKGSGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFPETVTSGTNVT 356
|||||
QY 351 ASGKGTATVSKDDGNTITVMYDVNVDALNVQNSGNWLDKAVAGSSGKVISGNVS 410
|||||
Db 357 ASGKGTATVSKDDGNTITVMYDVNVDALNVQNSGNWLDKAVAGSSGKVISGNVS 416
|||||
QY 411 PSKGMDETNNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDGD-ALN 469
|||||
Db 417 PSKGMDETNNINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSVDDEGALN 476
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QY 470 VGSKDKNKPVRITNTVAPGVKEGDTNVAQLKGVAQNLRIDNVGNARAGIAQAATAG 529
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Db 477 VGSKDKNKPVRITNTVAPGVKEGDTNVAQLKGVAQNLRIDNVGNARAGIAQAATAG 536
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QY 530 LVOAYLPGKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGFCASASVGY 589
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Db 537 LQAVYLPKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGFCASASVGY 596
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Db 597 QW 598

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AC QJPR8.
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).
GN GNA992 OR NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20175756; PubMed=10710308;
RA Piza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=H38;
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
RT membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF226383; AAF42532.1; -.
DR EMBL: AF157608; AAK6869.1; -.
SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;
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Query Match 89.2%; Score 2676; DB 2; Length 599;
Best Local Similarity 89.0%; Pred. No. 2.6e-105;
Matches 536; Conservative 18; Mismatches 34; Indels 14; Gaps 4;
QY 1 MNEILRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEE 60
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Db 60 -LEPVVRSALVIOFMIDKEGNGENEST-CNIGWSIYYDNNHTLHGATVTLTKAGDNLIKIK 117
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QY 121 -----NGTNFTYSLKDKDLTSLTSVTEKLSFANGKNVITSDTKGLNFAKETAG 170
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Db 118 NTNKNWNTNDSPTYSLLKDLTSLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 177
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QY 171 TNGDVTTHLNGIGSTLTDLLNTGATTNTNDVDDKRAASVKDVLNAGNNIKGVKP 230
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QY 470 VGSKDKNKPVRITNTVAPGVKEGDTNVAQLKGVAQNLRIDNVGNARAGIAQAATAG 529
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QY 530 LVOAYLPGKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGFCASASVGY 589
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Db 538 LVOAYLPGKSMMAIGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGFCASASVGY 597
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QY 590 QW 591
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Db 598 QW 599
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Search completed: July 3, 2002, 08:28:45  
Job time: 1166 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:09:07 ; Search time 168.6 Seconds  
(without alignments)  
389.351 Million cell updates/sec

Title: US-09-771-382-5  
Perfect score: 2999  
Sequence: 1 MNEILRIIMNSALNANWYVS.....TASGNSRGHCASASVGYQW 591

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

- 1: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1980.DAT:\*
- 2: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1981.DAT:\*
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- 5: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1984.DAT:\*
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- 11: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA1990.DAT:\*
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- 22: /SIDSL/gcgdata/hold-geneseq/geneeqp-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2999	100.0	591	20	AAV23741
2	2999	100.0	591	22	AAU06175
3	2984	99.5	591	20	AAV27202
4	2984	99.5	591	20	AAV23746
5	2984	99.5	591	22	AAU06171
6	2958	98.6	591	21	AAV57045
7	2952.5	98.4	592	20	AAV23737
8	2739.5	91.3	594	21	AAV23740
9	2739.5	91.3	594	21	AAV57044
10	2739.5	91.3	594	22	AAU06174
11	2721.5	90.7	594	20	AAV23739

12	2721.5	90.7	594	22	AAU06179	N. meningitidis BZ
13	2706.5	90.2	598	20	AAV23742	A surface protein
14	2706.5	90.2	598	22	AAU06177	N. meningitidis H1
15	2705.5	90.2	598	20	AAV23738	A surface protein
16	2705.5	90.2	598	22	AAU06178	N. meningitidis BZ
17	2676	89.2	599	20	AAV23743	A surface protein
18	2676	89.2	599	22	AAU06176	N. meningitidis H3
19	2554.5	85.2	592	20	AAV23744	A surface protein
20	2554.5	85.2	592	22	AAU06172	N. meningitidis H4
21	2538.5	84.6	512	22	AAU06182	N. meningitidis PM
22	2467	82.3	589	20	AAV23745	A surface protein
23	2467	82.3	589	22	AAU06173	N. meningitidis P2
24	2447.5	81.6	502	22	AAU06186	N. meningitidis PM
25	2445.5	81.5	592	22	AAU06180	N. meningitidis Z2
26	2416.5	80.6	592	20	AAV27203	Amino acid sequenc
27	2395	79.9	513	22	AAU06183	N. meningitidis H4
28	2230.5	74.4	604	22	AAU06181	N. meningitidis su
29	2096	69.9	433	22	AAU06185	N. meningitidis PM
30	1949	65.0	407	22	AAU06184	N. meningitidis PM
31	1245	41.5	2411	21	AAV23860	Haemophilus influe
32	1243	41.4	2353	17	AAV23857	Haemophilus influe
33	1221	40.7	245	20	AAV27201	Amino acid sequenc
34	1064.5	35.5	1094	21	AAV23858	Haemophilus influe
35	1054.5	35.2	1098	17	AAV23859	Haemophilus influe
36	985	32.8	679	21	AAV23855	Haemophilus influe
37	985	32.8	679	21	AAV23857	Haemophilus influe
38	749.5	25.0	1004	21	AAV23854	Haemophilus influe
39	738.5	24.6	1002	21	AAV23854	Haemophilus influe
40	694.5	23.2	1104	21	AAV23856	Haemophilus influe
41	694.5	23.2	1104	21	AAV23859	Haemophilus influe
42	600	20.0	116	21	AAV23832	Neisseria meningitidis
43	390.5	13.0	1778	22	AAV23877	Neisseria meningitidis
44	388	12.9	2314	22	AAV23877	Neisseria meningitidis
45	381.5	12.7	2053	22	AAV23877	Neisseria meningitidis

## ALIGNMENTS

RESULT 1

AAV23741 standard; Protein; 591 AA.

AAV23741:

08-SEP-1999 (first entry)

A surface protein of Neisseria meningitidis.

Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.

Neisseria meningitidis.

OS Neisseria meningitidis.

PN WO931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998: 98WO-AU01031.

PK 12-DEC-1997: 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PI (UYOU) UNIT QUEENSLAND.

Jennings MP, Moxon ER, Peak IRA; WPI, 1999-418754/35.

N-PSDB: AAV85793.

Neisseria meningitidis surface proteins useful for treating N. meningitidis infections



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OY 1 MNEILRIIWNLSALNMAWVVSSELTNRHTRASATVKTAVLATLTFATVQASANNEOEEDL 60
DB 1 meilirilinsalnawvvseltlrnhtrkrasatvtktavlatllfatvgasanneegee1 60
OY 61 YLDPVLRTAVLILVNSDKGEGEKEKEVEENSDMAVVFENEKGYLTAREITLKAGDNLIKIKO 120
DB 61 yldpvlrtavilivnsdkegekekeveensdwayvfnekgyltarelilkgadnlikixq 120
OY 121 NCTNPFYSLKQDLTDTSVGTGTEKLSFANGKNVNTISDPTKGLNFAKETAGTNGDTTVHLN 180
DB 121 nctnfyfslkqdltdtstgteklsfsangknvnitstdptkglnfaketagtngdtvhl 180
OY 181 GIGSTLTDLTLMTGATTNTNNDVTDDEKKRAASVADVNAGMNIGKVPGETTASDNVDF 240
DB 181 gigtstldtldtlmtgattntnndvtddekkraasvadvnagmnikgvpgettasdnvdf 240
OY 241 VRTYDVEFLSADTKTTTNNVESKDKGKTEYKIGAKTSVIREKDKLVTGDKGENGSS 300
DB 241 vrtydveflsadtktttnnveskdngkkteyvigaktsvirekdglvtgdkgenngss 300
OY 301 TDEGEGLYTAKEVIDAVNKAAGWRMKTATTANGOTGADEFTVTSCTNVPFASGKGTATV 360
DB 301 tdegegliytakevldavnkagwrmtktattangotgadefvtsctnvpfasgkgtatv 360
OY 361 SKDDGNTITVMYDVNVDALNNQLONSGMNLSKAVAGSSGKVIISGNVSPSKGKDETV 420
DB 361 skddgntitvmymdvngdallnnqlnsgwnlidskavagssgkvisgnvpskymde 420
OY 421 NINAGNNIEITRGNKIDATSMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKNPPV 480
DB 421 ninagnnieitrngknidatmtptofssvslgagadaptlisvdgalnvgskkdknp 480
OY 481 ITNNVAPGVKESDVTNVAOLKGYAQNLNRIIDVNDGNAKAGIAQAIATAGLVQATLPKGS 540
DB 481 itnnvapgvkesdvtvnvaqlkgyaqnlmriddvndgnaragiagaiaataglvqaylp 540
OY 541 MAIGGTYRGEAGYAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYQW 591
DB 541 maiggtyrgeagyalgyssisdgmwilkgtasgnsrghfgasasvgyqw 591

RESULT 3
AAV27202
ID AAV27202 standard; Protein: 591 AA.
XX
AC AAV27202;
XX
DT 24-SEP-1999 (first entry)
XX
DE Amino acid sequence of N. meningitidis protein ORF40-1.
XX
KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
XX
OS Neisseria meningitidis.
XX
PN WO936544-A2.
XX
PD 22-JUL-1999.
XX
PF 14-JAN-1999; 99WO-IB00103.
XX
PR 09-OCT-1998; 98GB-0022143.
XX
PR 14-JAN-1998; 98GB-0000760.
XX
PR 01-SEP-1998; 98GB-0019015.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Masiagnani V, Piazza M, Rappuoli R, Scarlato V;
XX
DR WPI; 1999-444400/37.
XX
DR N-PSDB; AAX99124.
XX
```

```
PT New protein and its nucleotide sequence, useful in vaccines or
PT diagnostic compositions for treating and/or preventing Neisseria
PT meningitidis infections
XX
PS Claim 1; Page 62; 123pp; English.
XX
CC The invention provides proteins (AAV27201-245) from Neisseria
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
CC encoding the proteins. Compositions comprising the protein, nucleic acid
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a
CC vaccine composition or a diagnostic composition. The composition is also
CC useful for treating or preventing an infection due to Neisseria
CC bacteria, especially Neisseria meningitidis.
XX
SQ Sequence 591 AA:

Query Match 99.5%; Score 2984; DB 20; Length 591;
Best Local Similarity 99.5%; Pred. No. 4.5e-168;
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MNEILRIIWNLSALNMAWVVSSELTNRHTRASATVKTAVLATLTFATVQASANNEOEEDL 60
DB 1 mneilirilinsalnawvvseltlrnhtrkrasatvtktavlatllfatvgasanneegee1 60
OY 61 YLDPVLRTAVLILVNSDKGEGEKEKEVEENSDMAVVFENEKGYLTAREITLKAGDNLIKIKO 120
DB 61 yldpvlrtavilivnsdkegekekeveensdwayvfnekgyltarelilkgadnlikixq 120
OY 121 NCTNPFYSLKQDLTDTSVGTGTEKLSFANGKNVNTISDPTKGLNFAKETAGTNGDTTVHLN 180
DB 121 nctnfyfslkqdltdtstgteklsfsangknvnitstdptkglnfaketagtngdtvhl 180
OY 181 GIGSTLTDLTLMTGATTNTNNDVTDDEKKRAASVADVNAGMNIGKVPGETTASDNVDF 240
DB 181 gigtstldtldtlmtgattntnndvtddekkraasvadvnagmnikgvpgettasdnvdf 240
OY 241 VRTYDVEFLSADTKTTTNNVESKDKGKTEYKIGAKTSVIREKDKLVTGDKGENGSS 300
DB 241 vrtydveflsadtktttnnveskdngkkteyvigaktsvirekdglvtgdkgenngss 300
OY 301 TDEGEGLYTAKEVIDAVNKAAGWRMKTATTANGOTGADEFTVTSCTNVPFASGKGTATV 360
DB 301 tdegegliytakevldavnkagwrmtktattangotgadefvtsctnvpfasgkgtatv 360
OY 361 SKDDGNTITVMYDVNVDALNNQLONSGMNLSKAVAGSSGKVIISGNVSPSKGKDETV 420
DB 361 skddgntitvmymdvngdallnnqlnsgwnlidskavagssgkvisgnvpskymde 420
OY 421 NINAGNNIEITRGNKIDATSMTPOFSSVSLGAGADAPTLISVDGALNVGSKKDKNPPV 480
DB 421 ninagnnieitrngknidatmtptofssvslgagadaptlisvdgalnvgskkdknp 480
OY 481 ITNNVAPGVKESDVTNVAOLKGYAQNLNRIIDVNDGNAKAGIAQAIATAGLVQATLPKGS 540
DB 481 itnnvapgvkesdvtvnvaqlkgyaqnlmriddvndgnaragiagaiaataglvqaylp 540
OY 541 MAIGGTYRGEAGYAIGYSSISDGMWIIKGTASGNSRGHFGASASVGYQW 591
DB 541 maiggtyrgeagyalgyssisdgmwilkgtasgnsrghfgasasvgyqw 591

RESULT 4
AAV23746
ID AAV23746 standard; Protein: 591 AA.
XX
AC AAV23746;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
DR Surface protein; surface glycoprotein; infection; vaccine;
XX
```

KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
XX (UYOU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI: 1999-418754/35.  
DR N-PSDB: AAX85798.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1: Page 127-128; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA:

Query Match 99.5%; Score 2984; DB 20; Length 591;  
Best Local Similarity 99.5%; Pred. No. 4,5e-168;  
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIIWSALNANWVSELTNRHTRKASATVKTAVLATLLEFPTVOASANNEOEEDL 60  
DB 1 mkkiyriiwnsalnawvsseltrnhtrkasatvktavlatllefptvoasanneegee 60  
QY 61 YIDPLRLVAVLIIVSDKEGEGEKEVENSMDAYFNEKGLTARETTIKAGDLKIKQ 120  
DB 61 yldpqrtrvaavliivnsdkegegekevensmdawayfnekgytarelitlkagdnkikq 120  
QY 121 NGNTFYSLKRDLDLTSGTEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTVHLN 180  
DB 121 ngntfyslkrdldltsgteklsfsangknvntsdtkglnfaketagtngdttvhl 180  
QY 181 GIGSLFLDTLNTGATFNTVNDVTDDEKKRAASVKDVLNAGMNKGVKPGTTASDNVDF 240  
DB 181 gisglfldtlntgatfntvndvtddekkraasvkdvlnagmnkgykpgttasdnvdf 240  
QY 241 VRTYTFVEFLSADTKTTVNVESKNGKTEYKIGAKTSYIKERKGLVTKGDKENGSS 300  
DB 241 vrtytvfeplsadtktttvnnveskngkteykigaktstykergkglvtgdkengss 300  
QY 301 TDEGGLVTAKEVIDAVNKAQRMAKTTTANGOTGOADKFEETVTSCTNVTFFASGKTATV 360  
DB 301 tdegglvtakevidavnkagrmaktttangotgoadkfeetvtsctnvtffasgkttatv 360  
QY 361 SKDDOGNTTVMVDVNVGDALNVNOLONGWINDSKAVAGSSGKVIISGNVSPSKGMDETV 420  
DB 361 skddognnttvmvdvnnvgdalanvnolongswnidskavagssgkviisgnvspkgmdetv 420  
QY 421 NINAAGNNEITRTNGKNIDIAITMTPOFSSVSLGAGADAPLTSLVDGDALVSGSKKNKPPR 480  
DB 421 ninaagnneitrtngknidiatmtmpofssvslgagadapltslvddalnvsgskknpvr 480

QY 481 ITNVAQVKEGDVNTVAQLKVAQNLNNRIDNVGNARAGIAQIATAGLVQAVLPGKSM 540  
DB 481 itnvapvkegdvntvvaqlkvagqnlmnridnvgnaragiagiataglvqaylpgksm 540  
QY 541 MAIGGTYRGAGYAIIGSSISDGNMIIKGTASGNSNGHFGASASVGYQW 591  
DB 541 maiggtyrgaayaiigyssisdgnmwlikgtasgnsrghfgasasvgyqw 591

RESULT 5  
ID AAU06171 standard; Protein; 591 AA.  
AC AAU06171;  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain PMC21.  
XX  
FH Location/Qualifiers  
FT Peptide  
FT /label= Signal\_peptide  
FT 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..108  
FT /label= V1  
FT /note= "Variable region 1"  
FT 52..591  
FT /label= Mature\_Nhha  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12."  
FT 109..120  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 121..124  
FT /label= V2  
FT /note= "Variable region 2"  
FT 125..188  
FT /label= C3  
FT /note= "Conserved region 3"  
FT 189..210  
FT /label= V3  
FT /note= "Variable region 3"  
FT 211..229  
FT /label= C4  
FT /note= "Conserved region 4"  
FT 230..236  
FT /label= V4  
FT /note= "Variable region 4"  
FT 237..591  
FT /label= C5  
FT /note= "Conserved region 5"

WO200155182-A1.  
02-AUG-2001.  
XX  
PD 25-JAN-2001; 2001WO-AU00069.  
XX  
PE 25-JAN-2000; 2000US-0177917.  
PR  
XX (UYOU ) UNIV QUEENSLAND.  
XX  
PA Peak IRA, Jennings MP;  
XX  
PI WPI: 2001-488774/53.  
DR N-PSDB: AAS09161.

XX New Nhma surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis .  
 XX  
 XX  
 PS Claim 9: Fig 1: 91pp: English.

CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhma  
 CC (AAU06182-AAU06186). The modified or mutant Nhma polypeptides are  
 CC characterized by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhma  
 CC from N. meningitidis strain PMC21 is 1 of 10 Nhma polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX  
 XX Sequence 591 AA:

Query Match 99.5%; Score 2984; DB 22: Length 591;  
 Best Local Similarity 99.5%; Pred. No. 4, 5e-168;  
 Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEIIRIINSAALNMAVVSSELTNRHTRKASATVKTAVLATLLEFATVQASANNEOEEDL 60  
 DB 1 mmkiryllinsalnawvvseltlrhtrkasatvktavlatllefavqasannegeedl 60  
 QY 61 YLDPVLRVAVLIVNSDKEGTEKEKEVEENSDMAVVFENEKGVLTAREITLKAGDNLKIQ 120  
 DB 61 yldpvrvaavllivnsdkegtekkeveensdwayvfenekgvltareitlkagdnlikiq 120  
 QY 121 NGTNFTYSKAKDLDLTSTGTEKLSFANGKNVNTSDPKGLNFAETAGTNGDTVHLN 180  
 DB 121 ngtnftyslkakldltstgvteklsfsangknvntsdtkglnfaketagntgdltvhl 180  
 QY 181 GIGSTLTDLTLMWAGATTNTNDVTDEKKRASVYKDVNAGNLIKGVPGTASDNVDF 240  
 DB 181 gigtstldtldtlnwagattntndvtdedekkrasvkvdivnagnlikgvpgtasdnvdf 240  
 QY 241 VRTYDVEFLSADTKTTTVNVESEKNGKTEVKGAKTSVIREKDGKLVYTGDKENGSS 300  
 DB 241 vrtydveflsadtktttvnvesekngkktevkgaktsvirekdgklvtgdkengss 300  
 QY 301 TPEGGLVYAKREVIDAVNKAQRMTTANGOTGADKEETVTSCTNVPFASGKTITATV 360  
 DB 301 tpegglvyakrevidavvnkagrmkttanngotgadkeetvtsctnvpfasgkttatv 360  
 QY 361 SKDDGNTIVMVDVNYGDALNNOLNSGMNLSKAVASSGCVISGNTSPSGKMDERY 420  
 DB 361 skddgntivmvdvnygdalnnolnsgmnlsskavassgcvisgntspsgkmdery 420  
 QY 421 NINAGNIEITRNKNIDIAISMTPOFSSVSLGAGADAPLTSLVDSDALNVGSKDKR 480  
 DB 421 ninagnieitrnknidiatismtpofssvslgagadapltslvdsgalnvgsdkdkr 480  
 QY 481 IINVAPGVESGVTNVAQLKGYAQNINNRIDVNDGNARAGIAOATITAGLVQATLFGSK 540  
 DB 481 iinvapgvsgvtvnvaqlkgyaqninnrdivndgnaragiaoatitaglvqatlfpgsk 540  
 QY 541 MAIGGTYGEGAGYAGYSISDGMWIKGTASGNSRGHFGASASVGQW 591  
 DB 541 maiggytygeagyalgysisdgmwilkgtasgnsrghfgasasvgyw 591

RESULT 6  
 AA57045  
 ID AA57045 standard: Protein: 591 AA.

XX  
 AC AA57045;  
 XX  
 DT 21-FEB-2000 (first entry)  
 XX  
 DE BASB029 amino acid sequence from N. meningitidis strain H44/76.  
 XX  
 KW BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
 XX infection; treatment; prevent; antibacterial drug.  
 XX Neisseria meningitidis.

Key Location/Qualifiers  
 FT Misc-difference 90 /note= "Encoded by AAT"  
 FT Misc-difference 92 /note= "Encoded by GAT"  
 FT Misc-difference 98 /note= "Encoded by AAC"  
 FT Misc-difference 108 /note= "Encoded by AATC"  
 FT Misc-difference 123 /note= "Encoded by ACA"  
 FT Misc-difference 269 /note= "Encoded by AAA"  
 FT Misc-difference 389 /note= "Encoded by CGT"

PN W0958683-A2.  
 PD 18-NOV-1999.  
 XX 07-MAY-1999; 99WO-EP03255.  
 PR 13-MAY-1998; 98GB-0010276.  
 XX (SMK ) SMTTKLINE BECHAM BIOLOGICALS.

PI Ruelle J;  
 DR WPI: 2000-053103/04.  
 XX N-PSDB: AA239865.  
 PT New polypeptide from neisseria meningitidis useful for diagnosis,  
 XX treatment or prevention of bacterial infections in mammal

Claim 4: Fig 2: 74pp: English.  
 This is the Neisseria meningitidis BASB029 amino acid sequence from  
 serogroup B strain H44/76. The BASB029 protein is homologous to the  
 Haemophilus influenzae surface fibril (HSF) protein. The invention  
 relates to BASB029 polynucleotide sequences (AA239864-239865) and  
 CC polypeptide sequences (AA57044-Y57045) and their immunogenic fragments.  
 CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
 CC meningitidis infection in a mammal. Compositions containing BASB029  
 CC polynucleotides and polypeptides are useful for generating an immune  
 CC response in an animal. A therapeutic composition comprising an antibody  
 CC directed against BASB029 is useful in treating humans with Neisseria  
 CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
 CC the stage of infection, type of infection, susceptibility to an  
 CC infection which results from increased or decreased expression of the  
 CC polynucleotide, and for therapeutic or prophylactic purposes,  
 CC particularly genetic immunisation. Antibodies against BASB029  
 CC polynucleotides and polypeptides are also useful for treating infections  
 CC particularly bacterial infections. The protein is useful in the  
 CC screening and development of antibacterial drugs. Fused recombinant  
 CC protein is useful for the stimulation of the immune system of an organism  
 CC receiving the protein.

Sequence 591 AA:

Query Match 98.6%; Score 2958; DB 21: Length 591;





XX	DE	A surface protein of <i>Neisseria meningitidis</i> .
XX	KW	Surface protein; surface glycoprotein; infection; vaccine;
XX	KW	Immunoreactive peptide.
XX	OS	<i>Neisseria meningitidis</i> .
XX	PN	WO9931132-A1.
XX	PD	24-JUN-1999.
XX	PF	14-DEC-1998; 98WO-AU01031.
XX	PR	12-DEC-1997; 97GB-0026398.
XX	PA	(ISIS-) ISIS INNOVATION LTD.
XX	PI	(UYOU) UNIV QUEBENS/LAND.
XX	PI	Jennings MP, Moxon ER, Peak IRA;
XX	DR	WPI: 1999-418754/35.
XX	DR	N-PSDB; AAX85792.
XX	PT	<i>Neisseria meningitidis</i> surface proteins useful for treating <i>N.</i>
XX	PT	<i>meningitidis</i> infections
XX	PS	Claim 1; Page 100-101; 132pp; English.
XX	CC	The present sequence represents a surface protein of <i>Neisseria</i>
XX	CC	<i>meningitidis</i> which is approximately 62 kDa. The <i>N. meningitidis</i>
XX	CC	surface glycoproteins, nucleic acids, the primers and optionally
XX	CC	a thermostable polymerase, or antibodies are useful in a kit for
XX	CC	the detection or diagnosis of <i>N. meningitidis</i> infection in humans.
XX	CC	The <i>N. meningitidis</i> surface glycoproteins can also be used to
XX	CC	prevent or treat <i>N. meningitidis</i> infection in humans, especially
XX	CC	in the form of vaccines. The proteins and antibodies can also
XX	CC	be used to identify immunoreactive peptides.
XX	Sequence	594 AA;

Query Match	91.3%	Score 2739.5	DB 20	Length 594
Best Local Similarity	91.8%	Pred. No. 1.2e-153		
Matches	549	Conservative 15	Mismatches 23	Indels 11
				Gaps 4
QY	1	MNEILRIIWSNALNAAVYVSELTFRNHTKRSATVKTAVLATLTLFTVQASANNEDEEDL	60	
Db	1	mkilyrlimsalnawavseltrnhctkraasatavatiatlifavgsttd---dddl	57	
QY	61	YLDPLRLRVAVLVVNSDKEGTGEKKKEVENSWMAYFENKGVLTARETLRKGDNIKKIQ	120	
Db	58	ylpqrqtravavstfsdkegltgeke-vledsmwgyfdkkygltagtllkxgdnlkixq	116	
QY	121	-----NCTNFYSLKRPDLTSTVGTEKLSPSANGKNKNTSPDKGLFAKETAGTND	174	
Db	117	ntnenltnassffyslkkdltdltsygtelktsiansnknrltsdctglnifakktaelngd	176	
QY	175	TTVHLNLTGISTITDPLNLNTGATTNVTNDNVTDDEKKRAASVCDVLNAGNNIKGVPDTTA	234	
Db	177	tlvhlnglsgstltdclntlgatctnndvtddekkraasvcdvlnaagnlkygvpkta	236	
QY	235	SDNVCFVRYTPDVELESDTKTTTNNVESKONGKTEVAKTSTYRKDGKLVYGRGX	294	
Db	237	sdnvcfvrltydclvelelsadctkctlnrvveskadngkrltevkigsaktsvlkkdgkllvygkx	296	
QY	295	GENSSDTDEGELVTAKEVIDAVNRAGWEMKTTTANGQTGAQDKFEPTVTSGTNVPFASQK	354	
Db	297	gensdstdkegelytakaevldavnkagwrmktctlangqygqadkfctvtsyglcnvtfasqk	356	
QY	355	GTTTAVNSDDOQNIIVMDVNYGDLNVNQLONSGNLIDSKRVAVAGSSGKVIAGNVSPSKG	414	
Db	357	gtttavnsddqgnltcmvqnvnygdalnvnyqnlqnsqgnlidskkaavagssgkviagsnvpskg	416	

OY	415	KKDEIVNINAGNNIETRRGKNIDIAATSMTPGESSYSLGAGADAPILSYDGD-ALNWGSK	473
OY	416		
DB	417	Kmdetvlnaagnlietrrgnkndiatstncpqtssvslgagadaprlsyddegaalnvsgk	476
OY	474	KKKKPVRIITNVPAPGVEGDDVTNVAQILGKYGAQNLNINRDIWDVDCNARAGIAQDAITAGLVQA	533
DB	477		
OY	534	YLPKGSMAAIGCGTYRGEAGYVIAIGYSSISDGCNMIITKGASGNSRCHFGASASVGYQW	591
DB	537	YLPKGSmaaiaggctyrgeagyalysysisdggnwilkgtasgnsrghfgasasvgyw	594
RESULT 9			
AAV57044	ID	AAV57044 standard; Protein; 594 AA.	
XX	AC	AAV57044;	
XX	XX	21-FEB-2000 (first entry)	
DE	XX	BASB029 amino acid sequence from N. meningitidis strain ATCC13090.	
XX	XX	BASB029: Neisseria meningitidis; surface fibril protein; HSF; diagnosis;	
KW	XX	infection; treatment; prevent; antibacterial drug.	
OS	XX	Neisseria meningitidis.	
XX	XX	Key	Location/Qualifiers
FT	XX	Misc-difference 104	
FT	XX	/note= "Encoded by AATC"	
PN	XX	WO958683-A2.	
PD	XX	18-NOV-1999.	
PF	XX	07-MAY-1999; 99WO-EP03255.	
PR	XX	13-MAY-1998; 98GB-0010276.	
XX	XX	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.	
PA	XX	Ruelle J;	
PI	XX	WPI; 2000-053103/04.	
DR	XX	N-PSDB; AAZ39864.	
PT	XX	New polypeptide from neisseria meningitidis useful for diagnosis,	
PS	XX	treatment or prevention of bacterial infections in mammal	
XX	XX	Claim 4; Fig 2; 74pp: English.	
XX	XX	This is the Neisseria meningitidis BASB029 amino acid sequence from	
CC	XX	serogroup B strain ATCC13090. The BASB029 protein is homologous to the	
CC	XX	Haemophilus influenzae surface fibril (HSF) protein. The invention	
CC	XX	relates to BASB029 polynucleotide sequences (AAZ39864-739865) and	
CC	XX	BASB029 polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.	
CC	XX	BASB029 polypeptides are useful in a method of diagnosing a Neisseria	
CC	XX	meningitidis infection in a mammal, compositions containing BASB029	
CC	XX	polynucleotides and polypeptides are useful for generating an immune	
CC	XX	response in an animal. A therapeutic composition comprising an antibody	
CC	XX	directed against BASB029 is useful in treating humans with Neisseria	
CC	XX	meningitidis disease. The polynucleotide is useful in the diagnosis of	
CC	XX	the stage of infection, type of infection, susceptibility to an	
CC	XX	infection which results from increased or decreased expression of the	
CC	XX	polynucleotide, and for therapeutic or prophylactic purposes,	
CC	XX	particularly genetic immunisation. Antibodies against BASB029	
CC	XX	polynucleotides and polypeptides are also useful for treating infections	
CC	XX	particularly bacterial infections. The protein is useful in the	
CC	XX	screening and development of antibacterial drugs. Fused recombinant	
CC	XX	protein is useful for the stimulation of the immune system of an organism	
XX	XX	receiving the protein.	



Qy	175	TTVHLNGSGSLPTLNTLNTGATTVNDNTDNDYDEDKRAASVKDVLNKGWNIKVKPPETTA	234
Db	177	ctvhngjgsllctdlntlgatcthvrdntdteekkkrasvkvdlmgawlkyykpgpta	236
Qy	235	SDNVDFVTVTVEFLSADPRTTTVNVESKDNKKEVKGAKTSVIREKDGKLVYTKDK	294
Db	237	sdnvdfvtrtytveflsadekcttctvneskdngrtrtevkigaktsvlkekdgkrlvtgkdk	296
Qy	295	GENSSSIDEGEGLVTAKEVIDAVNKKAGWRMKTTTANGQTQOADKEFTVTSGTNVTFASGK	354
Db	297	gendsltckgeglvtakevidavnkagwrmttltanqgtgackfevtsgtntvtfasgk	356
Qy	355	GTTTATVSKDDCGNTTVWADVNGALVYNOLONSGNMLDSKAVNGSSGKXVTSGNVSPSKG	414
Db	357	gtttatvskddcgnttlvngadvngalvynnglqnsqwnldskavngssgkvtslgnvspskg	416
Qy	415	KMDETVNIAGNNIETIRNGKNIDIAIATSMTPQFSSVSLGAGADAPLTLSVGD-ALANYSK	473
Db	417	kmdeetvniagnnietirngknidietatmsmpqfssvslgagadapltlsvddegallnygsk	476
Qy	474	KDKRPVRTINAVPGVKEGSDVTNVAQLKGVAONLNNRIDNVDGNARAGIAOLAIFAGLVQA	533
Db	477	dankrpvrltnavpgvkegsvtnvaqlkgvvaqnlnnhldvngnaraglaqalafaglvqa	536
Qy	534	YLPKSSMAIIGGTYRCGAGAIATSSISOGGNNIITKGTASGNSRGHFGASASVGYOW	591
Db	537	ylpksmaiaiggtyrcgagaiatssisoggnniitkgtasgnsrgthfgasasvgyow	594

RESULT 11  
AAV23739  
ID AAV23739 standard; Protein; 594 AA

DT 08-SEP-1999 (first entry)

A surface protein of *Neisseria meningitidis*.

**KW** Surface protein; surface glycoprotein; infection; vaccine;  
**KW** immunoreactive peptide.

OS *Neisseria meningitidis*.

PN WO9931132-A1

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

XX

XX

DR N-PSDB; AAX85791.

PT Neisseria meningitidis surface proteins useful for treating N. meningitidis infections

PS Claim 1; Page 95-97; 132pp; English.

CC The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also

CC be used to identify immunoreactive peptides  
XX  
SQ Sequence 594 AA;

Query Match	90.78;	Score 2721.5;	DB 20;	Length 594;
Best Local Similarity	91.68;	Pred. No. 1.3e-152;		
Matches 548;	Conservative 12;	Mismatches 27;	Indels 11;	Gaps 4;

Oy	1	MNEIIRITMNSALNAAWVVSSELTNNHTEKRAATYKTAVLATLLEPATYQASANNDEOED	60
Dd	1	mkklyrllmsalnlawwvvseltlnhckraatatavlatallfatyganaat---dddl	57
Oy	61	YLDPVLRTVAVLIVNSDKEGTGEKEYEENSDMAVFENEKVLTAREITLLKAGDNLIKQ	120
.Db	58	ylepqrtaaylslfrsdkegfygekged -snwayfdekrvllkagatlclikagnllkq	116
Oy	121	-----NOTNTTYSLKRLDLDTSVGCEKLISFSANGKNKVTSTPTCKLNPAKEFAGNGD	174
Dd	117	nluenentssfltylsklkalclsesveklsfgangnvnltscdkjntakeaengnd	176
Oy	175	TTVHLNGIGSLFTDTLLTWGATTWNNDNVDDKKRAASYVDVLMGNMKGVPGTTA	233
Dd	177	pvlhngysltldtllntgatctnvndvedekkraasvkxvlnmgmlkykpgpta	236
Oy	235	SDNWDEFVRTVEFLSADTKTTTVNNESSKDNGKTEVKIGAKTSVIKEKDKLVTKDK	294
Dd	237	sduvfvtlygtvelslsadtkcttnveskngkktewklgaktsvikkekqglvtgkg	296
Oy	295	GENGSTDEGGGLYTAKEVIDAVNKKAGRMTTTTANQTGADKFERYTSTNTTFASGK	355
Dd	297	dengsstlegelylvakevidavnkagwrmtctlangqtgadflevtsyntvltbsgk	356
Oy	355	GTTTAVSSDDCGNTTVMDVMWGALNLNOJONGSMNLDSKAAYSOGSSKVTSGNVSPSK	414
Dd	357	glttatscdgggnltkvkdvnvgdalinvnqlmgswnlkskavagssgkylsgnvspskg	416
Oy	415	KMDETVNINAGNNIEITFRNGKNIDIAISMPOFFSVSLGACADAPTLSYDGD-ALANYGK	473
Dd	417	kmdetvnlagnmlietrngnkhdatsemapqfsvslsgadaprlsvddeglinvnsk	476
Oy	474	KDNKFEVRIITNAPGVKEBDVTNVAQLKGVAONLNNRIDNDGNARAGIAQAIAIATAGLYQA	533
Dd	477	dnkfevrilttnavykgegdvtnvaqlkqvagnlmrldnvgnarengjaqaiaataglvqa	536
Oy	534	YLPKGSMAJGGGYTRGEGAYICATSSSIDSCGMNIITGTASGNSRGHPHGASASVGYOM	591
Dd	537	ylpbgsmajaggdvtrgeagyalysslsdggnmlkykbasgrnrglhgaasvgyw	594

RESULT	12
AAU06179	
ID	AAU06179 standard; Protein; 594 AA

AC AAU06179;

DT 24-OCT-2001 (first entry)

DE N. meningitidis BZ198 surface antigen Nhha polypeptide sequence.

KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX

FT	Region	1. .50
FT	Region	1. .50

FT /note= "Conserved region 1"

```

FT      /label= v1

```

Region	105.116
FT	



CC prevent or treat *N. meningitidis* infection in humans, especially  
 CC in the form of vaccines. The proteins and antibodies can also  
 CC be used to identify immunoreactive peptides.

XX Sequence 598 AA:

Query Match 90.2%; Score 2706.5; DB 20; Length 598;  
 Best Local Similarity 90.5%; Pred. No. 1e-151;  
 Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;

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QY 61 YLDPLVARTAVAVLVNSDKGTGKEKEVEENSDMAVVFNEKGVLTAEETITKADNLIKIK 120
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Db 58 ylepvgrtavlavlsfrskdkgelged-snavyidekrvllkagaillkagdnllkixg 116

QY 121 -----NGTNYSLKKDLTDLTSVGTETKLSFSAANGKNVNTSDPKGLNFAKETAG 170
   |:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 117 ntrenentndesfyslkkdltltsveteklsifgankvnltsdtkglnfaketag 176

QY 171 TNGDTRVHLNGIGSTLTDPLTNGATTNTNDVTDDEKKRAASVYKDVLAGNINIKVXP 230
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 177 tngdtrvhlnglsgstltdclntgatntvndvndidekkraasvcdvlnagvnlkgykp 236

QY 231 GTTASNDVFRVRYDVEPLSADTKTTTVNVEKDKNGKTEVIGAKTSYIRKDGKLV 290
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 237 gttasndvfrvrydveplfsadtklttvnveskdngkktvirkgtsvikkedqklv 296

QY 291 GKDKGENSGSTDEGLVTAKEVIDAVNKGAMKTTTANGOTGADKPEVTNSGTNVTF 350
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Db 297 gkdkgensgstdegevlvakevidavmkagvrmkcttanqgtgqadkfelvsgtkvlt 356

QY 351 ASGKGTATVSKDDQCNITVMYDVNVDALNVLQNSGNLDSKAVAGSSGKVISGNVS 410
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Db 357 asgngtatsvskddqcnltvkynvgdalnvglnsgnldskavagssgkvisgnvs 416

QY 411 PSKGKDETVNINAGNNIETTRNGKNIDTATSKTPOFSSVSLGADAPTLVSDGD-ALN 469
   |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 417 pskgkndetvnlagnnielttrngknidatstmpqfssvslgagadaptlsvddegaln 476

QY 470 VGSKKDKNKPVRTNVAPEGKEDVTNVAQLKGYAQNLRNIDVDCNARAGIAQATATAG 529
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Db 477 vgskkdknkpvrtnvapegkdvtnvaqlkgyaqnlmrnidvdcnaraaglaqatag 536

QY 530 LVQAVLPGRKSMAIGGTYRGEAGYAIIGYSISDGCNMIIKGTASGNSRCHFGASASVGY 589
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Db 537 lagaylpgrksmmaiggtyrgeagyaigysslsdgtgnwvikgtasgnsrghfgasasvgy 596

QY 590 QW 591
   ||.
Db 597 qw 598

```

RESULT 14

ID AA006177 standard; Protein; 598 AA.

AC AA006177;

DT 24-OCT-2001 (first entry)

DE *N. meningitidis* H15 surface antigen Nhma polypeptide sequence.

KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.

OS *Neisseria meningitidis* strain H15.

Key Location/Qualifiers

FT 1..50  
 FT Region /label= C1

```

FT FT /note= "Conserved region 1"
FT Region 51..104
FT /label= V1
FT /note= "Variable region 1"
FT Region 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT Region 117..130
FT /label= V2
FT /note= "Variable region 2"
FT Region 131..194
FT /label= C3
FT /note= "Conserved region 3"
FT Region 195..216
FT /label= V3
FT /note= "Variable region 3"
FT Region 217..235
FT /label= C4
FT /note= "Conserved region 4"
FT Region 236..242
FT /label= V4
FT /note= "Variable region 4"
FT Region 243..598
FT /label= C5
FT /note= "Conserved region 5"

PN WO200155182-A1.
PD 02-AUG-2001.
PD XX
PR 25-JAN-2001; 2001MO-AU000069.
PR XX
PA 25-JAN-2000; 2000US-0177917.
PA XX
PI (UYOU ) UNITV QUEENSLAND.
PI XX
PI Peak IRA, Jennings MP;
PI XX
DR WPI; 2001-488774/53.
DR XX
DR N-PSDB; AAS09167.
DR XX
PT New Nhma surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
PT XX
PS Claim 9; Fig 1; 91pp; English.
PS XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhma
XX (AA006182-AA006186). The modified or mutant Nhma polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhma
XX from N. meningitidis strain H15 is 1 of 10 Nhma polypeptide sequences
XX (AA006171-AA006180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
SQ Sequence 598 AA:

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Query Match 90.2%; Score 2706.5; DB 22; Length 598;

Best Local Similarity 90.5%; Pred. No. 1e-151;  
 Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;

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QY 1 MNEILRIINMSALNANVVSELTRNHTKRASATVKTAVALTLLFATVQASANNEQEDL 60
   ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 mkiylriwmsalnawvseltrnhtkrasatvatatllfatvganad---dddl 57

```

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OY 61 YLDPVLRVAVLIIVNSDEKTEGKEKEVENSMDWAYFNEKGVLTFAREITLAKGDNLIKIKO 120
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Db 58 yleprtravlsfrsfdckegteged -snwayfdekrvfkagaltlkagdnllkikg 116
OY 121 -----NCTNFTYSLKDKDLTDLTDSVTEKLSFSANGKNVITTSOTKGINFKETAG 170
   ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 117 ntneutnentndsflyslkklldltsveteleklsfganghkvntsdtkglnfaketaag 176
OY 171 TNGDFTVLNIGISFLPTLTINTGATVNTNDNVNDDKKRAASAKVDVNLNGMNIKGYKP 230
   ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 177 tngdptvlhnglsglltcltllntgatcltnvndvdeekkraasvkdvlnagwnlkgykp 236
OY 231 GTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKGKTEVKGAKTSVIREKDKGLVT 290
   ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 237 gttasdnvdfvrydtveflsadektltvnveskngkktvkkigaktsvlkekdgklvt 296
OY 291 GKDKGENSSSTDEGGLVTAKEVIDAVNKAQRMAKTTTANGOTGQADKFEVYTSCTNVT 350
   ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 297 gkgkngssstdegeglvtakevidavnkagwrmtltlangtgqadkfeytsqtkvltf 356
OY 351 ASGKGTATVSKDDOGNTVWVDVWGDALVNLONGSMNIDSKAVAGSSGKVTSGNWS 410
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Db 357 asnggtlatvskddqgnltvkvynvgdahnvnglqnsqwnldskavagssgkvlsqnv 416
OY 411 PSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDGD-ALN 469
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OY 530 LVOAALPGKSMWAIIGGTYRGAGYAIGYSSISDGNMNIKGTAGSNGRHGAGASVGY 589
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OY 590 QW 591
   ||
Db 597 qw 598

RESULT 15
AA23738
ID AAY23738 standard; Protein: 598 AA.
XX
AC AAY23738;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein: surface glycoprotein; infection; vaccine;
   immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN MO9931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-A001031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
   (UYOU) UNIV QUEENSLAND.
XX
PI Jennings MP, Moxon ER, Peak IRA;
XX
DR WPI: 1999-418754/35.
XX
DR N-PSDB; AAX85790.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
```

```
PT meningitidis infections
XX
PS Claim 1, Page 91-93; 132pp: English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match 90.2%; Score 2705.5; DB 20; Length 598;
Best Local Similarity 90.4%; Pred. No. 1.2e-151;
Matches 544; Conservative 14; Mismatches 29; Indels 15; Gaps 4;

OY 1 MNEILRIIWNALNMMVYSELTRNHTKRASATVKTAVLATLTFATVOASNNNEQEDL 60
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Db 1 mkslrrllwnsalnaawvvsellrnhckrasatvktavlatltafvanaad---dddl 57

OY 61 YLDPVLRVAVLIIVNSDEKTEGKEKEVENSMDWAYFNEKGVLTFAREITLAKGDNLIKIKO 120
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Db 58 yleprtravlsfrsfdckegteged -snwayfdekrvfkagaltlkagdnllkikg 116
OY 121 -----NCTNFTYSLKDKDLTDLTDSVTEKLSFSANGKNVITTSOTKGINFKETAG 170
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Db 117 ntneutnentndsflyslkklldltsveteleklsfganghkvntsdtkglnfaketaag 176
OY 171 TNGDFTVLNIGISFLPTLTINTGATVNTNDNVNDDKKRAASAKVDVNLNGMNIKGYKP 230
   ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| ||| ||||| |||
Db 177 tngdptvlhnglsglltcltllntgatcltnvndvdeekkraasvkdvlnagwnlkgykp 236
OY 231 GTTASDNVDFVRYDTVEFLSADTKTTTVNVESSKDKGKTEVKGAKTSVIREKDKGLVT 290
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OY 291 GKDKGENSSSTDEGGLVTAKEVIDAVNKAQRMAKTTTANGOTGQADKFEVYTSCTNVT 350
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Db 297 gkgkngssstdegeglvtakevidavnkagwrmtltlangtgqadkfeytsqtkvltf 356
OY 351 ASGKGTATVSKDDOGNTVWVDVWGDALVNLONGSMNIDSKAVAGSSGKVTSGNWS 410
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OY 411 PSKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLSDGD-ALN 469
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Db 417 pskgmdeitvlnagnnieitrngknidiatmtpofssvslgagadaptlsvddegaln 476
OY 470 VGSKKDNKPVRTITNAPGVKESGDTNVAOLKGVAONLNRRIDNVGNARAGIAQAIAIATAG 529
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Db 477 vgskdanpvriltvnvapgvgedvtnvaqlkqvagqlnmrldnvgnaraglaqalataag 536
OY 530 LVOAALPGKSMWAIIGGTYRGAGYAIGYSSISDGNMNIKGTAGSNGRHGAGASVGY 589
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OY 590 QW 591
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Db 597 qw 598
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Search completed: July 3, 2002, 08:09:09  
Job time: 495 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:10:17 ; Search time 64.11 Seconds  
(without alignments)  
225.168 Million cell updates/sec

Title: US-09-771-382-5  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2999	100.0	591	US-09-377-155-11	Sequence 11, Appl
2	2999	100.0	591	US-09-669-974-11	Sequence 11, Appl
3	2984	99.5	591	US-09-377-155-21	Sequence 21, Appl
4	2984	99.5	591	US-09-669-974-21	Sequence 21, Appl
5	2952.5	98.4	592	US-09-377-155-2	Sequence 2, Appl
6	2952.5	98.4	592	US-09-669-974-2	Sequence 2, Appl
7	2739.5	91.3	594	US-09-377-155-9	Sequence 9, Appl
8	2739.5	91.3	594	US-09-669-974-9	Sequence 9, Appl
9	2721.5	90.7	594	US-09-377-155-7	Sequence 7, Appl
10	2721.5	90.7	594	US-09-669-974-7	Sequence 7, Appl
11	2706.5	90.2	598	US-09-377-155-13	Sequence 13, Appl
12	2706.5	90.2	598	US-09-669-974-13	Sequence 13, Appl
13	2705.5	90.2	598	US-09-377-155-5	Sequence 5, Appl
14	2705.5	90.2	598	US-09-669-974-5	Sequence 5, Appl
15	2676	89.2	599	US-09-377-155-15	Sequence 15, Appl
16	2676	89.2	599	US-09-669-974-15	Sequence 15, Appl
17	2554.5	85.2	592	US-09-377-155-17	Sequence 17, Appl
18	2554.5	85.2	592	US-09-669-974-17	Sequence 17, Appl
19	2467	82.3	589	US-09-377-155-19	Sequence 19, Appl
20	2467	82.3	589	US-09-669-974-19	Sequence 19, Appl
21	1245	41.5	2411	US-09-268-347-36	Sequence 36, Appl
22	1243	41.4	2353	US-08-913-942-4	Sequence 33, Appl
23	1243	41.4	2353	US-08-377-155-33	Sequence 33, Appl
24	1243	41.4	2353	US-09-669-974-33	Sequence 33, Appl
25	1242	41.4	2354	US-09-268-347-47	Sequence 47, Appl
26	1180.5	39.4	607	US-08-409-995-6	Sequence 6, Appl
27	1180.5	39.4	607	US-08-685-467-6	Sequence 6, Appl

28	1180.5	39.4	607	US-08-913-942-6	Sequence 6, Appl
29	1180.5	39.4	1912	US-08-409-995-4	Sequence 4, Appl
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31	1064.5	35.5	1094	US-09-268-347-32	Sequence 32, Appl
32	1054.5	35.2	1098	US-08-409-995-2	Sequence 2, Appl
33	1054.5	35.2	1098	US-08-685-467-2	Sequence 2, Appl
34	1054.5	35.2	1098	US-09-377-155-32	Sequence 32, Appl
35	1054.5	35.2	1098	US-08-913-942-32	Sequence 32, Appl
36	1054.5	35.2	1098	US-09-669-974-32	Sequence 32, Appl
37	1054.5	35.2	1098	US-09-268-347-44	Sequence 44, Appl
38	1036.5	34.6	658	US-08-409-995-5	Sequence 5, Appl
39	1036.5	34.6	658	US-08-685-467-5	Sequence 5, Appl
40	1036.5	34.6	658	US-08-913-942-5	Sequence 5, Appl
41	985	32.8	679	US-08-913-942-15	Sequence 15, Appl
42	985	32.8	679	US-09-268-347-26	Sequence 26, Appl
43	749.5	25.0	1004	US-09-268-347-30	Sequence 30, Appl
44	738.5	24.6	1002	US-09-268-347-24	Sequence 24, Appl
45	694.5	23.2	1104	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1					
US-09-377-155-11					
Sequence 11, Application US/09377155					
Patent NO. 6197312					
GENERAL INFORMATION:					
APPLICANT: PEAR, Ian Richard Anselm					
APPLICANT: JENNINGS, Michael Paul					
APPLICANT: MOXON, E. Richard					
TITLE OF INVENTION: NOVEL SURFACE ANTIGEN					
FILE REFERENCE: 065064/0128					
CURRENT APPLICATION NUMBER: US/09/377,155					
CURRENT FILING DATE: 1999-08-19					
PRIOR APPLICATION NUMBER: PCT/AU98/01031					
PRIOR FILING DATE: 1998-12-14					
PRIOR APPLICATION NUMBER: GB 9726398.2					
PRIOR FILING DATE: 1997-12-12					
NUMBER OF SEQ ID NOS: 33					
SOFTWARE: Patent In Ver. 2.0					
SEQ ID NO 11					
LENGTH: 591					
TYPE: PRT					
ORGANISM: Neisseria meningitidis					
US-09-377-155-11					
Query Match					
Best Local Similarity 100.0%, Score 2999; DB 4; Length 591;					
Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;					
OY	1	MNELIRINMSALNMAVYVSELNRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL	60		
DB	1	MNELIRINMSALNMAVYVSELNRNHTKRASATVKTAVLATLLFATVQASANNEDEEDL	60		
OY	61	YIDPVLRVAVLVINSDEKGTGEKEVEENSDMAVYFNEKGVLTAREITLAKADNLKIKO	120		
DB	61	YIDPVLRVAVLVINSDEKGTGEKEVEENSDMAVYFNEKGVLTAREITLAKADNLKIKO	120		
OY	121	NGNFTYSLKKDLTDLTSVTEKLSFSAKNGKNVITSDFKGLNFAKETAGTNDTTHLN	180		
DB	121	NGNFTYSLKKDLTDLTSVTEKLSFSAKNGKNVITSDFKGLNFAKETAGTNDTTHLN	180		
OY	181	GIGSTLTDLTLNLTGATTTNTNDVTTDEKKRAASVDVNLNAGNINIGVKGPTASDNVDF	240		
DB	181	GIGSTLTDLTLNLTGATTTNTNDVTTDEKKRAASVDVNLNAGNINIGVKGPTASDNVDF	240		
OY	241	VRTYDFVEELSDTKTTTVNVEKDKNGKTEVKGATSVYKEDKLVYTKDKGENSS	300		
DB	241	VRTYDFVEELSDTKTTTVNVEKDKNGKTEVKGATSVYKEDKLVYTKDKGENSS	300		
OY	301	TDEGBELVTAKEVIDAVNNAKGMKTTTANGQYTGADKPEFTVSGTNVTFASGKTATV	360		

```
|||||
Db 301 TDEGGGLTAKAEVIDAVNKGARMKTTTANGOTGADKFEIYVTSCTNVTFAAGKGTATV 360
Qy 361 SKDDGNTITVMYDVNVDGALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDET 420
Db 361 SKDDGNTITVMYDVNVDGALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDET 420
Qy 421 NINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLTSDGDALNVGSKDKNPVR 480
Db 421 NINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLTSDGDALNVGSKDKNPVR 480
Qy 481 ITNVAAPVKEGCVTVAOLKGYAQNINRINVDGNARAGIAQAIATAGLVQAYILPGKSM 540
Db 481 ITNVAAPVKEGCVTVAOLKGYAQNINRINVDGNARAGIAQAIATAGLVQAYILPGKSM 540
Qy 541 MAIGGTYRGEAGYAIQYSSISDGGNMIITKGTASGNSRCHFGASASVGYQW 591
Db 541 MAIGGTYRGEAGYAIQYSSISDGGNMIITKGTASGNSRCHFGASASVGYQW 591
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## RESULT 2

```
US-09-669-974-11
; Sequence 11, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669, 974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 11
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-11
```

Query Match 100.0%; Score 2999; DB 4; Length 591;

Best Local Similarity 100.0%; Pred. No. 4.8e-224;

Matches 591; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 MNEILRIIWSALNMAWVYSELTRNHTRKASATVKTAVLATLLFATVOASANNEQEDL 60
Db 1 MNEILRIIWSALNMAWVYSELTRNHTRKASATVKTAVLATLLFATVOASANNEQEDL 60
Qy 61 YLDPVLRVAVLIIVNSDEKGEKKEVEENSDMAVYFNEKGYLTAREITLAKGDMUKIKQ 120
Db 61 YLDPVLRVAVLIIVNSDEKGEKKEVEENSDMAVYFNEKGYLTAREITLAKGDMUKIKQ 120
Qy 121 NGTNFTYSLKKDLTJLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVDL 180
Db 121 NGTNFTYSLKKDLTJLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVDL 180
Qy 181 GIGSTLTJTLNTGATTNTNDNVTDDKKRAASVKDVLNAGMNIKGVPPTTASDNDVF 240
Db 181 GIGSTLTJTLNTGATTNTNDNVTDDKKRAASVKDVLNAGMNIKGVPPTTASDNDVF 240
Qy 241 VRTYDVEFLSADTKTTTVNVESKDNKGKTEYKIGAKTSVIEKDGKLVTKGDKGENSS 300
Db 241 VRTYDVEFLSADTKTTTVNVESKDNKGKTEYKIGAKTSVIEKDGKLVTKGDKGENSS 300
Qy 301 TDEGGGLTAKAEVIDAVNKGARMKTTTANGOTGADKFEIYVTSCTNVTFAAGKGTATV 360
Db 301 TDEGGGLTAKAEVIDAVNKGARMKTTTANGOTGADKFEIYVTSCTNVTFAAGKGTATV 360
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Db 301 TDEGGGLTAKAEVIDAVNKGARMKTTTANGOTGADKFEIYVTSCTNVTFAAGKGTATV 360
Qy 361 SKDDGNTITVMYDVNVDGALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDET 420
Db 361 SKDDGNTITVMYDVNVDGALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDET 420
Qy 421 NINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLTSDGDALNVGSKDKNPVR 480
Db 421 NINAGNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLTSDGDALNVGSKDKNPVR 480
Qy 481 ITNVAAPVKEGCVTVAOLKGYAQNINRINVDGNARAGIAQAIATAGLVQAYILPGKSM 540
Db 481 ITNVAAPVKEGCVTVAOLKGYAQNINRINVDGNARAGIAQAIATAGLVQAYILPGKSM 540
Qy 541 MAIGGTYRGEAGYAIQYSSISDGGNMIITKGTASGNSRCHFGASASVGYQW 591
Db 541 MAIGGTYRGEAGYAIQYSSISDGGNMIITKGTASGNSRCHFGASASVGYQW 591
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## RESULT 3

```
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21
```

Query Match 99.5%; Score 2984; DB 4; Length 591;

Best Local Similarity 99.5%; Pred. No. 6.9e-223;

Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 MNEILRIIWSALNMAWVYSELTRNHTRKASATVKTAVLATLLFATVOASANNEQEDL 60
Db 1 MNEILRIIWSALNMAWVYSELTRNHTRKASATVKTAVLATLLFATVOASANNEQEDL 60
Qy 61 YLDPVLRVAVLIIVNSDEKGEKKEVEENSDMAVYFNEKGYLTAREITLAKGDMUKIKQ 120
Db 61 YLDPVLRVAVLIIVNSDEKGEKKEVEENSDMAVYFNEKGYLTAREITLAKGDMUKIKQ 120
Qy 121 NGTNFTYSLKKDLTJLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVDL 180
Db 121 NGTNFTYSLKKDLTJLTSVGTSEKLSFSANGKNVNTSDTKGLNFAKETAGTNGDTTVDL 180
Qy 181 GIGSTLTJTLNTGATTNTNDNVTDDKKRAASVKDVLNAGMNIKGVPPTTASDNDVF 240
Db 181 GIGSTLTJTLNTGATTNTNDNVTDDKKRAASVKDVLNAGMNIKGVPPTTASDNDVF 240
Qy 241 VRTYDVEFLSADTKTTTVNVESKDNKGKTEYKIGAKTSVIEKDGKLVTKGDKGENSS 300
Db 241 VRTYDVEFLSADTKTTTVNVESKDNKGKTEYKIGAKTSVIEKDGKLVTKGDKGENSS 300
Qy 301 TDEGGGLTAKAEVIDAVNKGARMKTTTANGOTGADKFEIYVTSCTNVTFAAGKGTATV 360
Db 301 TDEGGGLTAKAEVIDAVNKGARMKTTTANGOTGADKFEIYVTSCTNVTFAAGKGTATV 360
Qy 361 SKDDGNTITVMYDVNVDGALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDET 420
Db 361 SKDDGNTITVMYDVNVDGALNVNOLONGMNLDSKAVAGSSGKVIISGNVSPSKGMDET 420
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Db 361 SKDDGNTITVMDVNVGDLANVNOLONSGMNLDKRAVAGSSSKVTSIGNVSPSKGMDETV 420
QY 421 NINAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKDNKPYR 480
Db 421 NINAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKDNKPYR 480
QY 481 ITNVAPEGEGVTVNAQLKGYAQNLRNRIIDVNDGNARAGIAQALATAGLVQAYLPGKSM 540
Db 481 ITNVAPEGEGVTVNAQLKGYAQNLRNRIIDVNDGNARAGIAQALATAGLVQAYLPGKSM 540
QY 541 MAIGGTYRGEAGYALGYSSISDGMWIKGTASGNSRCHFGASASVGYQW 591
Db 541 MAIGGTYRGEAGYALGYSSISDGMWIKGTASGNSRCHFGASASVGYQW 591
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```
RESULT 4
US-09-669-974-21
: Sequence 21, Application US/09669974
: Patent No. 6333173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669, 974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 21
: LENGTH: 591
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-669-974-21
```

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Query Match 99.5%; Score 2984; DB 4; Length 591;
Best Local Similarity 99.5%; Pred. No. 6.9e-223;
Matches 588; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MNEILRIIWSALNMAVYVSELTNRHTRKASATVKTAVLATLLEFATVOASANNEOEEDL 60
Db 1 MNEILRIIWSALNMAVYVSELTNRHTRKASATVKTAVLATLLEFATVOASANNEOEEDL 60
QY 61 YLDPVLRVAVLIYNSDEKGEKEKEVEENSDMAVYFNEKGYLTPAREITLAKGDLKIK 120
Db 61 YLDPVLRVAVLIYNSDEKGEKEKEVEENSDMAVYFNEKGYLTPAREITLAKGDLKIK 120
QY 121 NCTNFTYSLKDLTDLISVTEKLSFSANGKNVNTSDTKGLNPAKETAGTNGDTTVALH 180
Db 121 NCTNFTYSLKDLTDLISVTEKLSFSANGKNVNTSDTKGLNPAKETAGTNGDTTVALH 180
QY 181 GIGSLTDLTDLNTGATNTNDNVTDDEKRAASVADVNLNAGMNIKGYKPGTTASDNVDF 240
Db 181 GIGSLTDLTDLNTGATNTNDNVTDDEKRAASVADVNLNAGMNIKGYKPGTTASDNVDF 240
QY 241 VRTYDVEFLSADTKTTTVNVNVEKDNKKTEVEKIGAKTSVIEKDKGLVTGKDKGENSS 300
Db 241 VRTYDVEFLSADTKTTTVNVNVEKDNKKTEVEKIGAKTSVIEKDKGLVTGKDKGENSS 300
QY 301 TDEGEGVLTAKVYIDAVNKAQRKATTTTANGOTGADKEFEYVTSCTNVTTFASGKTATV 360
Db 301 TDEGEGVLTAKVYIDAVNKAQRKATTTTANGOTGADKEFEYVTSCTNVTTFASGKTATV 360
QY 361 SKDDGNTITVMDVNVGDLANVNOLONSGMNLDKRAVAGSSSKVTSIGNVSPSKGMDETV 420
Db 361 SKDDGNTITVMDVNVGDLANVNOLONSGMNLDKRAVAGSSSKVTSIGNVSPSKGMDETV 420
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Db 361 SKDDGNTITVMDVNVGDLANVNOLONSGMNLDKRAVAGSSSKVTSIGNVSPSKGMDETV 420
QY 421 NINAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKDNKPYR 480
Db 421 NINAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKDNKPYR 480
QY 481 ITNVAPEGEGVTVNAQLKGYAQNLRNRIIDVNDGNARAGIAQALATAGLVQAYLPGKSM 540
Db 481 ITNVAPEGEGVTVNAQLKGYAQNLRNRIIDVNDGNARAGIAQALATAGLVQAYLPGKSM 540
QY 541 MAIGGTYRGEAGYALGYSSISDGMWIKGTASGNSRCHFGASASVGYQW 591
Db 541 MAIGGTYRGEAGYALGYSSISDGMWIKGTASGNSRCHFGASASVGYQW 591
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```
RESULT 5
US-09-377-155-2
: Sequence 2, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 2
: LENGTH: 592
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-2
```

```
Query Match 98.4%; Score 2952.5; DB 4; Length 592;
Best Local Similarity 98.5%; Pred. No. 1.9e-220;
Matches 583; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MNEILRIIWSALNMAVYVSELTNRHTRKASATVKTAVLATLLEFATVOASANNEOEEDL 59
Db 1 MNEILRIIWSALNMAVYVSELTNRHTRKASATVKTAVLATLLEFATVOASANNEOEEDL 59
QY 60 YLDPVLRVAVLIYNSDEKGEKEKEVEENSDMAVYFNEKGYLTPAREITLAKGDLKIK 119
Db 60 YLDPVLRVAVLIYNSDEKGEKEKEVEENSDMAVYFNEKGYLTPAREITLAKGDLKIK 119
QY 120 NCTNFTYSLKDLTDLISVTEKLSFSANGKNVNTSDTKGLNPAKETAGTNGDTTVALH 179
Db 120 NCTNFTYSLKDLTDLISVTEKLSFSANGKNVNTSDTKGLNPAKETAGTNGDTTVALH 179
QY 181 NGISGLTDLTDLNTGATNTNDNVTDDEKRAASVADVNLNAGMNIKGYKPGTTASDNVDF 239
Db 181 NGISGLTDLTDLNTGATNTNDNVTDDEKRAASVADVNLNAGMNIKGYKPGTTASDNVDF 239
QY 240 VRTYDVEFLSADTKTTTVNVNVEKDNKKTEVEKIGAKTSVIEKDKGLVTGKDKGENS 299
Db 240 VRTYDVEFLSADTKTTTVNVNVEKDNKKTEVEKIGAKTSVIEKDKGLVTGKDKGENS 299
QY 300 TDEGEGVLTAKVYIDAVNKAQRKATTTTANGOTGADKEFEYVTSCTNVTTFASGKTATV 359
Db 300 TDEGEGVLTAKVYIDAVNKAQRKATTTTANGOTGADKEFEYVTSCTNVTTFASGKTATV 359
QY 360 VSKDDGNTITVMDVNVGDLANVNOLONSGMNLDKRAVAGSSSKVTSIGNVSPSKGMDET 419
Db 360 VSKDDGNTITVMDVNVGDLANVNOLONSGMNLDKRAVAGSSSKVTSIGNVSPSKGMDET 419
QY 420 VNNAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKDNKPYR 479
Db 420 VNNAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDGDALNVGSKKDNKPYR 479
```

Db 421 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKNRPV 480  
QY 480 RITNAPGVKRGDYTNVAQLKGVAONLNRRIDNDGNARAGIAIATAGLVQAYLPKRS 539  
Db 481 RITNAPGVKRGDYTNVAQLKGVAONLNRRIDNDGNARAGIAIATAGLVQAYLPKRS 540  
QY 540 MMAIGGTYRGEAGYALGYSSISDGMMIIGKTASGNSRGHFGASASVGYOM 591  
Db 541 MMAIGGTYRGEAGYALGYSSISDGMMIIGKTASGNSRGHFGASASVGYOM 592

## RESULT 6

US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 98.4%; Score 2952.5; DB 4; Length 592;

Best Local Similarity 98.4%; Pred. No. 1.9e-220;  
Matches 583; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 MNELIRITMNSALNAAVYVSELTNRHTRKASATYKATVATLTLFATYQASANNEDQED 59  
Db 1 MNKIRITMNSALNAAVYVSELTNRHTRKASATYKATVATLTLFATYQASANNEDPRKD 60  
QY 60 LYDPLVLTAVLVINSDEKSTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIK 119  
Db 61 LYDPLVLTAVLVINSDEKSTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIK 120  
QY 120 ONGNFTYSLKDLTDLTSVTEKLSFSAANGKNVITSDTGLNPAKTAAGTNGDTVHL 179  
Db 121 ONGNFTYSLKDLTDLTSVTEKLSFSAANGKNVITSDTGLNPAKTAAGTNGDTVHL 180  
QY 180 NGISLTLDLTLNTGATTVNDVYTDDEKRRASVYKDYLVNAGMNIKVKKGTASDNDV 239  
Db 181 NGISLTLDLTLNTGATTVNDVYTDDEKRRASVYKDYLVNAGMNIKVKKGTASDNDV 240  
QY 240 FVRTYDYVEFLSADTKTTTVAVESKDKGKTEVKIGAKTSVIKEKDKLVYKDKGENGS 299  
Db 241 FVRTYDYVEFLSADTKTTTVAVESKDKGKTEVKIGAKTSVIKEKDKLVYKDKGENGS 300  
QY 300 STDGEGVLTAKYEVDAVNAKGMKRTTANGOTGADKFEVTVSGTVTFASGKGTAT 359  
Db 301 STDGEGVLTAKYEVDAVNAKGMKRTTANGOTGADKFEVTVSGTVTFASGKGTAT 360  
QY 360 VSKDQGNITVAVYVNDALNVNOLONGMNLDSKAAGSSGKVIISGNVSPSKGMDT 419  
Db 361 VSKDQGNITVAVYVNDALNVNOLONGMNLDSKAAGSSGKVIISGNVSPSKGMDT 420  
QY 420 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKNRPV 479

Db 421 VNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGALNVGSKDKNRPV 480  
QY 480 RITNAPGVKRGDYTNVAQLKGVAONLNRRIDNDGNARAGIAIATAGLVQAYLPKRS 539  
Db 481 RITNAPGVKRGDYTNVAQLKGVAONLNRRIDNDGNARAGIAIATAGLVQAYLPKRS 540  
QY 540 MMAIGGTYRGEAGYALGYSSISDGMMIIGKTASGNSRGHFGASASVGYOM 591  
Db 541 MMAIGGTYRGEAGYALGYSSISDGMMIIGKTASGNSRGHFGASASVGYOM 592

## RESULT 7

US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 91.3%; Score 2739.5; DB 4; Length 594;

Best Local Similarity 91.8%; Pred. No. 5.7e-204;  
Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;

QY 1 MNELIRITMNSALNAAVYVSELTNRHTRKASATYKATVATLTLFATYQASANNEDQED 60  
Db 1 MNKIRITMNSALNAAVYVSELTNRHTRKASATYKATVATLTLFATYQASANNEDPRKD 57  
QY 61 LYDPLVLTAVLVINSDEKSTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIK 120  
Db 58 YLEPVORTAVLVINSDEKSTGEKEVEENSDMAVYFNEKGVLTAREITLKAGDNLIKIK 116  
QY 121 -----NGNFTYSLKDLTDLTSVTEKLSFSAANGKNVITSDTGLNPAKTAAGTNGD 174  
Db 117 NTNENTNASFTYSLKDLTDLTSVTEKLSFSAANGKNVITSDTGLNPAKTAAGTNGD 176  
QY 175 TTVHLNGISLTLDLTLNTGATTVNDVYTDDEKRRASVYKDYLVNAGMNIKVKKGTAS 234  
Db 177 TTVHLNGISLTLDLTLNTGATTVNDVYTDDEKRRASVYKDYLVNAGMNIKVKKGTAS 236  
QY 235 SDNDFVARTYVEFLSADTKTTTVAVESKDKGKTEVKIGAKTSVIKEKDKLVYKDK 294  
Db 237 SDNDFVARTYVEFLSADTKTTTVAVESKDKGKTEVKIGAKTSVIKEKDKLVYKDK 296  
QY 295 GENGSTDEGEGVLTAKYEVDAVNAKGMKRTTANGOTGADKFEVTVSGTVTFASGK 354  
Db 297 GENGSTDEGEGVLTAKYEVDAVNAKGMKRTTANGOTGADKFEVTVSGTVTFASGK 356  
QY 355 GTTATVSKDQGNITVAVYVNDALNVNOLONGMNLDSKAAGSSGKVIISGNVSPSKG 414  
Db 357 GTTATVSKDQGNITVAVYVNDALNVNOLONGMNLDSKAAGSSGKVIISGNVSPSKG 416  
QY 415 KMDFTVNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGALNVGSK 473  
Db 417 KMDFTVNINAGNNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSDGALNVGSK 476  
QY 474 KDNRPVRLITNAPGVKRGDYTNVAQLKGVAONLNRRIDNDGNARAGIAIATAGLVQ 533

|||||  
Db 477 DANKPVRITNVA PGVEGDTVNAQLKGVAQNLNHNHIDVDGNARAGIAQAATATAGLVQA 536  
QY 534 YLPKSMIAIGGTYRGEGVAIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591  
|||||  
Db 537 YLPKSMIAIGGTYRGEGVAIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 594

## RESULT 8

US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 91.3%; Score 2739.5; DB 4; Length 594;  
Best Local Similarity 91.8%; Pred. No. 5.7e-204;  
Matches 549; Conservative 15; Mismatches 23; Indels 11; Gaps 4;

QY 1 MNELIRIINWSALNMAVVVSELTRNHTKRASATVKTAVLATLILFATVOASANNEDEEDL 60  
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| : : ||  
Db 1 MNKIRIINWSALNMAVVVSELTRNHTKRASATVKTAVLATLILFATVOASTD--DDDL 57  
61 YLDPVLRVAVLIIVNSDKGTEGKEKEVEENSDMAVYFENKGVLTAREITLTKAGDNLKIQ 120  
||:| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 58 YLEPQRTAVLVSPRSDEKTEGEKE-VIEDSNMGVYFEDKGVLTAGTTLTKAGDNLKIQ 116  
121 -----NGTNFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDPKGLNFAKETAGTNGD 174  
| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 117 NTNEMTNMSSFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDPKGLNFAKETAGTNGD 176  
175 TTVHLNGIGSTLDTLTLNLTGATTNTNDVTDDEKRRASVAVDVLNAGNINIGVKGPGTTA 234  
|||||  
Db 177 TTVHLNGIGSTLDTLTLNLTGATTNTNDVTDDEKRRASVAVDVLNAGNINIGVKGPGTTA 236  
235 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVAKIGKTSYIKKDKGLVYGKDK 294  
|||||  
QY 235 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVAKIGKTSYIKKDKGLVYGKDK 294  
|||||  
Db 235 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVAKIGKTSYIKKDKGLVYGKDK 296  
235 GENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGADKPEFTVSGTNVTFASGK 354  
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 297 GENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGADKPEFTVSGTNVTFASGK 356  
355 GTTATVSKDQGNITVYVNVGDALNVNOLONGNLDLSKAVAGSSGKVIISGNVSPSGK 414  
|||||  
QY 355 GTTATVSKDQGNITVYVNVGDALNVNOLONGNLDLSKAVAGSSGKVIISGNVSPSGK 414  
|||||  
Db 357 GTTATVSKDQGNITVYVNVGDALNVNOLONGNLDLSKAVAGSSGKVIISGNVSPSGK 416  
415 KMDEYNINAGNIIETTRGNKIDATSMTPOFSSVSLGAGADAPTLVSDGALNVGSK 473  
|||||  
Db 417 KMDEYNINAGNIIETTRGNKIDATSMTPOFSSVSLGAGADAPTLVSDGALNVGSK 476  
474 KKNKPVRTITNVA PGVEGDTVNAQLKGVAQNLNHNHIDVDGNARAGIAQAATATAGLVQA 533  
|||||

|||||  
Db 477 DANKPVRITNVA PGVEGDTVNAQLKGVAQNLNHNHIDVDGNARAGIAQAATATAGLVQA 536  
QY 534 YLPKSMIAIGGTYRGEGVAIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591  
|||||  
Db 537 YLPKSMIAIGGTYRGEGVAIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 594

## RESULT 9

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentln Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 90.7%; Score 2721.5; DB 4; Length 594;  
Best Local Similarity 91.6%; Pred. No. 1.4e-202;  
Matches 548; Conservative 12; Mismatches 27; Indels 11; Gaps 4;

QY 1 MNELIRIINWSALNMAVVVSELTRNHTKRASATVKTAVLATLILFATVOASANNEDEEDL 60  
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 1 MNKIRIINWSALNMAVVVSELTRNHTKRASATVKTAVLATLILFATVOANAYD--DDDL 57  
61 YLDPVLRVAVLIIVNSDKGTEGKEKEVEENSDMAVYFENKGVLTAREITLTKAGDNLKIQ 120  
||:| || || ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 58 YLEPQRTAVLVSPRSDEKTEGKEGED-SMNAVYFEDKRVLKAGATITLTKAGDNLKIQ 116  
121 -----NGTNFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDPKGLNFAKETAGTNGD 174  
| : ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 117 NTNEMTNMSSFTYSLAKDLTDLTSVTEKLSFSAANGKNVITSDPKGLNFAKETAGTNGD 176  
175 TTVHLNGIGSTLDTLTLNLTGATTNTNDVTDDEKRRASVAVDVLNAGNINIGVKGPGTTA 234  
|||||  
Db 177 TTVHLNGIGSTLDTLTLNLTGATTNTNDVTDDEKRRASVAVDVLNAGNINIGVKGPGTTA 236  
235 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVAKIGKTSYIKKDKGLVYGKDK 294  
|||||  
Db 235 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVAKIGKTSYIKKDKGLVYGKDK 296  
237 SONVDFVRTYDVEFLSADTKTTTVNVEESKDKGKTEVAKIGKTSYIKKDKGLVYGKDK 296  
295 GENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGADKPEFTVSGTNVTFASGK 354  
||:| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||  
Db 297 GENGSTDEGEGLVTAKEVIDAVNKGARMKTTTANGOTGADKPEFTVSGTNVTFASGK 356  
355 GTTATVSKDQGNITVYVNVGDALNVNOLONGNLDLSKAVAGSSGKVIISGNVSPSGK 414  
|||||  
QY 355 GTTATVSKDQGNITVYVNVGDALNVNOLONGNLDLSKAVAGSSGKVIISGNVSPSGK 414  
|||||  
Db 357 GTTATVSKDQGNITVYVNVGDALNVNOLONGNLDLSKAVAGSSGKVIISGNVSPSGK 416  
415 KMDEYNINAGNIIETTRGNKIDATSMTPOFSSVSLGAGADAPTLVSDGALNVGSK 473  
|||||  
Db 417 KMDEYNINAGNIIETTRGNKIDATSMTPOFSSVSLGAGADAPTLVSDGALNVGSK 476  
474 KKNKPVRTITNVA PGVEGDTVNAQLKGVAQNLNHNHIDVDGNARAGIAQAATATAGLVQA 533  
|||||  
Db 477 DINKPVRTITNVA PGVEGDTVNAQLKGVAQNLNHNHIDVDGNARAGIAQAATATAGLVQA 536  
534 YLPKSMIAIGGTYRGEGVAIGYSSISDGNWIIKGTASGNSRHFASASVGYOW 591

[illegible]

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Db      537  YLPKSMMAIGGTYRGEAGYAI GYSSIDSGNMWIIKKTASGNSRGHFASASVGYOM 594
      RESULT 11
      US-09-377-155-13
      ; Sequence 13, Application US/09377155
      ; Patent No. 6197312
      ; GENERAL INFORMATION:
      ; APPLICANT: PEAK, Ian Richard Anselm
      ; APPLICANT: JENNINGS, Michael Paul
      ; APPLICANT: MOXON, E. Richard
      ; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
      ; FILE REFERENCE: 065064/0128
      ; CURRENT APPLICATION NUMBER: US/09/377,155
      ; CURRENT FILING DATE: 1999-08-19
      ; PRIOR APPLICATION NUMBER: PCF/AU98/01031
      ; PRIOR FILING DATE: 1998-12-14
      ; PRIOR APPLICATION NUMBER: GB 9726398.2
      ; PRIOR FILING DATE: 1997-12-12
      ; NUMBER OF SEQ ID NOS: 33
      ; SOFTWARE: PatentIn Ver. 2.0
      ; SEQ ID NO 13
      ; LENGTH: 598
      ; TYPE: PRF
      ; ORGANISM: Neisseria meningitidis
      ; US-09-377-155-13

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Query Match	90.2%	Score 2706.5	DB 4	Length 598
Best Local Similarity	90.5%	Pred. No. 2.1e-201		
Matches 545, Conservative	13	Mismatches 29	Indels 15	Gaps 4

Query Match	Similarity	90.7%	Score	2721.5	DB	4	Length	594
Best Local	Similarity	91.6%	Pred.	No. 1.4e-202				
Matches	548	Conservative	12	Mismatches	27	Indels	11	Gaps
Qy	1	MNEILRIIMNSALNAMYVSELTRNHHYKASATVKTAVLATLTLFATVQASANNEOEEDL	60					
Db	1	MNKIRRIIMNSALNAMYVSELTRNHHYKASATVKTAVLATLTLFATVQANAND---	DDTL	57				
Qy	61	YLDPLVPLTAVAVIYVSDKEGTEKREKVEENSMAVYFENKGVLTFAREILKRGDNLIKQ	120					
Db	58	YLEPQKRAVVLSEFSDDEGTEKREKTED-SMAYVYFPEDEKRLKAGATILKAGDNLIKQ	116					
Qy	121	-----NCTNFTYSLKKDLJDLTSVGETEKLSEFSAANGKNVITSDTKGLNFAKETAGTND	174					
Db	117	NTNENTNINSFPTYSLKDKLTLDTLSYETEKLSEFGANGKNVITSDTKGLNFAKETAGTND	176					
Qy	175	TTVHLNGIGSTLTDTLMLMGATTNTNNVNPDEKKRAASVQDVLNAGNINIGVAPGCTA	234					
Db	177	PLVHLNGIGSTLTDTLMLMGATTNTNDVVDDEKKRAASVQDVLNAGNINIGVAPGCTA	236					
Qy	235	SDNVDFVRYDTVEFLSADTKTTTVNVVESKDGKKTVEYKIGAKTSYIKEDDKLVTGKDR	294					
Db	237	SDNVDFVRYDTVEFLSADTKTTTVNVVESKDGKKTVEYKIGAKTSYIKEDDKLVTGKGR	296					
Qy	295	GENSSSTPEGEGELTFAKEVLDVAVNKAAGRMKTTTNGGTGQADKEETVSGNNVFAASK	354					
Db	297	DENSSSTDEGELTFAKEVLDVAVNKAAGRMKTTTNGGTGQADKEETVSGNNVFAASK	356					
Qy	355	GTTATVSKDDGNGITVMVDVNGDALNNQNLNSGMNLDSKVAVASSSGKVIISGNVPSKQ	414					
Db	357	GTTATVSKDDGNGITVVKVDVNGDALNNQNLNSGMNLDSKVAVASSSGKVIISGNVPSKQ	416					
Qy	415	KMDETVNINAGNNEITETNGKNIDATISMTPOFSSVSLGAGADAPLTSLVDG-ALNVGSK	473					
Db	417	KMDETVNINAGNNEITETNGKNIDATISMAPOFSSVSLGAGADAPLTSLVDGALNVGSK	476					
Qy	474	KDNKFEVRIITNNAVGVKEGVDVNTVAOLKGVQAMNNRINDVNDONARAGIAQALATATAGLVQA	533					
Db	477	DTNKFEVRIITNNAVGVKEGVDVNTVAOLKGVQAMNNRINDVNDONARAGIAQALATATAGLVQA	536					
Qy	534	YLPQKSMALIGGTYRGEGVYVIGVSSISDGGNNWIIKGAISGNSGHPGASVGYQW	591					

Qy	1	MNLTIRIIMNSALAAWYVSELTIRNHRKRASATVTKAVLTLLTFAIYQASANEDEED	60
Qy	1	MNLTIRIIMNSALAAWYVSELTIRNHRKRASATVTKAVLTLLTFAIYQASANEDEED	60
Db	1	MNLTIRIIMNSALAAWYVSELTIRNHRKRASATVTKAVLTLLTFAIYQASANEDEED	57
Qy	61	YLDVFLKTVAAVLINSDRKEGTGEKEKEEENSDAWYVNEKGVLTAREITLKAGDNLIKQ	120
Db	58	YLEPVQRTAAVLSPRSDKEGTGEKEGTED-SNMAVYFDEKRRVLKAGAITLKAGDNLIKQ	116
Qy	121	-----NGTFFYLSLKOLDLTLSVGTSEKESFANGKNVITSDTGLGNPAKKTAG	170
Db	117	NTNENTNENTNDSSFTYSLKLDLTLSVETEKLSFANGKNVITSDTGLGNPAKKTAG	176
Qy	171	TNGDTYHLNIGISTLTDLTLNTGATNTNDVTDDEKKRAASVKDVLNAGNINIKVPR	230
Db	177	TNGDPTYHLNIGISTLTDLTLNTGATNTNDVTDDEKKRAASVKDVLNAGNINIKVPR	236
Qy	231	GTTASDNDVDFVRIYDFVEFLSADTKRTTVVNESKDNCKKTEVKGATSVYKEKDGKLV	290
Db	237	GTTASDNDVDFVRIYDFVEFLSADTKRTTVVNESKDNCKKTEVKGATSVYKEKDGKLV	296
Qy	291	GKMDGENSSSTDEEBEGLVTAKEVIDAANKGWRKTTTANGQGTQOAKFEVTSIGTWT	350
Db	297	GKMDGENSSSTDEEBEGLVTAKEVIDAANKGWRKTTTANGQGTQOAKFEVTSIGTWT	356
Qy	351	ASGKGTATVASKDOGNITVYDVVNDGADALVNLOLQNSGNLJLSKAAVAGSSGKVISGN	410
Db	357	ASGKGTATVASKDOGNITVYDVVNDGADALVNLOLQNSGNLJLSKAAVAGSSGKVISGN	416
Qy	411	PSKGMDETVINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDGD-ALN	468
Db	417	PSKGMDETVINAGNNIETIRNGKNIDIASMTPOFSSVSLGAGADAPLTVSDDEGALN	476
Qy	470	VGSKDKDKPVKITVAVGVEGDVTNAOLKGVQONLNRRDNDVGNARAGIQAIFTAG	529
Db	477	VGSDANKPVKITVAVGVEGDVTNAOLKGVQONLNRRDNDVGNARAGIQAIFTAG	536
Qy	530	LYQAYLTPGKSMMAIGGGTYRREAGAYTAIGYSSISDGGNMIIKGTASGNSRGHFGASASV	589
Db	537	LAQAYLTPGKSMMAIGGGTYRREAGAYTAIGYSSISDGTGMWIKGTASGNSRGHFGASASV	596
Qy	590	QW 591	

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Db 597 QW 598

RESULT 12
US-09-669-974-13
; Sequence 13, Application US/09669974
; Patent No. 6333173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 13
; LENGTH: 598
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
US-09-669-974-13

Query Match 90.2%; Score 2706.5; DB 4; Length 598;
Best Local Similarity 90.5%; Pred. No. 2.1e-201;
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;

QY 1 MNELIRIINMSALNANWVSELRNHTKRASATYKTVATLTLLFATVQAANNEDEEDL 60
DB 1 MNELIRIINMSALNANWVSELRNHTKRASATYKTVATLTLLFATVQAANNTD---DDDL 57
QY 61 YLDPVLTAVLVNDSKEGTGEKEKEVENSMDAVYFNEKGVLTAREITLKAGDNLKIKO 120
DB 58 YLEPVORTAVVLSPRSDEKTEGEKEDG--SNAVYFDEKRVLKAGAITLKAGDNLKIKO 116
QY 121 -----NGTNFTYSLKKDLTDLTSVGTETKLSFGANGNKVNTSDTGLNFAKCTAG 170
DB 117 NTNENTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGNKVNTSDTGLNFAKCTAG 176
QY 171 TNGDTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKRRASVKVYLAAGNVIKGVK 230
DB 177 TNGDPVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKRRASVKVYLAAGNVIKGVK 236
QY 231 GTTASDNVDFVRYDYVEFLSADTKTTTVNVEKDKNGKTEVKGAKTSYIKEDGKLV 290
DB 237 GTTASDNVDFVRYDYVEFLSADTKTTTVNVEKDKNGKTEVKGAKTSYIKEDGKLV 296
QY 291 GKDKGENSGSTDBEGGLVTAKEVIDAVNKAQWRKTTTANGQGTGQADKFETVTSGTWTF 350
DB 297 GKDKGENSGSTDBEGGLVTAKEVIDAVNKAQWRKTTTANGQGTGQADKFETVTSGTWTF 356
QY 351 ASGKGTATVSKDQGITVYDVNVGDALNVNOLONGNLDLSKAAVAGSSGKVIISGNVS 410
DB 357 ASGNGTATVSKDQGITVYDVNVGDALNVNOLONGNLDLSKAAVAGSSGKVIISGNVS 416
QY 411 PSKGKDETVNINAGNIEITRNGKNIDITSMTPQSSVSLGAGADAPTLSDVGD-ALN 469
DB 417 PSKGKDETVNINAGNIEITRNGKNIDITSMTPQSSVSLGAGADAPTLSDVDEBALN 476
QY 470 VGSKKDKRPVITNVAGVEGDTVNAQLKGYAQNLNINIDVNDGARRAGIAQALATAG 529
DB 477 VGSKDANKPVRITNVAGVEGDTVNAQLKGYAQNLNINIDVNDGARRAGIAQALATAG 536
QY 530 LVQAYILPKGSMMAIGGCTYGEAGYALGYSSISDGGNMIITKGTASGNSRHFPGASASVGY 589
DB 530 LVQAYILPKGSMMAIGGCTYGEAGYALGYSSISDGGNMIITKGTASGNSRHFPGASASVGY 589
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Db 537 LQAYILPKGSMMAIGGCTYGEAGYALGYSSISDPTGNWVIKGTASGNSRHFPGASASVGY 596
QY 590 QW 591
Db 597 QW 598

RESULT 13
US-09-377-155-5
; Sequence 5, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 5
; LENGTH: 598
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
US-09-377-155-5

Query Match 90.2%; Score 2705.5; DB 4; Length 598;
Best Local Similarity 90.4%; Pred. No. 2.5e-201;
Matches 544; Conservative 14; Mismatches 29; Indels 15; Gaps 4;

QY 1 MNELIRIINMSALNANWVSELRNHTKRASATYKTVATLTLLFATVQAANNEDEEDL 60
DB 1 MNELIRIINMSALNANWVSELRNHTKRASATYKTVATLTLLFATVQAANNTD---DDDL 57
QY 61 YLDPVLTAVLVNDSKEGTGEKEKEVENSMDAVYFNEKGVLTAREITLKAGDNLKIKO 120
DB 58 YLEPVORTAVVLSPRSDEKTEGEKEDG--SNAVYFDEKRVLKAGAITLKAGDNLKIKO 116
QY 121 -----NGTNFTYSLKKDLTDLTSVGTETKLSFGANGNKVNTSDTGLNFAKCTAG 170
DB 117 NTNENTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGNKVNTSDTGLNFAKCTAG 176
QY 171 TNGDTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKRRASVKVYLAAGNVIKGVK 230
DB 177 TNGDPVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKRRASVKVYLAAGNVIKGVK 236
QY 231 GTTASDNVDFVRYDYVEFLSADTKTTTVNVEKDKNGKTEVKGAKTSYIKEDGKLV 290
DB 237 GTTASDNVDFVRYDYVEFLSADTKTTTVNVEKDKNGKTEVKGAKTSYIKEDGKLV 296
QY 291 GKDKGENSGSTDBEGGLVTAKEVIDAVNKAQWRKTTTANGQGTGQADKFETVTSGTWTF 350
DB 297 GKDKGENSGSTDBEGGLVTAKEVIDAVNKAQWRKTTTANGQGTGQADKFETVTSGTWTF 356
QY 351 ASGKGTATVSKDQGITVYDVNVGDALNVNOLONGNLDLSKAAVAGSSGKVIISGNVS 410
DB 357 ASGNGTATVSKDQGITVYDVNVGDALNVNOLONGNLDLSKAAVAGSSGKVIISGNVS 416
QY 411 PSKGKDETVNINAGNIEITRNGKNIDITSMTPQSSVSLGAGADAPTLSDVGD-ALN 469
DB 417 PSKGKDETVNINAGNIEITRNGKNIDITSMTPQSSVSLGAGADAPTLSDVDEBALN 476
QY 470 VGSKKDKRPVITNVAGVEGDTVNAQLKGYAQNLNINIDVNDGARRAGIAQALATAG 529
DB 477 VGSKDANKPVRITNVAGVEGDTVNAQLKGYAQNLNINIDVNDGARRAGIAQALATAG 536
QY 530 LVQAYILPKGSMMAIGGCTYGEAGYALGYSSISDGGNMIITKGTASGNSRHFPGASASVGY 589
DB 530 LVQAYILPKGSMMAIGGCTYGEAGYALGYSSISDGGNMIITKGTASGNSRHFPGASASVGY 589
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[illegible]

RESULT 14  
US-09-669-

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: Sequence 5, Application US/09669974
: Patent No. 6331173
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/669,974
: CURRENT FILING DATE: 2000-09-26
: PRIOR APPLICATION NUMBER: US 09/377,155
: PRIOR FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: Patentln Ver. 2.0
: SEQ ID NO 5
: LENGTH: 598
: TYPE: prt
: ORGANISM: Neisseria meningitidis
: US-09-669-974-5

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Query Match	90.2%;	Score 2705.5;	DB 4;	Length 598;
Best Local Similarity	90.4%;	Pred. No. 2.5e-201;		
Matches 544;	Conservative 14;	Mismatches 29;	Indels 15;	Gaps 4

Oy	1	MNEIIRITIMNSALNAWVVSSELTNRHNRKRAATYKTAVALTILEPATYQOASNNEDCEEDL	60
Dd	1	MNKISRIITMNSALNAWVVSSELTNRHNRKRAATYATATVALTILEPATYQOANATD---DDDL	57
Oy	61	YLDPLVLTVAVLIVNSDKEGTGEK EKV EENS DMAVYENEGVLTAREITTLAKGDNLIKQ	120
Dd	58	YLEPQRTAVVLSFRSDEGTGEKEGED -SNMAVYEDKKVYLKAAGITTLKAGDNLIKQ	116
Oy	121	-----NGTNPYSLKKDLDLTVSGYGEKLSFGANGKVVITSDTGLNPAKKTAG	170
Dd	117	NTNENTNENTNDSSTYSYLKDLTDLTVSETEKLSFGANGKVVITSDTGLNPAKKTAG	176
Oy	171	TNGDTPVHLANGISGTLTDLTLNTGATNTVNTDNTYDDEKKRAASVKKVLANAGWIKVKP	230
Dd	177	TNGDTPVHLANGISGTLTDLTLNTGATNTVNTDNTYDDEKKRAASVKKVLANAGWIKVKP	236
Oy	231	GTTASDNDVFPRTDYVEFLSADTKTTTVVNESKNGKTEVTKGATSVYKEKDKGLVT	290
Dd	237	GTTASDNDVFPRTDYVEFLSADTKTTTVVNESKNGKRTVEVTKGATSVYKEKDKGLVT	296
Oy	291	GKDGGENSSVDEDEGGLTAK EVDANKAGWRKTTTANGQTOGAKPFVTVSGTWTF	350
Dd	297	GKDGGENSSVDEDEGGLTAK EVDANKAGWRKTTTANGQTOGAKPFVTVSGTWTF	356
Oy	351	ASGKGTTATVSKDQGNITTVYDVNVGDLVNLQNSGWNLDJSKAVAGSSGKVISGNVS	410
Dd	357	ASGKGTTATVSKDQGNITTVYDVNVGDLVNLQNSGWNLDJSKAVAGSSGKVISGNVS	416
Oy	411	PSKGMDETVINAGNNIETTRNGKNIDIATSMTPQSSVSLGAGADPTLSVDCG-ALN	466
Dd	417	PSKGMDETVINAGNNIETTRNGKNIDIATSMTPQSSVSLGAGADPTLSVDCGALN	476
Oy	470	VGSKDKNKPVLTITVAPGVKREGDVTNTAOLKGVANQNLNRRIDNDVGNARAGIQAITAG	529

Db	477	VGSDDANPVRITNVAGVYKGEVDYNTVAOLKGVNQNNRINDVNDGNAARAGIAQAATATAG	536
Oy	530	LVQAYLPKRSMMALGGGTGYREAGYATCGSYISIDGGMMITKGTASGNSRSHFGASASVGY	589
Db	537	LAQAYLPKRSMMALGGGTGYREAGYATCGSYISIDTGMWVTKGTASGNSRSHFGTSASVGY	596
Oy	590	QW 591	
Db	597	QW 598	

RESULT 15  
US-09-377-1

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1      Sequence 15, Application US/09377155
2      Patent No. 6197312
3      GENERAL INFORMATION:
4      APPLICANT: PEAK, Ian Richard Anselm
5      APPLICANT: JENNINGS, Michael Paul
6      APPLICANT: MOKON, E. Richard
7      TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
8      FILE REFERENCE: 065064,0/128
9      CURRENT APPLICATION NUMBER: US/09/377,155
10     CURRENT FILING DATE: 1999-08-19
11     PRIOR APPLICATION NUMBER: PCT/AU98/01031
12     PRIOR FILING DATE: 1998-12-14
13     PRIOR APPLICATION NUMBER: GB 9726398.2
14     PRIOR FILING DATE: 1997-12-12
15     NUMBER OF SEQ ID NOS: 33
16     SOFTWARE: PatentIn Ver. 2.0
17     SEQ ID NO 15
18     LENGTH: 599
19     TYPE: PRT
20     ORGANISM: Neisseria meningitidis
21     US-09-377-155-15

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Query Match	89.2%;	Score 2676;	DB 4;	length 599;
Best Local Similarity	89.0%;	Pred. NO. 4.8e-199;		
Matches 536;	Conservative 18;	Mismatches 34;	Indels 14;	Gaps 4;

OY	1	MNELIRITIMNSALNAWAVVSELTZRNHRKRAATVKTVLTTLEFATVOASANNEDEEDD	60
Dd	1	NNKIYRIIMNSALNAWAVSELTRNHRKRASATYKTIVLATLLEFATVOAANAATEDDEEE-	59
OY	61	YLDPVLRTVAVLIVNSDKECTGEKEVEBDAVVFENEKVLTARETILKADNLKIKO	120
Dd	60	-LEEVSALALQPMIREKGENSEST-GNIGMSIYYDNMTLHGAVTILKADNLKIKO	117
OY	121	-----NGHEFTSLKNDLDELTSVGEEKLSFGANKNKNTISDTGLMFAKETAG	170
Dd	118	NTKNKNENTNMDSFFYSLKDLFDLTSVETEKLSFGANKNKNTISDTGLMFAKETAG	177
OY	171	TNGDT'VHLANGISGTLTDLTLLTGATTNVINDNVTDDEKKRAASVKDYLNAGNNIKGVP	230
Dd	178	TNGDT'VHLANGISGTLTDLTLLTGATTNVINDNVTDDEKKRAASVKDYLNAGNNIKGVP	237
OY	231	GTPASDNDVPR'RYTDYEPFLSADTKTTTVAVESKDNRKTEVAKIGASTSYRKDGKLYT	290
Dd	238	GTPASDNDVPH'HYTDYEFBSADTKTTTVAVESKDNRKTEVAKIGASTSYRKDGKLYT	297
OY	291	GKDXGENSGSTDECEGLVTAKEVIDAENVAKGWRKTTTJANGOTGOADKFETVTSGTNYTF	350
Dd	298	GKXGENSGSTDECEGLVTAKEVIDAENVAKGWRKTTTJANGOTGOADKFETVTSGTNYTF	357
OY	351	ASGGTATATVSKDDOGNITWYKYDVNVGDALINVNOLOMSGNLLDSKAANGSSGVISGNVS	410
Dd	358	ASGGTATATVSKDDOGNITWYKYDVNVGDALINVNOLOMSGNLLDSKAANGSSGVISGNVS	417
OY	411	PSRKMDETIVINAGNNIEITRNKNIDIAITSMTPORSSVSLGAGADAPLSDVG-DALN	469
Dd	418	PSRKMDETIVINAGNNIEITRNKNIDIAITSMTPORSSVSLGAGADAPLSDVDGALN	477
OY	470	VGSKKNDPVARITVABPVKEGDVTVNAOLKGYAOULNBRINDVDCNARAGICAOAIATAG	529



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Db 478 VGSKDANKPVRIITNVAPGVKEGDPVTNVAQLKGVAQNLNRRIDNVDCNARAGIAQAIAATAG 537
QY 530 LVQAYILPGKSMMAIGGTYRGEGYTAIGYSSISDGGNWIIGKTASGNSRGRHFGASASVGY 589
Db 538 LVQAYILPGKSMMAIGGTYRGEGYTAIGYSSISDGGNWIIGKTASGNSRGRHFGASASVGY 597
QY 590 QW 591
Db 598 QW 599
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Job time: 531 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:09:09 ; Search time 168.6 Seconds  
(without alignments)  
394.622 Million cell updates/sec

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Perfect score: 3060  
Sequence: 1 MNKYIRIWNALNAWAVS.....TASGSRGHFGASAVGVQW 599

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3060	100.0	599	20 AAY23743	A surface protein
2	3060	100.0	599	22 AAU06176	N. meningitidis H3
3	2824.5	92.3	598	20 AAY23742	A surface protein
4	2824.5	92.3	598	22 AAU06177	N. meningitidis H1
5	2821.5	92.2	598	20 AAY23738	A surface protein
6	2821.5	92.2	598	22 AAU06178	N. meningitidis B2
7	2802.5	91.6	594	20 AAY23739	A surface protein
8	2802.5	91.6	594	22 AAU06179	N. meningitidis B2
9	2762.5	90.3	594	20 AAY23740	A surface protein
10	2762.5	90.3	594	21 AAY57044	BASB029 amino acid
11	2762.5	90.3	594	22 AAU06174	N. meningitidis EG

12	2699.5	88.2	592	20 AAY23744	A surface protein
13	2699.5	88.2	592	21 AAU06172	N. meningitidis H4
14	2696	88.1	591	21 AAY57045	BASB029 amino acid
15	2694	88.0	589	20 AAY23745	A surface protein
16	2694	88.0	589	22 AAU06173	N. meningitidis P2
17	2685	87.7	591	20 AAY27202	Amino acid sequenc
18	2685	87.7	591	22 AAY23746	A surface protein
19	2685	87.7	591	22 AAU06171	N. meningitidis PM
20	2676	87.5	591	20 AAY23741	A surface protein
21	2676	87.5	591	22 AAU06175	N. meningitidis EG
22	2663.5	87.0	592	20 AAY23737	A surface protein
23	2587.5	84.6	592	22 AAU06180	N. meningitidis Z2
24	2551.5	83.4	592	20 AAY27203	Amino acid sequenc
25	2472	80.8	513	22 AAU06183	N. meningitidis H4
26	2453.5	80.2	512	22 AAU06182	N. meningitidis PM
27	2371.5	77.5	502	22 AAU06186	N. meningitidis PM
28	2231.5	72.9	604	22 AAU06181	N. meningitidis su
29	2032	66.4	433	22 AAU06185	N. meningitidis PM
30	1886	61.6	407	22 AAU06184	N. meningitidis PM
31	1271	41.5	2353	17 AAR99393	Haemophilus adhesi
32	1246	40.7	2411	21 AAB23860	Haemophilus influe
33	1070.5	35.0	1098	17 AAR99392	Haemophilus influe
34	1053.5	34.4	1094	21 AAB23858	Haemophilus influe
35	1008	32.9	679	17 AAR99394	Haemophilus adhesi
36	1008	32.9	679	21 AAB23855	Haemophilus influe
37	970.5	31.7	245	20 AAY27201	Amino acid sequenc
38	758.5	24.8	1004	21 AAB23857	Haemophilus influe
39	743.5	24.3	1002	21 AAB23854	Haemophilus influe
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42	600	19.6	116	21 AAB37832	Neisserial conserv
43	401.5	13.1	2123	22 AAE00701	Moraxella catarrha
44	398.5	13.0	1992	17 AAW04505	Moraxella 200 kDa
45	398.5	13.0	1992	22 AAB69133	M. catarrhalis str

#### ALIGNMENTS

RESULT 1  
AAY23743  
ID AAY23743 standard; Protein; 599 AA.  
XX  
AC AAY23743;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW Immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-AL.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI: 1999-418754/35.  
DR N-PSDB; AAY85795.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX

PS Claim 1; Page 114-115; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 599 AA;

Query Match 100.0%; Score 3060; DB 20; Length 599;  
Best Local Similarity 100.0%; Pred. No. 7.9e-171;  
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVCAANATDEDEEL 60  
Db 1 mnkiyriiwsalnawavseltrnhtkrasatvktavlatllfatvqanatedeeseel 60

Qy 61 EPVRSALVLFQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120  
Db 61 epvrsalvlfqfmidkegngengestgnigwsiyydnhntlhgatvtlkagdnlkikqntn 120

Qy 121 KNTNENTNDSSFTYSLKDLTDLASVTEKLSFGANGKXVNTSDTKCLNFAKETAGTNG 180  
Db 121 kntnentndssftysllkdlldlsveteklsfgangknkvnitsdtkgnlfaketagtn 180

Qy 181 DTTVHLNGIGSTLDTLNTGATTNVTNDVTDOKKRAASVKDVLNAGWNKIGVKPGTT 240  
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Qy 241 ASDNVDFVHTYDTEFLSADTKTNTVNVESKDNKGRTEVKTAGTSVIKEKDKGLVTGKG 300  
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Qy 301 KGENGSSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTQADKFEFVTSGTNVTFASG 360  
Db 301 kgensstdegeglvtakevldavnkagwrmtttangotqadkfetvtsgtntvtfasg 360

Qy 361 KGTATVSKDQGNITVKYIDYVNGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420  
Db 361 kgtatvskdqqnitvkydyvngdalnvnglqnsqwnldskavagssgkvisgnvpsk 420

Qy 421 GKMDETVNIAGNIEITRNKNIIDIAFSMTPPQSSVSLGAGADAPTLVSVDKGLALNVGS 480  
Db 421 gkmdetvniagnieitrngknidiatsmtppqfssvslgagadaptilsvdkgalnvgs 480

Qy 481 KDANKPVRITNVAPQVKEGDTNVNOLKGAQNLNRRINDVGNARAGIAQAIATAGLVQ 540  
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Qy 541 AYLPGKSMMAIGGTYREAGYAIYGSISDPGNNIIRKGTASGNSRHFASASVGYQW 599  
Db 541 aylpgksmmaiggytyreagyaiygsisdpgnniirkgtsagnsrhfgasasvgyqw 599

RESULT 2  
AAU06176  
ID AAU06176 standard; Protein; 599 AA.  
XX AAU06176;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE *N. meningitidis* H38 surface antigen Noha polypeptide sequence.  
XX Surface antigen Noha; meningococcal disease; meningitis vaccine.  
KW  
XX *Neisseria meningitidis* strain H38.  
OS

XX PH Key Location/Qualifiers  
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FT /note= "Conserved region 1"  
FT Region 51..105  
FT /label= V1  
FT /note= "Variable region 1"  
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FT /note= "Conserved region 5"  
XX WO200155182-A1.  
PN  
XX  
XX 02-AUG-2001.  
XX  
XX 25-JAN-2001; 2001WO-AU000069.  
XX  
XX 25-JAN-2000; 2000US-0177917.  
XX (UYOU ) UNIV QUEENSLAND.  
XX Peak IRA, Jennings MP;  
PI  
XX WPI; 2001-488774/53.  
DR N-PSDB; AAS09166.  
XX  
XX New Noha surface antigen polypeptides and polynucleotides from  
PT *Neisseria meningitidis*, useful in producing vaccines for treating or  
PT preventing broad spectrum of *Neisseria meningitidis* -  
XX Claim 9; Fig 1; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel *Neisseria*  
CC meningitidis mutant polypeptides of the surface antigen Noha  
CC (AAU06182-AAU06186). The modified or mutant Noha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of *N. meningitidis*, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of *N. meningitidis* strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Noha  
CC from *N. meningitidis* strain H38 is 1 of 10 Noha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different *N. meningitidis* strains given in  
XX the present invention.  
SQ Sequence 599 AA;

Query Match 100.0%; Score 3060; DB 22; Length 599;  
Best Local Similarity 100.0%; Pred. No. 7.9e-171;  
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 mnkiyriiwnlsalnawavseltrnhtkrasatvktavlatllfatvqanatdedeeel 60  
QY 61 EPVRSALVQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120  
Db 61 epvrsalvqfmidkegngengestgnigwsyiyddhntlhgatvtlkagdnlikqkntn 120  
QY 121 KNTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNG 180  
Db 121 kntnentndssfyslkkdltdltsveteklsfgangknvntsdctkglnfaketagting 180  
QY 181 DTTVHLNGIGSTLTDLLNTGATNTVNDYDDKKRAASVKDVLNAGWNITKGVKPGTT 240  
Db 181 dttvhlngigstltdllntgattntvndytdkkrasvkdvlmagwnikgvkpgtt 240  
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Db 241 asdnvdfvhtydtveflsadtktttvnveskngkrtvekgaktsvikekdglvtgkg 300  
QY 301 KGENGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGOADKFTETVTSGTNVTFASG 360  
Db 301 kgensstdegeglvtakevidavnkagwrmtnttngotgoadkftetvtsgtntvtfasg 360  
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Db 421 gkmdetvniagnnieitrngknidatmtptqfssvslgagadaptslvddkglngvsg 480  
QY 481 KDANKPVRITNVAPVKEGDTVNVQALKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 540  
Db 481 kdankpvrntnvapvkegdtvnnvqalkgvaqlnrnidnvdgnaraglaaiaataglvq 540  
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Db 541 aylpgksmmaigggtyrgeagyaigyssisdgggnwiikgtasgnsrghfgasasvgyqw 599

## RESULT 3

AA06177  
ID AA06177 standard; Protein; 598 AA.

AC AA06177;

DT 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

DE Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.

XX Neisseria meningitidis.

OS WO9931132-A1.

XX 24-JUN-1999.

PD 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85794.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

PS Claim 1; Page 108-110; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 598 AA;

Query Match 92.3%; Score 2824.5; DB 20; Length 598;  
Best Local Similarity 92.7%; Pred. No. 4.4e-157;  
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

QY 1 MNKIYRIIWNLSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60

Db 1 mnkiyriiwnlsalnawavseltrnhtkrasatvktavlatllfatvqanat-d-dddyl 59

QY 61 EPVRSALVQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120

Db 60 epvrtavvlsfrskgegtednsnwavfydkrvlkagailkagdnlikqkntn 119

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Db 120 entnentndssfyslkkdltdltsveteklsfgangknvntsdctkglnfaketagting 179

QY 181 DTTVHLNGIGSTLTDLLNTGATNTVNDYDDKKRAASVKDVLNAGWNITKGVKPGTT 240

Db 180 dptvhlngigstltdllntgattntvndytdkkrasvkdvlmagwnikgvkpgtt 239

QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKSKNGKRTVEKIGAKTSVIEKDKGLVTGKG 300

Db 240 asdnvdfvhtydtveflsadtktttvnveskngkrtvekgaktsvikekdglvtgkg 299

QY 301 KGENGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGOADKFTETVTSGTNVTFASG 360

Db 300 kgensstdegeglvtakevidavnkagwrmtnttngotgoadkftetvtsgtntvtfasg 359

QY 361 KGTATVSKDDQGNITVKYDNNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420

Db 360 ngttatvskddgnitvkydnnvgdalnvnqlnsgwnldskavagssgkvisgnvpsk 419

QY 421 GKMDETVNIAGNNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLSVDDKGLNNGVS 480

Db 420 gkmdetvniagnnieitrngknidatmtptqfssvslgagadaptslvddkglngvsg 479

QY 481 KDANKPVRITNVAPVKEGDTVNVQALKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 540

Db 480 kdankpvrntnvapvkegdtvnnvqalkgvaqlnrnidnvdgnaraglaaiaataglaq 539

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Db 540 aylpgksmmaigggtyrgeagyaigyssisdgggnwiikgtasgnsrghfgasasvgyqw 598

## RESULT 4

AAU06177  
ID AAU06177 standard; Protein; 598 AA.

AC AAU06177;

DT 24-OCT-2001 (first entry)

XX N. meningitidis H15 surface antigen Noha polypeptide sequence.

XX Surface antigen Noha; meningococcal disease; meningitis vaccine.

XX	OS	Neisseria meningitidis strain H15.	
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FT	FT		/label= C1
FT	FT		/note= "Conserved region 1"
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FT	FT		/note= "Variable region 1"
FT	FT	Region	105..116
FT	FT		/label= C2
FT	FT		/note= "Conserved region 2"
FT	FT	Region	117..130
FT	FT		/label= V2
FT	FT		/note= "Variable region 2"
FT	FT	Region	131..194
FT	FT		/label= C3
FT	FT		/note= "Conserved region 3"
FT	FT	Region	195..216
FT	FT		/label= V3
FT	FT		/note= "Variable region 3"
FT	FT	Region	217..235
FT	FT		/label= C4
FT	FT		/note= "Conserved region 4"
FT	FT	Region	236..242
FT	FT		/label= V4
FT	FT		/note= "Variable region 4"
FT	FT	Region	243..598
FT	FT		/label= C5
FT	FT		/note= "Conserved region 5"
XX	XX	WO200155182-A1.	
XX	XX	02-AUG-2001.	
XX	XX	25-JAN-2001; 2001WO-AU00069.	
XX	XX	25-JAN-2000; 2000US-0177917.	
XX	XX	(UYQU ) UNIV QUEENSLAND.	
PI	Peak IRA, Jennings MP;		
XX	WPI; 2001-488774/53.		
DR	N-PSDB; AAS09167.		
XX	New Noha surface antigen polypeptides and polynucleotides from		
PT	Neisseria meningitidis, useful in producing vaccines for treating or		
PT	preventing broad spectrum of Neisseria meningitidis		
XX	Claim 9; Fig 1; 91pp; English.		
XX	The present invention relates to the isolation of novel Neisseria		
CC	meningitidis mutant polypeptides of the surface antigen Noha		
CC	(AAU06182-AAU06186). The modified or mutant Noha polypeptides are		
CC	characterised by deletions of non-conserved amino acids, particularly		
CC	the deletion of variable regions. The deletion mutants are useful in		
CC	diagnostics, therapeutic and prophylactic vaccines against a broader		
CC	spectrum of N. meningitidis, and in designing and/or screening of		
CC	medicaments. The mutant proteins when used as a vaccine can effectively		
CC	immunise against a broader spectrum of N. meningitidis strains than		
CC	would be expected from a corresponding wild-type surface antigen.		
CC	The present sequence representing the wild type surface antigen Noha		
CC	from N. meningitidis strain H15 is 1 of 10 Noha polypeptide sequences		
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in		
CC	the present invention.		
XX	Sequence 598 AA;		
SQ			
Query Match	92.3%; Score 2824.5; DB 22; Length 598;		
Best Local Similarity	92.7%; Pred. No. 4.4e-157;		

Matches	555;	Conservative	14;	Mismatches	29;	Indels	1;	Gaps	1;
Qy	1	MNKIVRIIWN	SALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEBEL	60					
Db	1	mmklyriiwn	salsawvseltrnhtkrasatvatavlatllfatvqanad-dddlyl	59					
Qy	61	EPVVR	SALVLFQFMIDKEGNGENESTGNIGWIIYDNNHNTLHGATVTLKAGDNKLTKQNTN	120					
Db	60	epvqr	tavvlsfrsdkegtgekedtsednwavfdekrvilkagaitlkagdnklkqntn	119					
Qy	121	KNTNENT	NDSSFTYSLKKDLTDLTSVETEKLSFGANGNKVNITSDTKGLNFAKETAGTNG	180					
Db	120	entnntndss	ftyslkkdldtsveteklsfgangnkvnitstdtkglnfaketagtn	179					
Qy	181	DTTVHLNG	IGISLTLDTLNTGATTNVTDKKRAASVKDVLNAGWNIKGVPCTT	240					
Db	180	dptvhlng	igistldtllntgattntdndvtddekkraasvkvlnagwnikgvpctt	239					
Qy	241	ASDNVDFVHTY	VEFLSADTKTTTVNVYESKDNKRTVEIKGAKTSVTEKDGKLVTKG	300					
Db	240	asdnvdfvrt	ydtveflsadtktttvnveskdngkktvkgaktsvtekdgklvtgk	299					
Qy	301	KGNGS	STDEGEGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFEFTVTSCTNVT	360					
Db	300	kdengsstde	geglvtakevidavnkagwrmtttangqtgqadkftvtsctnvtfsg	359					
Qy	361	KGTTATVSK	DDQGNITVKYDVNVGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSPSK	420					
Db	360	ngttatvsk	ddqgnitvkvynvgdnlvngsqwnldskavagssgkvisgnvpsk	419					
Qy	421	GKMDETVNI	NAGNIEITRNKNIDIAFMTPTQFSSVSLGAGADAPTLSDVDKALNVGS	480					
Db	420	gkmdetvni	nagnieitrngknidiatsmtpqfssvslgagadaptlsvddegalnvs	479					
Qy	481	KDANKPVRIT	NVAPVKEGDTNVVAQLKGVAQNLRNDVGNARAGIAQAIATAGLVQ	540					
Db	480	kdanpvr	itnvapvkegdtnvvaqlkgvaqnlrnrndvgnaraglaqaiataglaq	539					
Qy	541	AYLPCKSM	MAITGGGTYRGEAGYAIYSSISDGNWIKGTASGNSRHFASASVGYOW	599					
Db	540	aylpcksm	maigggtyrgeagyaigyssisdgtnwvlgktagsgnsrghfgasasvgyqw	598					
RESULT	5								
AAV23738									
ID	AAV23738	standard; Protein; 598	AA.						
XX	AAV23738;								
AC	AAV23738;								
XX	08-SEP-1999	(first entry)							
DT	08-SEP-1999	(first entry)							
XX									
DE		A surface protein of Neisseria meningitidis.							
XX		Surface protein; surface glycoprotein; infection; vaccine;							
KW		immunoreactive peptide.							
XX		Neisseria meningitidis.							
OS		Neisseria meningitidis.							
XX		WO9931132-A1.							
XX		24-JUN-1999.							
XX		14-DEC-1998; 98WO-AU01031.							
XX		12-DEC-1997; 97GB-0026398.							
PR		(ISIS-) ISIS INNOVATION LTD.							
XX		(UYQU ) UNIV QUEENSLAND.							
PA		Jennings MP, Moxon ER, Peak IRA;							
XX		WPI; 1999-418754/35.							
DR		N-PSDB; AAX85790.							

```
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PS Claim 1; Page 91-93; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match          92.2%; Score 2821.5; DB 20; Length 598;
Best Local Similarity 92.7%; Pred. No. 6.5e-157;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 1 MKKIRIINWNSALNAWVSELTNRHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 mkksirliwnsalnawvseiltnrhtkrasatvatavlatllfatvqanatl-dddl 59
QY 61 EPVRSALVQPMIDKEGNESTCIGNWSIYYDNNHNTLHGATVTLKAGDNLIKQNTN 120
Db 60 epvqrtavvisrdsqegtegekedtsnwavyfdekrvfkagaitckagdnlikqnc 119
QY 121 KNTNENTNDSSEFYSLLKDLTDLTSTVETKLSFGANGKVNITSDTKGLNFAKETAGTNG 180
Db 120 entnentndssftyslkkaldtstveteklsfgangkvnitsdtkglinfaketagtn 179
QY 181 DRTVHLNGIGSLTDLTLNLTGATFNTVNDVDDKKRAASVKDVLNAGWNKIGVKPGTT 240
Db 180 dptvhlngigsltdtlntgattntvndvddkkraasvkdvltnagwnikgvpkgtt 239
QY 241 ASDNVDFVHTYDTVEFLSADTHTTVNVESKDKGRTEVKIGAKTSVKEKGKLVTKG 300
Db 240 asdnvdfvtydtveflsadtktttvnveskdngkrtevkigaktsvikekgklvtgk 299
QY 301 KGENSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKPETVTSGTNTVTFASG 360
Db 300 kgensstdegeglvtakevidavnkagwrmttttangtggadkftetvtsgtkvtfasg 359
QY 361 KGTATVSKDDGNTVTKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 360 ngttatvskddgnttkydyvngvdalnvqnqlqnswnldskavagssgkvisgnvpsk 419
QY 421 GKWDEVTNINAGNNIEITRNGKNIDTATSWTPQFSVSLGAGADAPTLSVDKDGALNVCS 480
Db 420 gkmdetvnlagnnleitrngknidatstmpqfssvslgagadapltlsvddgelnvcs 479
QY 481 KDANKPVRITNVPAGKEGDVTNVAQLKGVAQNLNRRIDVNGNARAGIAQAIAATAGLVQ 540
Db 480 kdankpvrntnvpagkegdvtnvaqlkgvaqnlrridvngnarnaraglaiaataglaq 539
QY 541 AYLPGKSMMAIGGYRGAGYAIGYSSISDGNWIIKTAGSNGSRGHFGASASVGYQW 599
Db 540 aylpgksmmaiggytyrgeaygaigyssisdtgnwviktagasngsrghfgtasvgyqw 598

RESULT 6
AAU06178
ID AAU06178 standard; Protein; 598 AA.
XX
AC AAU06178;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis Bz10 surface antigen Nhha peptide sequence.
```

```
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
KW Neisseria meningitidis strain Bz10.
OS
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..104 /label= V1
FT /note= "Variable region 1"
FT Region 105..116 /label= C2
FT /note= "Conserved region 2"
FT Region 117..130 /label= V2
FT /note= "Variable region 2"
FT Region 131..194 /label= C3
FT /note= "Conserved region 3"
FT Region 195..216 /label= V3
FT /note= "Variable region 3"
FT Region 217..235 /label= C4
FT /note= "Conserved region 4"
FT Region 236..242 /label= V4
FT /note= "Variable region 4"
FT Region 243..598 /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
PF 25-JAN-2001; 2001WO-AU00069.
PR 25-JAN-2000; 2000US-0177917.
XX (UYQU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
DR WPI; 2001-488774/53.
DR N-PSDB; AAS09168.
XX
PT New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
PS Claim 9; Fig 1; 9lpp; English.
XX
CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC medicaments. The mutant proteins when used as a vaccine can effectively
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain Bz10 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC the present invention.
XX
SQ Sequence 598 AA;
```





XX N. meningitidis Bz198 surface antigen Nhha polypeptide sequence.  
 XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
 KW Neisseria meningitidis strain Bz198.  
 OS  
 XX Key Location/Qualifiers  
 XX Region 1..50  
 FT /label= C1  
 FT /note= "Conserved region 1"  
 FT Region 51..104  
 FT /label= V1  
 FT /note= "Variable region 1"  
 FT Region 105..116  
 FT /label= C2  
 FT /note= "Conserved region 2"  
 FT Region 117..126  
 FT /label= V2  
 FT /note= "Variable region 2"  
 FT Region 127..190  
 FT /label= C3  
 FT /note= "Conserved region 3"  
 FT Region 191..212  
 FT /label= V3  
 FT /note= "Variable region 3"  
 FT Region 213..231  
 FT /label= C4  
 FT /note= "Conserved region 4"  
 FT Region 232..238  
 FT /label= V4  
 FT /note= "Variable region 4"  
 FT Region 239..594  
 FT /label= C5  
 FT /note= "Conserved region 5"  
 XX WO200155182-A1.  
 PN  
 XX 02-AUG-2001.  
 PD  
 XX 25-JAN-2001; 2001WO-AU00069.  
 PF  
 XX 25-JAN-2000; 2000US-0177917.  
 PR  
 XX (UYQU ) UNIV QUEENSLAND.  
 PA  
 XX Peak IRA, Jennings MP;  
 PI  
 XX WPI; 2001-488774/53.  
 DR N-PSDB; AAS09169.  
 DR  
 XX New Nhha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis .  
 XX  
 XX Claim 9; Fig 1; 91pp; English.  
 PS  
 XX The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC immunisants. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha  
 CC from N. meningitidis strain Bz198 is 1 of 10 Nhha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX Sequence 594 AA;  
 SQ

Query Match 91.6%; Score 2802.5; DB 22; Length 594;  
 Best Local Similarity 92.5%; Pred. No. 8.3e-156;  
 Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;  
 QY 1 MNKIYRIIWNNSALNNAWVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATDEDEEEL 60  
 DB 1 mkiyriiwnsalnawvavseltrnhtkrasatavlatlilfatvqanatd-dddlyl 59  
 QY 61 EPVRSALVLQFMIDKEGENESTIGNWSIYYDNHNLHGATVTLKAGDNLIKIKONTN 120  
 DB 60 epvrtavvlfrskdtegtedshwvfyfdekrvlkagaitlkagdnlikikg--- 116  
 QY 121 KNTNENTNDSSFTYSLKDLTDLTSVETKLSFGANGKNVNITSDTKGLNFAKETAGTNG 180  
 DB 117 -ntnentndssftyslkkdltdltsveteklsfgangknvnitsdckglnfaketagtng 175  
 QY 181 DTTVHLNGIGSTLTDTLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKIGVPGT 240  
 DB 176 dptvhlingigstltdtllntgattnvtndvddkkraasvkdvlmagwnikgvkpgtt 235  
 QY 241 ASDNVDFVHTYDFVFLSADTKTTTVNVESKONGKTEVKIGAKTSVIEKEKDKLVTKG 300  
 DB 236 asdnvdfvrtvdfvflsadtktttvnveskdngkktvkgaktsviekdkglvtgk 295  
 QY 301 KGENSSDDEGGLVTAKEVIDAVNKAGRMKTTTANGOTGOADKFTETVTSCTNVTFASG 360  
 DB 296 kdengssddegglvtakevidavnkagrmktttangotgoadkftetvtsctnvtfasg 355  
 QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSK 420  
 DB 356 kgtatvskddqgnitvkydvnvvgdalnvnqlnsgnwldkavagssgkvisgnvspk 415  
 QY 421 GKMDETVNIAGNNIEITRNGKNIDIATSKTPOFSSVSLGAGADAPTLSDVDDKALNVGS 480  
 DB 416 gkmdetvniagnnieitrngknidiatsmapqfssvslgagadaptlsvdddegalnvgs 475  
 QY 481 KDANKPVRITNVAPGVKEGDTVNAOLKGAONLNRIIDNVGNARAGIAQAATATAGLVQ 540  
 DB 476 kdnkpvritnvapgvkegdtvnalolkgvaonlnriidnvgnaraglaqataglvq 535  
 QY 541 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASGVQW 599  
 DB 536 aylpgksmmaiggyrgeagyaigyssisdggnwiikgtasgnsrghfgasasgvqw 594  
 RESULT 9  
 AAY23740  
 ID AAY23740 standard; Protein; 594 AA.  
 XX  
 AC AAY23740;  
 XX  
 DT 08-SEP-1999 (first entry)  
 XX  
 DE A surface protein of Neisseria meningitidis.  
 XX  
 KW Surface protein; surface glycoprotein; infection; vaccine;  
 KW immunoreactive peptide.  
 XX  
 OS Neisseria meningitidis.  
 XX  
 PN WO9931132-A1.  
 XX  
 PD 24-JUN-1999.  
 XX  
 PF 14-DEC-1998; 98WO-AU01031.  
 XX  
 PR 12-DEC-1997; 97GB-0026398.  
 XX  
 PA (ISIS-) ISIS INNOVATION LTD.  
 PA (UYQU ) UNIV QUEENSLAND.  
 XX

PI Jennings MP, Moxon ER, Peak IRA;  
XX WPI; 1999-418754/35.  
DR N-PSDB; AAX85792.  
XX  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
XX Claim 1; Page 100-101; 132pp; English.  
XX  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX Sequence 594 AA;  
SQ  
  
Query Match 90.3%; Score 2762.5; DB 20; Length 594;  
Best Local Similarity 91.7%; Pred. No. 1.8e-153;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
  
Qy 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVKTAVALTLLEFATVOANATDEDEEL 60  
Db 1 mnkyriiwsalnawavseltrnhtkrasatvatavlatllefatqastdd-dddlyl 59  
  
Qy 61 EPVRSALVLOFMIDKEGNGENSTGNIGWYIYDNNHTLHGATVTLKAGDNLKIKQNTN 120  
Db 60 epvrtavvlsfrsdkegtevednsnwgvyfdkkgvltagtitikagdnllkq--- 116  
  
Qy 121 KNTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180  
Db 117 -ntnentnassfyslkkdltdltsvteklfsfnsnknvntsdtkglnfakkttaetng 175  
  
Qy 181 DTTVHLNGIGSLTDLTLNLTGATNTVNDVTDDBKRAASVDVNLNAGWNKGVKPGTT 240  
Db 176 dttvhngigsltdltnltgatntvndvtdbdkraasvdkvnlagnwnkvgkpgtt 235  
  
Qy 241 ASDNVDFVHTYDTEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIEKDGKLVTKGK 300  
Db 236 asdhvdfvtydteflsadtktttvnveskdngkrtevkigaktsviekdgklvtgkd 295  
  
Qy 301 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFETVTSCTWVTASG 360  
Db 296 kgengsstdgeglvtakevldavnkagwrmktttangqtgqadkfetvtsctwvtfasg 355  
  
Qy 361 KGTATVSKDQGNITVKYDYNVGDALNVNOLNSGWNLDKAVAGSGKVIYSGNVSPSK 420  
Db 356 kgtatvskdqgnitvmydvngvdalnvnqlngsgwnldskavagsgkviyngnvspsk 415  
  
Qy 421 GKMDETVINAGNIEITRNKNIDIAITSMPTQFSSVSLGAGADAPTLSDVDKALNVGS 480  
Db 416 gkmdetvinagnieitrnknidiatmtptqfssvslgagadaptlsvddegalnvg 475  
  
Qy 481 KDANKPVRIITNAPGVKEGDTNVAQLKGVAQNLRNDRDNDVGNARAGIAIATAGLVQ 540  
Db 476 kdankpvritnapgvkegdtnvaqlkgvaqnlnrhdndvgnaragiaiataglvq 535  
  
Qy 541 AYLPGKSMMAIGGTYRGEAGYAIYSSISDGGNWIITKGASGNSRHFHGASASVGVQW 599  
Db 536 aylpgksmmaiggytyrgeagyaigyssisdgggnwiitkgasgnsrghfghgasasvgyqw 594  
  
RESULT 10  
AAY57044  
ID AAY57044 standard; Protein; 594 AA.  
XX  
AC AAY57044;

XX 21-FEB-2000 (first entry)  
DT  
DE BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
XX  
XX BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
XX Neisseria meningitidis.  
OS  
XX  
XX Key Location/Qualifiers  
FH Misc-difference 104 /note= "Encoded by AATC"  
FT  
FN WO9958683-A2.  
XX  
PD 18-NOV-1999.  
XX  
PF 07-MAY-1999; 99WO-EP03255.  
XX  
PR 13-MAY-1998; 98GB-0010276.  
XX  
PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
XX  
PI Ruelle J;  
XX  
XX WPI: 2000-053103/04.  
DR N-PSDB; AAZ39864.  
XX  
PT New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
XX  
XX Claim 4; Fig 2; 74pp; English.  
XX  
CC This is the Neisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing a Neisseria  
CC meningitidis and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 594 AA;

Query Match 90.3%; Score 2762.5; DB 21; Length 594;  
Best Local Similarity 91.7%; Pred. No. 1.8e-153;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
  
Qy 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVKTAVALTLLEFATVOANATDEDEEL 60  
Db 1 mnkyriiwsalnawavseltrnhtkrasatvatavlatllefatqastdd-dddlyl 59  
  
Qy 61 EPVRSALVLOFMIDKEGNGENSTGNIGWYIYDNNHTLHGATVTLKAGDNLKIKQNTN 120  
Db 60 epvrtavvlsfrsdkegtevednsnwgvyfdkkgvltagtitikagdnllkq--- 116  
  
Qy 121 KNTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180  
Db 117 -ntnentnassfyslkkdltdltsvteklfsfnsnknvntsdtkglnfakkttaetng 175

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QY 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKRAASVKDVLNAGWNIKGVKPGTT 240
DB 176 dtvhlngigstltdtllntgattntdntdvddekkraasvkdvlndagwnikgvkpgtt 235
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTNNVESKDKGRKTEVIGAKTSVIEKDKGLVTGKG 300
DB 236 asdnvdfvhtydtveflsadtktttnnveskdngkrtevigaktsviekdgklvtgkd 295
QY 301 KGENSGSTDEGEGLVTAKEVIDAVNKAAGRMTTANGQTGQADKPEETVTSCTNVTTFASG 360
DB 296 kgendsstdkgeglvtakevidavnkagwrmtttangqtgqadkfetvtsgtnvtfsg 355
QY 361 KGTATVSKDDCGNITVKYDYNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNNVSPSK 420
DB 356 kgtatvskddcgntvkmymydvngdnlvngqlnsgwnldskavagssgkvisgnvpsk 415
QY 421 GKMDFTVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
DB 416 gkmdetvniagnieitrngknidiatsmtpfssvslgagadaptlsvdddegalnvg 475
QY 481 KDANKPVRTNVPAGVKEGDTNVAQLKGAQNLRNIDVNGNARAGIAQAIAATAGLVQ 540
DB 476 kdankpvrtnvpagvkegdtnvvaqlkgvaqnlrnhldnvdngnaraglaqalataglvq 535
QY 541 AYLPKSMMAIGGTYRGAGYAIGYSSTSDGNNWIIKGTASGNSRHFGASASVGYOW 599
DB 536 aylpksmmaiggytyrgagyaigyssisdggnwliktasgnsrghfgasasvgyow 594

RESULT 11
AAU06174
ID AAU06174 standard; Protein; 594 AA.
XX
AC AAU06174;
XX
DT 24-OCT-2001 (first entry)
DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.
XX
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain EG327.
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT 51..104 /label= V1
FT /note= "Variable region 1"
FT 105..116 /label= C2
FT /note= "Conserved region 2"
FT 117..126 /label= V2
FT /note= "Variable region 2"
FT 127..190 /label= C3
FT /note= "Conserved region 3"
FT 191..212 /label= V3
FT /note= "Variable region 3"
FT 213..231 /label= C4
FT /note= "Conserved region 4"
FT 232..238 /label= V4
FT /note= "Variable region 4"
FT 239..594 /label= C5
FT /note= "Conserved region 5"
XX
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WO200155182-A1.

XX

02-AUG-2001.

XX

25-JAN-2001; 2001WO-AU000069.

XX

25-JAN-2000; 2000US-0177917.

XX

(UYOU ) UNIV QUEENSLAND.

PA

Peak IRA, Jennings MP;

XX

WPI; 2001-488774/53.

DR

N-PSDB; AAS09164.

XX

New Nhha surface antigen polypeptides and polynucleotides from Neisseria meningitidis, useful in producing vaccines for treating or preventing broad spectrum of Neisseria meningitidis -

XX

Claim 9; Fig 1; 91pp; English.

XX

The present invention relates to the isolation of novel Neisseria meningitidis mutant polypeptides of the surface antigen Nhha (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are characterised by deletions of non-conserved amino acids, particularly the deletion of variable regions. The deletion mutants are useful in diagnostics, therapeutic and prophylactic vaccines against a broader spectrum of N. meningitidis, and in designing and/or screening of

CC

medicaments. The mutant proteins when used as a vaccine can effectively

CC

immunise against a broader spectrum of N. meningitidis strains than

CC

would be expected from a corresponding wild-type surface antigen.

CC

The present sequence representing the wild type surface antigen Nhha

CC

from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences

CC

(AAU06171-AAU06180) from 10 different N. meningitidis strains given in

CC

the present invention.

XX

SQ Sequence 594 AA;

Query Match 90.3%; Score 2762.5; DB 22; Length 594;  
Best Local Similarity 91.7%; Pred. No. 1.8e-153;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

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QY 1 MNKIYRIWNSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 1 mkiyriwnsalnawvavseltrnhtkrasatvktavlatllfatvqasttd-dddlyl 59
QY 61 EPVRSALVLQFMIDKEGNGENESTGNIGWSIYYDNNHTLHGATVTLKAGDNLKIKONTN 120
DB 60 epvrtavvlsfrskgegtednsngvyfdkkgvltagtitlkagdnlikkq--- 116
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
DB 117 -ntnentnassftyslkkdltdltsveteeklsfsaansknvntsdtkgnfakktetng 175
QY 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKRAASVKDVLNAGWNIKGVKPGTT 240
DB 176 dtvhlngigstltdtllntgattntdntdvddekkraasvkdvlndagwnikgvkpgtt 235
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTNNVESKDKGRKTEVIGAKTSVIEKDKGLVTGKG 300
DB 236 asdnvdfvhtydtveflsadtktttnnveskdngkrtevigaktsviekdgklvtgkd 295
QY 301 KGENSGSTDEGEGLVTAKEVIDAVNKAAGRMTTANGQTGQADKPEETVTSCTNVTTFASG 360
DB 296 kgendsstdkgeglvtakevidavnkagwrmtttangqtgqadkfetvtsgtnvtfsg 355
QY 361 KGTATVSKDDCGNITVKYDYNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNNVSPSK 420
DB 356 kgtatvskddcgntvkmymydvngdnlvngqlnsgwnldskavagssgkvisgnvpsk 415
QY 421 GKMDFTVNIAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
DB 416 gkmdetvniagnieitrngknidiatsmtpfssvslgagadaptlsvdddegalnvg 475
```

```
Db 416 gkndetvniagnnieitrngknidiatsmtpqfssvslgagadapltlsvddgalnvgs 475
QY 481 KDANKPVRITNVAPGVKEGSDVTNVAQLKGYAQNLRIDNVGNARAGIAQAIAATAGLVQ 540
Db 476 kdankpvrinrvapgvkegavtnvaqlkgyaqnlhnhidnvgnaragiaaiaataglvq 535
QY 541 AYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 599
Db 536 aylpksmmaig999tyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 594

RESULT 12
AAY23744
ID AAY23744 standard; Protein; 592 AA.
XX
AC AAY23744;
XX
DT 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN W09931132-A1.
XX
PD 24-JUN-1999.
XX
PF 14-DEC-1998; 98WO-AU01031.
XX
PR 12-DEC-1997; 97GB-0026398.
XX
PA (ISIS-) ISIS INNOVATION LTD.
PA (UTQU ) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
XX WPI: 1999-418754/35.
XX N-PSDB; AAX85796.
XX
PT Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
PS Claim 1; Page 118-120; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 592 AA;

Query Match 88.2%; Score 2699.5; DB 20; Length 592;
Best Local Similarity 91.2%; Pred. No. 8.5e-150;
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

QY 1 MNKYRIIWNALNANWAVASELFRNHFKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 mnklyriiwnsalnawavaseltrnhktrasatvktavlatllfratvqanatedeeseel 60
QY 61 EPVVRSAVLVQFMIDKEGNGENESTGNIGWSIYYDNTLHG-ATVTLKAGDNLKIKQNT 119
Db 61 esvqrs-vvgsiqasmeqvelet---islsmtdnskefvdpyivvltkagdnkikq-- 114
QY 120 NKNTNENTNDSSFTYSLKKDLTDLTSTVETEKLSFGANGKNVNITSDPKGLNFAKETAGTN 179
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Db 115 --ntnentnassfyslkkdlgtlinveteklsifgankkvnlisdcgkgnfaketagtn 172
QY 180 GDTTVHLNGISGLTDTLLNTGATTTNVTNDNVTDDKKRAASVKDVLNAGWNKGVKPGT 239
Db 173 gdtvhlngisgltdmlntgattnvtdndvtddekkraasvkdvlinaagwnlkgvkgpgt 232
QY 240 TASDNVDVFVHTYDTEFLSADTKTTTNNVESKDNKRKTEYKIGAKTSVVIKEKGKLVTK 299
Db 233 tasdnvdfvrtlyteflsadtkttttnveskdngkktvkigaktsvikekgkklvtgk 292
QY 300 KGKENGSSDDEGLVTAKEVIDAVNKAGWRMKTITTANGOTGQADKXETVTSGTNVTTFAS 359
Db 293 kgkengsstdegeglvtakevidavnkagwrmtktttangtgdqdkfetytsgtkvtfas 352
QY 360 KGKTTATVSKDDOGNTTVKYDVNVGDALNVNQLNSQWNLDSKAVAGSSGKVTSGNVSPS 419
Db 353 gngttatvskddggnltcvkydvngdnlvngnlqnsqwnlidskavagssgkvvisgnavsps 412
QY 420 KGKMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDDKALNVG 479
Db 413 kgkmdetvinagnnieitrngknidiatsmtpqfssvslgagadapltlsvddgalnvq 472
QY 480 SKDANKPVRITNVAPGVKEGSDVTNVAQLKGYAQNLRIDNVGNARAGIAQAIAATAGLV 539
Db 473 skdankpvrinrvapgvkegavtnvaqlkgyaqnlhnhidnvgnaragiaaiaataglv 532
QY 540 QAYLPKSMMAIGGGTYRGEAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 599
Db 533 qaylpksmmaig999tyrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyqw 592

RESULT 13
AAU06172
ID AAU06172 standard; Protein; 592 AA.
XX
AC AAU06172;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis H41 surface antigen NnhA polypeptide sequence.
XX
KW Surface antigen NnhA; meningococcal disease; meningitis vaccine.
XX
OS Neisseria meningitidis strain H41.
XX
FH Key Location/Qualifiers
FT Peptide 1..51 /label= Signal_peptide
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..102 /label= V1
FT /note= "Variable region 1"
FT Protein 52..592 /label= Mature_NnhA
FT /note= "Predicted mature protein, specifically
FT claimed in claim 12"
FT Region 103..114 /label= C2
FT /note= "Conserved region 2"
FT Region 115..124 /label= V2
FT /note= "Variable region 2"
FT Region 125..188 /label= C3
FT /note= "Conserved region 3"
FT Region 189..210 /label= V3
FT /note= "Variable region 3"
FT Region 211..229 /label= C4
FT
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FT      /note= "Conserved region 4"
FT      230..236
FT      /label= V4
FT      /note= "Variable region 4"
FT      237..592
FT      /label= C5
FT      /note= "Conserved region 5"
XX      WO200155182-A1.
XX      02-AUG-2001.
XX      25-JAN-2001; 2001WO-AU00069.
XX      25-JAN-2000; 2000US-0177917.
XX      (UQUU ) UNIV QUEENSLAND.
XX      Peak IRA, Jennings MP;
XX      WPI: 2001-488774/53.
XX      N-PSDB; AAS09162.
XX      New Nhaa surface antigen polypeptides and polynucleotides from
PT      Neisseria meningitidis, useful in producing vaccines for treating or
PT      preventing broad spectrum of Neisseria meningitidis .
XX      Claim 9; Fig 1; 9lpp; English.
XX      The present invention relates to the isolation of novel Neisseria
CC      meningitidis mutant polypeptides of the surface antigen Nhaa
CC      (AAU06182-AAU06186). The modified or mutant Nhaa polypeptides are
CC      characterised by deletions of non-conserved amino acids, particularly
CC      the deletion of variable regions. The deletion mutants are useful in
CC      diagnostics, therapeutic and prophylactic vaccines against a broader
CC      spectrum of N. meningitidis, and in designing and/or screening of
CC      medicaments. The mutant proteins when used as a vaccine can effectively
CC      immunise against a broader spectrum of N. meningitidis strains than
CC      would be expected from a corresponding wild-type surface antigen.
CC      The present sequence representing the wild type surface antigen Nhaa
CC      from N. meningitidis strain H41 is 1 of 10 Nhaa polypeptide sequences
CC      (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
CC      the present invention.
XX      Sequence 592 AA;
SQ
Query Match      88.2%; Score 2699.5; DB 22; Length 592;
Best Local Similarity 91.2%; Pred. No. 8.5e-150;
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;
QY      1 MKKIYRIIWSNALNRAWAVSELRHTRKRSATVTVTAVALTLFATVQANATDEDEEEL 60
DB      1 mkkiiyriiwnsalnrawavseltrhtrkrsatvktavlatllfatvqanatede 60
QY      61 EPVRSALVLPQFMIDKEGENESGTGSIYYDHNHNTLHG-ATVTLKAGDNLTKONT 119
DB      61 esvqrs-vvgsiqasmegsvelet---slsmtndskefvdpyivvtlkagdnlikq-- 114
QY      120 NKNTNNTNDSFTYSLKDLFDLTVSETEKLSFGANGKNVNITSDTKGLNFAKETAGTN 179
DB      115 --ntnentnassftysllkdkllnveteklsfsgangkknvniisdtkglnfaketagn 172
QY      180 GDTTVHLNIGISGTLTDLTLNLTGATTVNNDVTDKKRAASVKDVLNAGWNIKGVKPGT 239
DB      173 gdttvhlngisgtldmlntgattvntdndvtddekkraasvkdvlmagwnikgvkpgt 232
QY      240 TASDNVDFVHTYDVFELISADFTVTVNVESKDNGKRTVEKIGAKTSVTKEDGKLVTKG 299
DB      233 tasdnvdfvrtvdytvefilsadkttvntvveskdngkrtvekgaktsvikekdgkvlv 292
QY      300 KGKGENSSTDEGGLVTAKEVIDAYNKAGWRMKTITANGQTQADKFETVTSCTNVTFAS 359

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DB      293 gkgengsstdeglvtakevidavnkagwrmtktttangtqgqadkfetvtsgtkvtfas 352
QY      360 GKGTTATVSKDDQGNITVYDVNVGDALNVNOLQNSGWNLDKAVAGSSGKVTSGNVSPS 419
DB      353 gngttatvskddqgnitvkydvnvgdalnvnlqnsqwnldskavagsgkvtsignvps 412
QY      420 KGKMDETVNIAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLSVDDKALNYG 479
DB      413 kgkmdetvniagnnieitrcngknidiatmtppqfssvslgagadaptilsvddegalnvg 472
QY      480 SKDANKPVRITNWAPGVREGDVTNVAQLKGVAQNLNRRIDNVGDNARAGIAQAIATAGLV 539
DB      473 skdankpvrtnvapgvkegdvtvnaqlkgvagnlnrridnvnngnragiaqaiataglv 532
QY      540 QAYLPCKSMMAIGGGTYRGEAGYATIGYSSISDGGNWIKGTASGNSRHFHGASASVGYQW 599
DB      533 qaylpcksmmaigggtyrgeagyaigysisaggnwilkgtasgnsrhfgasasvgyqw 592

```

## RESULT 14

AAV57045  
ID AAV57045 standard; Protein; 591 AA.

XX AC AAV57045;

XX DT 21-FEB-2000 (first entry)

DE BASB029 amino acid sequence from N. meningitidis strain H44/76.

KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;  
infection; treatment; prevent; antibacterial drug.

XX OS Neisseria meningitidis.

Key	Location/Qualifiers
Misc-difference 90	/note= "Encoded by AAT"
Misc-difference 92	/note= "Encoded by GAT"
Misc-difference 98	/note= "Encoded by AAC"
Misc-difference 108	/note= "Encoded by AATC"
Misc-difference 123	/note= "Encoded by ACA"
Misc-difference 269	/note= "Encoded by AAA"
Misc-difference 389	/note= "Encoded by CGT"

XX WO9958683-A2.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-EP03255.

XX 13-MAY-1998; 98GB-0010276.

XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Ruelle J;

XX WPI: 2000-053103/04.

XX N-PSDB; AAZ39865.

XX New polypeptide from neisseria meningitidis useful for diagnosis,  
treatment or prevention of bacterial infections in mammal

XX Claim 4; Fig 2; 74pp; English.

XX This is the Neisseria meningitidis BASB029 amino acid sequence from  
serogroup B strain H44/76. The BASB029 protein is homologous to the  
Haemophilus influenzae surface fibril (HSF) protein. The invention

relates to BASB029 polynucleotide sequences (AAZ39864-239865) and polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments. BASB029 polypeptides are useful in a method of diagnosing a *Neisseria meningitidis* infection in a mammal. Compositions containing BASB029 polynucleotides and polypeptides are useful for generating an immune response in an animal. A therapeutic composition comprising an antibody directed against BASB029 is useful in treating humans with *Neisseria meningitidis* disease. The polynucleotide is useful in the diagnosis of the stage of infection, type of infection, susceptibility to an infection which results from increased or decreased expression of the polynucleotide, and for therapeutic or prophylactic purposes, particularly genetic immunisation. Antibodies against BASB029 polynucleotides and polypeptides are also useful for treating infections particularly bacterial infections. The protein is useful in the screening and development of antibacterial drugs. Fused recombinant protein is useful for the stimulation of the immune system of an organism receiving the protein.

XX	AA	AY23745;	
XX	AC		
XX	XX		
XX	DT	08-SEP-1999 (first entry)	
XX	XX		
DE	XX	A surface protein of Neisseria meningitidis.	
XX	DE		
KW	KW	Surface protein; surface glycoprotein; infection; vaccine; immunoreactive peptide.	
KW	XX		
XX	XX		
OS	OS	Neisseria meningitidis.	
XX	XX		
PN	PN	WO99311132-A1.	
XX	XX		
PD	PD	24-JUN-1999.	
XX	XX		
XX	PF	14-DEC-1998; 98WO-AU01031.	
XX	PF		
XX	PR	12-DEC-1997; 97GB-0026398.	
XX	PA	(ISIS-) ISIS INNOVATION LTD.	
PA	PA	(UYQU ) UNIV QUEENSLAND.	
XX	XX		
PI	PI	Jennings MP, Moxon ER, Peak IRA;	
XX	XX		
DR	DR	WPI; 1999-418754/35.	
DR	DR	N-PSDB; AAX85797.	
XX	XX		
PT	PT	Neisseria meningitidis surface proteins useful for treating N.	
PT	PT	meningitidis infections	
XX	PS	Claim 1; Page 122-124; 132pp; English.	
XX	XX		
CC	CC	The present sequence represents a surface protein of Neisseria	
CC	CC	meningitidis which is approximately 62 kDa. The N. meningitidis	
CC	CC	surface glycoproteins, nucleic acids, the primers and optionally	
CC	CC	a thermostable polymerase, or antibodies are useful in a kit for	
CC	CC	the detection or diagnosis of N. meningitidis infection in humans.	
CC	CC	The N. meningitidis surface glycoproteins can also be used to	
CC	CC	prevent or treat N. meningitidis infection in humans, especially	
CC	CC	in the form of vaccines. The proteins and antibodies can also	
CC	CC	be used to identify immunoreactive peptides.	
XX	XX		
SQ	SQ	Sequence 589 AA;	

RESULT 15

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Db 349 sngttatvskddggnitvkydvnvgdalnvnlqnsqwnldskavagsgkvvisgnvsp 408
    |||||
QY 419 SKGKMDETVNIAGNNIEITRNCKNIDIAITSMTPQFSSVSLGAGADAPTLSDVDDKALNV 478
    |||||
Db 409 skgkmdetvniagnnieitrngknidiatmtptfssvslgagadaptlsvddegaln 468
    |||||
QY 479 GSKDANKPVRITNVAPVKEGDTVNAQLKVAQNLNRRIDNVNVDGNARAGIAQAIATAGL 538
    |||||
Db 469 gskdankpvrित्रnavpvkegdivnvaqlxgvaqnlrridnvngnaraglaiaatagl 528
    |||||
QY 539 VQAYLPCKSMAIGGTYRGEAGYAICYSSISDGGNWIINKGTASGNSRGHFGASASVGYQ 598
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Db 529 aqaylpqksmmaigggtylgeagyaigyssisdtgnwvkgtagsgnrgfhfgtsasvgyq 588
    |||||
QY 599 W 599
Db 589 w 589
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

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Title: US-09-771-382-6  
Perfect score: 3060  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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6: /cgn2\_6/ptodata/2/1aa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3060	100.0	599	4	US-09-377-155-15
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4	2824.5	92.3	598	4	US-09-669-974-13
5	2821.5	92.2	598	4	US-09-377-155-5
6	2821.5	92.2	598	4	US-09-669-974-5
7	2802.5	91.6	594	4	US-09-377-155-7
8	2802.5	91.6	594	4	US-09-669-974-7
9	2762.5	90.3	594	4	US-09-377-155-9
10	2762.5	90.3	594	4	US-09-669-974-9
11	2699.5	88.2	592	4	US-09-377-155-17
12	2699.5	88.2	592	4	US-09-669-974-17
13	2694	88.0	589	4	US-09-377-155-19
14	2694	88.0	589	4	US-09-669-974-19
15	2685	87.7	591	4	US-09-377-155-21
16	2685	87.7	591	4	US-09-669-974-21
17	2676	87.5	591	4	US-09-377-155-11
18	2676	87.5	591	4	US-09-669-974-11
19	2663.5	87.0	592	4	US-09-377-155-2
20	2663.5	87.0	592	4	US-09-669-974-2
21	1271	41.5	2353	4	US-09-377-155-33
22	1271	41.5	2353	4	US-08-913-942-4
23	1271	41.5	2353	4	US-09-669-974-33
24	1270	41.5	2354	4	US-09-268-347-30
25	1246	40.7	2411	4	US-09-268-347-36
26	1199.5	39.2	607	1	US-08-409-995-6
27	1199.5	39.2	607	3	US-08-685-467-6

28	1199.5	39.2	607	4	US-08-913-942-6	Sequence 6, Appli
29	1199.5	39.2	1912	1	US-08-409-995-4	Sequence 4, Appli
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32	1070.5	35.0	1098	3	US-08-685-467-2	Sequence 2, Appli
33	1070.5	35.0	1098	4	US-09-377-155-32	Sequence 32, Appli
34	1070.5	35.0	1098	4	US-08-913-942-2	Sequence 2, Appli
35	1070.5	35.0	1098	4	US-09-669-974-32	Sequence 32, Appli
36	1070.5	35.0	1098	4	US-09-268-347-44	Sequence 44, Appli
37	1053.5	34.4	1094	4	US-09-268-347-32	Sequence 32, Appli
38	1050.5	34.3	658	1	US-08-409-995-5	Sequence 5, Appli
39	1050.5	34.3	658	3	US-08-685-467-5	Sequence 5, Appli
40	1050.5	34.3	658	4	US-08-913-942-5	Sequence 5, Appli
41	1008	32.9	679	4	US-08-913-942-15	Sequence 15, Appli
42	1008	32.9	679	4	US-09-268-347-26	Sequence 26, Appli
43	758.5	24.8	1004	4	US-09-268-347-30	Sequence 30, Appli
44	743.5	24.3	1002	4	US-09-268-347-24	Sequence 24, Appli
45	701.5	22.9	1104	4	US-09-268-347-28	Sequence 28, Appli

ALIGNMENTS

RESULT 1

US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match	100.0%	Score 3060;	DB 4;	Length 599;
Best Local Similarity	100.0%;	Pred. No. 7.2e-233;		
Matches 599;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	MNKIYRIIWNALNAWAVSELTRNHTKRASATVKTAVLATLTLFATVQANATDEDEEEL	60	
Db	1	MNKIYRIIWNALNAWAVSELTRNHTKRASATVKTAVLATLTLFATVQANATDEDEEEL	60	
QY	61	EPVRSALVQFMIDKEGNESTGNIGSIYDHNHTLHGATVTLKAGDNLKIKQNTN	120	
Db	61	EPVRSALVQFMIDKEGNESTGNIGSIYDHNHTLHGATVTLKAGDNLKIKQNTN	120	
QY	121	KNTNENTNDSSFTYSLLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG	180	
Db	121	KNTNENTNDSSFTYSLLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG	180	
QY	181	DTTVHLNGIGSTLTDPLLNATGATVNTNDVDDKKRAASVKDVLNAGNWKGVKPGTT	240	
Db	181	DTTVHLNGIGSTLTDPLLNATGATVNTNDVDDKKRAASVKDVLNAGNWKGVKPGTT	240	
QY	241	ASDNVDFVHTYDTEVFLSADTKTTTNNVESKONGKTEVKGAKTSVKEKDGKLVTKG	300	
Db	241	ASDNVDFVHTYDTEVFLSADTKTTTNNVESKONGKTEVKGAKTSVKEKDGKLVTKG	300	
QY	301	KGNSSTDBEGELVTAKEVIDAVNKAGRMKTMTTANGQTQADKPEVTVTSGTNTVTFASG	360	

Db 301 KGENSGTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSCTNVTFSAG 360  
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420  
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420  
QY 421 GKMDETVINAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKGALNVGS 480  
Db 421 GKMDETVINAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKGALNVGS 480  
QY 481 KDANKPVRITNAPGVKEGDTVNVQAOLKGYAQNLNRRIDNVNDRAGIAQAIAATAGLVQ 540  
Db 481 KDANKPVRITNAPGVKEGDTVNVQAOLKGYAQNLNRRIDNVNDRAGIAQAIAATAGLVQ 540  
QY 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFSGASASVGYQW 599  
Db 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFSGASASVGYQW 599

## RESULT 2

US-09-669-974-15

; Sequence 15, Application US/09669974

; Patent No. 633173

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/669,974

; PRIOR FILING DATE: 2000-09-26

; PRIOR APPLICATION NUMBER: US 09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 15

; LENGTH: 599

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-669-974-15

Query Match 100.0%; Score 3060; DB 4; Length 599;  
Best Local Similarity 100.0%; Pred. No. 7.2e-233;  
Matches 599; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 1 MNKIYRIIWSALNAWAVASELTNRNHTKRASATVKTAVLATLFLPATVOANATDEDEEEL 60  
Db 1 MNKIYRIIWSALNAWAVASELTNRNHTKRASATVKTAVLATLFLPATVOANATDEDEEEL 60  
QY 61 EPVVSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120  
Db 61 EPVVSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120  
QY 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNG 180  
Db 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNG 180  
QY 181 DTTVHLNGIGSTLDTLLNTGATTNVNDVDDKKRAASVKDVLNAGNWKVKPGTT 240  
Db 181 DTTVHLNGIGSTLDTLLNTGATTNVNDVDDKKRAASVKDVLNAGNWKVKPGTT 240  
QY 241 ASDNVDPVHTYDVTVEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 300  
Db 241 ASDNVDPVHTYDVTVEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 300  
QY 301 KGENSGTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSCTNVTFSAG 360

Db 301 KGENSGTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSCTNVTFSAG 360  
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420  
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420  
QY 421 GKMDETVINAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKGALNVGS 480  
Db 421 GKMDETVINAGNNEIETRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKGALNVGS 480  
QY 481 KDANKPVRITNAPGVKEGDTVNVQAOLKGYAQNLNRRIDNVNDRAGIAQAIAATAGLVQ 540  
Db 481 KDANKPVRITNAPGVKEGDTVNVQAOLKGYAQNLNRRIDNVNDRAGIAQAIAATAGLVQ 540  
QY 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFSGASASVGYQW 599  
Db 541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFSGASASVGYQW 599

## RESULT 3

US-09-377-155-13

; Sequence 13, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 13

; LENGTH: 598

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

US-09-377-155-13

Query Match 92.3%; Score 2824.5; DB 4; Length 598;  
Best Local Similarity 92.7%; Pred. No. 2.5e-214;  
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

QY 1 MNKIYRIIWSALNAWAVASELTNRNHTKRASATVKTAVLATLFLPATVOANATDEDEEEL 60  
Db 1 MNKIYRIIWSALNAWAVASELTNRNHTKRASATVKTAVLATLFLPATVOANATD-DDDLYL 59  
QY 61 EPVVSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 120  
Db 61 EPVVSALVLQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQNTN 119  
QY 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNG 180  
Db 121 KNTNENTNDSFYSYSLKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTNG 179  
QY 181 DTTVHLNGIGSTLDTLLNTGATTNVNDVDDKKRAASVKDVLNAGNWKVKPGTT 240  
Db 181 DTTVHLNGIGSTLDTLLNTGATTNVNDVDDKKRAASVKDVLNAGNWKVKPGTT 239  
QY 241 ASDNVDPVHTYDVTVEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 300  
Db 241 ASDNVDPVHTYDVTVEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 299  
QY 301 KGENSGTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSCTNVTFSAG 360  
Db 301 KGENSGTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQOADKFETVTSCTNVTFSAG 359  
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420

Db 360 NCTTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 419  
QY 421 GKMDETVNIAGNNIETIRNGKNIDIATSWTPOFSSVSLGAGADAPTLSVDDKAGALNVGS 480  
Db 420 GKMDETVNIAGNNIETIRNGKNIDIATSWTPOFSSVSLGAGADAPTLSVDDKAGALNVGS 479  
QY 481 KDANKPVRTNTPAVGKEGDTVNAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQ 540  
Db 480 KDANKPVRTNTPAVGKEGDTVNAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQ 539  
QY 541 AYLPGKSMMAIGGGTYRGAGYAIGYSSISDGTGNNWIKGTASGNSRGHFGASASVGYQW 599  
Db 540 AYLPGKSMMAIGGGTYRGAGYAIGYSSISDGTGNNWIKGTASGNSRGHFGASASVGYQW 598

## RESULT 4

US-09-669-974-13  
; Sequence 13, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-13

Query Match 92.3%; Score 2824.5; DB 4; Length 598;  
Best Local Similarity 92.7%; Pred. No. 2.5e-214;  
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;  
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLVL 59  
QY 61 EPVRSALVLPQWIDKEGNESTGNIWSIYDNNHTLHGATVTLKAGDNLKIKQNTN 120  
Db 60 EPVQRTAVVLSFRSDKEGTEGSDSNWYVFDEKRVLKAGAITLKAGDNLKIKQNTN 119  
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTG 180  
Db 120 ENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTG 179  
QY 181 DPTVHLNGIGSLTDLTLNLTGATNTVNDVDDKKRAASVKDVLNAGWNIKGKPGGT 240  
Db 180 DPTVHLNGIGSLTDLTLNLTGATNTVNDVDDKKRAASVKDVLNAGWNIKGKPGGT 239  
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVEKNGKRTVEKIGAKTSVKEKDGKLVTKGK 300  
Db 240 ASDNVDFVHTYDTVEFLSADTKTTTVNVEKNGKRTVEKIGAKTSVKEKDGKLVTKGK 299  
QY 301 KGENSSSTDEGELVTAKEVIDAVNKGAWRMKTITANGOTGQADKFETVTSCTNVTFSAG 360  
Db 300 KGENSSSTDEGELVTAKEVIDAVNKGAWRMKTITANGOTGQADKFETVTSCTNVTFSAG 359  
QY 361 KGTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 420  
Db 360 KGTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 419

Db 360 NCTTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 419  
QY 421 GKMDETVNIAGNNIETIRNGKNIDIATSWTPOFSSVSLGAGADAPTLSVDDKAGALNVGS 480  
Db 420 GKMDETVNIAGNNIETIRNGKNIDIATSWTPOFSSVSLGAGADAPTLSVDDKAGALNVGS 479  
QY 481 KDANKPVRTNTPAVGKEGDTVNAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQ 540  
Db 480 KDANKPVRTNTPAVGKEGDTVNAQLKGVAQNLRNIDVNGNARAGIAQAIAATAGLVQ 539  
QY 541 AYLPGKSMMAIGGGTYRGAGYAIGYSSISDGTGNNWIKGTASGNSRGHFGASASVGYQW 599  
Db 540 AYLPGKSMMAIGGGTYRGAGYAIGYSSISDGTGNNWIKGTASGNSRGHFGASASVGYQW 598

## RESULT 5

US-09-377-155-5  
; Sequence 5, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-5

Query Match 92.2%; Score 2821.5; DB 4; Length 598;  
Best Local Similarity 92.7%; Pred. No. 4.3e-214;  
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;  
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLVL 59  
QY 61 EPVRSALVLPQWIDKEGNESTGNIWSIYDNNHTLHGATVTLKAGDNLKIKQNTN 120  
Db 60 EPVQRTAVVLSFRSDKEGTEGSDSNWYVFDEKRVLKAGAITLKAGDNLKIKQNTN 119  
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTG 180  
Db 120 ENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTG 179  
QY 181 DPTVHLNGIGSLTDLTLNLTGATNTVNDVDDKKRAASVKDVLNAGWNIKGKPGGT 240  
Db 180 DPTVHLNGIGSLTDLTLNLTGATNTVNDVDDKKRAASVKDVLNAGWNIKGKPGGT 239  
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVEKNGKRTVEKIGAKTSVKEKDGKLVTKGK 300  
Db 240 ASDNVDFVHTYDTVEFLSADTKTTTVNVEKNGKRTVEKIGAKTSVKEKDGKLVTKGK 299  
QY 301 KGENSSSTDEGELVTAKEVIDAVNKGAWRMKTITANGOTGQADKFETVTSCTNVTFSAG 360  
Db 300 KGENSSSTDEGELVTAKEVIDAVNKGAWRMKTITANGOTGQADKFETVTSCTNVTFSAG 359  
QY 361 KGTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 420  
Db 360 KGTATVSKDDGNTITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSK 419  
QY 421 GKMDETVNIAGNNIETIRNGKNIDIATSWTPOFSSVSLGAGADAPTLSVDDKAGALNVGS 480

Db 420 GKMDVTNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 479  
QY 481 KDANKPVRITNVPAGVKEGDTVNTVAOLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 540  
Db 480 KDANKPVRITNVPAGVKEGDTVNTVAOLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 539  
QY 541 AYLPGKSMAIGGTYRGEAGYAGYSSISDGTGNWVILKGTASGNSRHFSGASVGYQW 599  
Db 540 AYLPGKSMAIGGTYRGEAGYAGYSSISDGTGNWVILKGTASGNSRHFSGASVGYQW 598

RESULT 6  
US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 92.2%; Score 2821.5; DB 4; Length 598;  
Best Local Similarity 92.7%; Pred. No. 4.3e-214; Indels 1; Gaps 1;  
Matches 555; Conservative 13; Mismatches 30;  
QY 1 MNKIYRIIWSALNANWAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATDDEEEL 60  
Db 1 MNKIYRIIWSALNANWAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATD-DDDLYL 59  
QY 61 EPVRSALVLFQMDKEGNGENESTGNISYIYDHNHTLHGATVTLKAGDNLKIKONTN 120  
Db 60 EPVQRTAVLVSFRSDKEGTEGKEDSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTN 119  
QY 121 KNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180  
Db 120 ENTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179  
QY 181 DTTVHLNGIGSTLTDLLNTGATTNVNDVDDKKRAASVKDVLNAGWNKIKVKGPGTT 240  
Db 180 DPTVHLNGIGSTLTDLLNTGATTNVNDVDDKKRAASVKDVLNAGWNKIKVKGPGTT 239  
QY 241 ASDNVDFVHYDYTFEFLSADTKTTTVNVEKDNKRTVEVIGAKTSVKEKDGKLVTKGK 300  
Db 240 ASDNVDFVHYDYTFEFLSADTKTTTVNVEKDNKRTVEVIGAKTSVKEKDGKLVTKGK 299  
QY 301 KGENSSTDEGGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFFETVSGTNVTFASG 360  
Db 300 KGENSSTDEGGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFFETVSGTNVTFASG 359  
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVQNLQNSGWNLDKAVAGSGKVISGNVSPSK 420  
Db 360 NGTATVSKDDQGNITVKYDYNVGDALNVQNLQNSGWNLDKAVAGSGKVISGNVSPSK 419  
QY 421 GKMDVTNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 480  
Db 420 GKMDVTNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 479

Db 420 GKMDVTNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 479  
QY 481 KDANKPVRITNVPAGVKEGDTVNTVAOLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 540  
Db 480 KDANKPVRITNVPAGVKEGDTVNTVAOLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 539  
QY 541 AYLPGKSMAIGGTYRGEAGYAGYSSISDGTGNWVILKGTASGNSRHFSGASVGYQW 599  
Db 540 AYLPGKSMAIGGTYRGEAGYAGYSSISDGTGNWVILKGTASGNSRHFSGASVGYQW 598

RESULT 7  
US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 91.6%; Score 2802.5; DB 4; Length 594;  
Best Local Similarity 92.5%; Pred. No. 1.3e-212;  
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWSALNANWAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATDDEEEL 60  
Db 1 MNKIYRIIWSALNANWAVAVSELTRNHTKRASATVKTAVLATLTLFATVQANATD-DDDLYL 59  
QY 61 EPVRSALVLFQMDKEGNGENESTGNISYIYDHNHTLHGATVTLKAGDNLKIKONTN 120  
Db 60 EPVQRTAVLVSFRSDKEGTEGKEDSNNAVYFDEKRVLKAGAITLKAGDNLKIKO--- 116  
QY 121 KNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180  
Db 117 -NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175  
QY 181 DTTVHLNGIGSTLTDLLNTGATTNVNDVDDKKRAASVKDVLNAGWNKIKVKGPGTT 240  
Db 176 DPTVHLNGIGSTLTDLLNTGATTNVNDVDDKKRAASVKDVLNAGWNKIKVKGPGTT 235  
QY 241 ASDNVDFVHYDYTFEFLSADTKTTTVNVEKDNKRTVEVIGAKTSVKEKDGKLVTKGK 300  
Db 236 ASDNVDFVHYDYTFEFLSADTKTTTVNVEKDNKRTVEVIGAKTSVKEKDGKLVTKGK 295  
QY 301 KGENSSTDEGGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFFETVSGTNVTFASG 360  
Db 296 KGENSSTDEGGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFFETVSGTNVTFASG 355  
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVQNLQNSGWNLDKAVAGSGKVISGNVSPSK 420  
Db 356 KGTATVSKDDQGNITVKYDYNVGDALNVQNLQNSGWNLDKAVAGSGKVISGNVSPSK 415  
QY 421 GKMDVTNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 480  
Db 416 GKMDVTNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 475  
QY 481 KDANKPVRITNVPAGVKEGDTVNTVAOLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 540

Db 476 KDTNKPVRITNAPVKGEGDVTNVAOLKGVQAOQLNNRDNVDGNARAGIAQAATAGLVQ 535  
QY 541 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFCASASVGYQW 599  
Db 536 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFCASASVGYQW 594

## RESULT 8

US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 6333173

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 91.6%; Score 2802.5; DB 4; Length 594;  
Best Local Similarity 92.5%; Pred. No. 1.3e-212;  
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKAVLATLLFATVQANAT-DBDLYL 59  
QY 61 EPVRSALVQFMIDKEGNESTGNIGSIYDNNHTLHGATVTLKAGDNLKIKONTN 120  
Db 60 EPQRTAVVLSFRSDEGTEGEGEDTSNWAYFDEKRVLKAGAITLKAGDNLKIKQ-- 116  
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180  
Db 117 -NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 175  
QY 181 DTTVHLNGIGSTLTDLLNTGATTNTNDVTDKKRAASVKDVLNAGWNKGVKPGTT 240  
Db 176 DPTVHLNGIGSTLTDLLNTGATTNTNDVTDKKRAASVKDVLNAGWNKGVKPGTT 235  
QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVESKNGKRTVEKIGAKTSVIREKDGKLVTKGK 300  
Db 236 ASDNVDFVHTYDVEFLSADTKTTTVNVESKNGKRTVEKIGAKTSVIREKDGKLVTKGK 295  
QY 301 KGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKEETVSGTNVTFASG 360  
Db 296 KGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKEETVSGTNVTFASG 355  
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420  
Db 356 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 415  
QY 421 GKMDETVNIAGNNIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGS 480  
Db 416 GKMDETVNIAGNNIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGS 475  
QY 481 KDANKPVRITNAPVKGEGDVTNVAOLKGVQAOQLNNRDNVDGNARAGIAQAATAGLVQ 540  
Db 476 KDANKPVRITNAPVKGEGDVTNVAOLKGVQAOQLNNRDNVDGNARAGIAQAATAGLVQ 535

Db 476 KDTNKPVRITNAPVKGEGDVTNVAOLKGVQAOQLNNRDNVDGNARAGIAQAATAGLVQ 535  
QY 541 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFCASASVGYQW 599  
Db 536 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFCASASVGYQW 594

## RESULT 9

US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 90.3%; Score 2762.5; DB 4; Length 594;  
Best Local Similarity 91.7%; Pred. No. 1.9e-209;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKAVLATLLFATVQASTTD-DBDLYL 59  
QY 61 EPVRSALVQFMIDKEGNESTGNIGSIYDNNHTLHGATVTLKAGDNLKIKONTN 120  
Db 60 EPQRTAVVLSFRSDEGTEGEGEDTSNNGVYFDKRGVLTAGTITLKAGDNLKIKQ-- 116  
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180  
Db 117 -NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 175  
QY 181 DTTVHLNGIGSTLTDLLNTGATTNTNDVTDKKRAASVKDVLNAGWNKGVKPGTT 240  
Db 176 DTTVHLNGIGSTLTDLLNTGATTNTNDVTDKKRAASVKDVLNAGWNKGVKPGTT 235  
QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVESKNGKRTVEKIGAKTSVIREKDGKLVTKGK 300  
Db 236 ASDNVDFVHTYDVEFLSADTKTTTVNVESKNGKRTVEKIGAKTSVIREKDGKLVTKGD 295  
QY 301 KGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKEETVSGTNVTFASG 360  
Db 296 KGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGOADKEETVSGTNVTFASG 355  
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420  
Db 356 KGTATVSKDDQGNITVKYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 415  
QY 421 GKMDETVNIAGNNIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGS 480  
Db 416 GKMDETVNIAGNNIETRNKKNIDATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGS 475  
QY 481 KDANKPVRITNAPVKGEGDVTNVAOLKGVQAOQLNNRDNVDGNARAGIAQAATAGLVQ 540  
Db 476 KDANKPVRITNAPVKGEGDVTNVAOLKGVQAOQLNNRDNVDGNARAGIAQAATAGLVQ 535  
QY 541 AYLPGKSMAIGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRHFCASASVGYQW 599

Db 536 AYLPGKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 594  
|||||

## RESULT 10

US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 90.3%; Score 2762.5; DB 4; Length 594;  
Best Local Similarity 91.7%; Pred. No. 1.9e-209;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

Qy 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLFLFATVOANATDEDEEEL 60  
Db 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLFLFATVOASTTD-DDDLYL 59  
Qy 61 EPVYRSALVLOFMIDKEGNGENESTGNIGSIYYDNNHTLHGATVTLKAGDNLKIKQNTN 120  
Db 60 EPVORTAVLFRSDKEGTGEKETEYEDSNMGVYFDKGVLTAGTITLKAGDNLKIKQ--- 116  
Qy 121 KNTNENTNDSFFYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180  
Db 117 -NTNENTNASSFFYSLLKDLTDLTSVETEKLSFSANKNVITSDTKGLNFAKTAETNG 175  
Qy 181 DTTVHLNGIGSTLTDLLNTGATTNVDNVTDDKKRAASVKDVLNAGWNKIGVKPGTT 240  
Db 176 DTTVHLNGIGSTLTDLLNTGATTNVDNVTDDKKRAASVKDVLNAGWNKIGVKPGTT 235  
Qy 241 ASDNVDFVHTYDVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLVTKG 300  
Db 236 ASDNVDFVHTYDVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLVTKG 295  
Qy 301 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFFETVTSCTNVTASG 360  
Db 296 KGENGSTDKGEGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFFETVTSCTNVTASG 355  
Qy 361 KGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDLSKAVAGSGKVISGNVSPSK 420  
Db 356 KGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDLSKAVAGSGKVISGNVSPSK 415  
Qy 421 GKMDETVINAGNIEITRNGKNIDTATSPQFSSVSLGAGADAPTLSDVDKCALNVGS 480  
Db 416 GKMDETVINAGNIEITRNGKNIDTATSPQFSSVSLGAGADAPTLSDVDDEGALNVGS 475  
Qy 481 KDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLNNDNVDGNARAGIAQAIATAGLVQ 540  
Db 476 KDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLNNDNVDGNARAGIAQAIATAGLVQ 535  
Qy 541 AYLPGKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 599  
|||||

Db 536 AYLPGKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 594  
|||||

## RESULT 11

US-09-377-155-17  
; Sequence 17, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-17

Query Match 88.2%; Score 2699.5; DB 4; Length 592;  
Best Local Similarity 91.2%; Pred. No. 1.7e-204;  
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

Qy 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLFLFATVOANATDEDEEEL 60  
Db 1 MNKYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLFLFATVOANATDEDEEEL 60  
Qy 61 EPVYRSALVLOFMIDKEGNGENESTGNIGSIYYDNNHTLHG-ATVTLKAGDNLKIKQNT 119  
Db 61 ESVQRS-VVGSIQASMEGSVELET--ISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQ-- 114  
Qy 120 KNTNENTNDSFFYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 179  
Db 115 -NTNENTNASSFFYSLLKDLTGLINVEETEKLSFGANGKNVITSDTKGLNFAKETAGTN 172  
Qy 180 GDTTVHLNGIGSTLTDLLNTGATTNVDNVTDDKKRAASVKDVLNAGWNKIGVKPGT 239  
Db 173 GDTTVHLNGIGSTLTDMLLNTGATTNVDNVTDDKKRAASVKDVLNAGWNKIGVKPGT 232  
Qy 240 TASDNVDFVHTYDVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLVTKG 299  
Db 233 TASDNVDFVHTYDVEFLSADTKTTTVNVESKDNKGRTEVKIGAKTSVIKEKDGKLVTKG 292  
Qy 300 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFFETVTSCTNVTAS 359  
Db 293 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTGOADKFFETVTSCTNVTAS 352  
Qy 360 KGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDLSKAVAGSGKVISGNVSPS 419  
Db 353 NGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDLSKAVAGSGKVISGNVSPS 412  
Qy 420 KGKMDETVINAGNIEITRNGKNIDTATSPQFSSVSLGAGADAPTLSDVDKCALNVG 479  
Db 413 KGKMDETVINAGNIEITRNGKNIDTATSPQFSSVSLGAGADAPTLSDVDDEGALNVG 472  
Qy 480 SKDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLNNDNVDGNARAGIAQAIATAGLV 539  
Db 473 SKDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLNNDNVDGNARAGIAQAIATAGLV 532  
Qy 540 QAYLPGKSMMAIGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRHFHGASASVGYQW 599  
Db 533 QAYLPGKSMMAIGGTYLGEAGYATGYSSISAGGNWIILKGTASGNSRHFHGASASVGYQW 592  
|||||

## RESULT 12

US-09-669-974-17  
; Sequence 17, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-17

Query Match 88.2%; Score 2699.5; DB 4; Length 592;  
Best Local Similarity 91.2%; Pred. No. 1.7e-204;  
Matches 547; Conservative 11; Mismatches 33; Indels 9; Gaps 4;

QY	1	MNKYRIIWNLSALNAVAVSELTRNHTKRASATVKAVLATLLFATVQANATDEDEEEL	60
DB	1	MNKYRIIWNLSALNAVAVSELTRNHTKRASATVKAVLATLLFATVQANATDEDEEEL	60
QY	61	EPVRSALVQFMIDKEGNGENESTGNIGWSIYYDNHNTLHG--ATVTLKAGDNLIKQNT	119
DB	61	ESVQRS--VVGSIQASMEGSELEET---ISLSMTNDSKEFVDPIVTVTLKAGDNLIKQ--	114
QY	120	NKNTNENTDSSFTYSILKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTN	179
DB	115	--NTNENTNASSFTYSILKKDLTGLINIVETEKLSFGANGKNVNIISDTKGLNFAKETAGTN	172
QY	180	GDPTVHLNGIGSLTDLTLNTGATTNVNDVDDKKRAASVKDVLNAGWNKGVKPGT	239
DB	173	GDPTVHLNGIGSLTDLMLNTGATTNVNDVDDKKRAASVKDVLNAGWNKGVKPGT	232
QY	240	TASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEKDKGLVTGK	299
DB	233	TASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEKDKGLVTGK	292
QY	300	KGKENGSSSTDEGEGLVTAKEVIDAVNKAAGRMTTTTANGOTGOADKFEVTSGTNTVTFAS	359
DB	293	KGKENGSSSTDEGEGLVTAKEVIDAVNKAAGRMTTTTANGOTGOADKFEVTSGTNTVTFAS	352
QY	360	KGKGTATVSKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPS	419
DB	353	GNCTATVSKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSPS	412
QY	420	KGKMDVTNINAGNNTIETRNKNIDIAATSMTPQFSSVSLGAGADAPTLTSDVDDKGLNVG	479
DB	413	KGKMDVTNINAGNNTIETRNKNIDIAATSMTPQFSSVSLGAGADAPTLTSDVDDKGLNVG	472
QY	480	SKDANKPVRITNVAPGKEGDVTNVAQLKGVAQNANRINDVNDGNARAGTAQAIATAGLV	539
DB	473	SKDANKPVRITNVAPGKEGDVTNVAQLKGVAQNANRINDVNDGNARAGTAQAIATAGLV	532
QY	540	QAYLPKSMMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW	599
DB	533	QAYLPKSMMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW	592

## RESULT 13

US-09-377-155-19  
; Sequence 19, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 589  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-19

Query Match 88.0%; Score 2694; DB 4; Length 589;  
Best Local Similarity 89.7%; Pred. No. 4.6e-204;  
Matches 539; Conservative 14; Mismatches 34; Indels 14; Gaps 3;

QY	1	MNKYRIIWNLSALNAVAVSELTRNHTKRASATVKAVLATLLFATVQANATDEDEEEL	60
DB	1	MNKYRIIWNLSALNAVAVSELTRNHTKRASATVKAVLATLLFATVQANATDEDEEEL	60
QY	61	EPVRSALVQFMIDKEGNGENESTGNIGWSIYYDNHNTLHGATVTLKAGDNLIKQNTN	120
DB	61	ESVRSALVQFMIDKEGNGEIESTGIGWSIYYDDHTLHGATVTLKAGDNLIKQ--	117
QY	121	KNTNENTDSSFTYSILKKDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTN	180
DB	118	-----SGKDFYSLKKELDLTDLTSVETEKLSFGANGKNVNIISDTKGLNFAKETAGTN	170
QY	181	DTTVHLNGIGSLTDLTLNTGATTNVNDVDDKKRAASVKDVLNAGWNKGVKPGTT	240
DB	171	DTTVHLNGIGSLTDLTLNTGATTNVNDVDDKKRAASVKDVLNAGWNKGVKPGTT	228
QY	241	A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEKDKGLVTG	298
DB	229	TGSENVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEKDKGLVTG	288
QY	299	KGKENGSSSTDEGEGLVTAKEVIDAVNKAAGRMTTTTANGOTGOADKFEVTSGTNTVTF	358
DB	289	KGKENGSSSTDEGEGLVTAKEVIDAVNKAAGRMTTTTANGOTGOADKFEVTSGTNTVTF	348
QY	359	SGKGTATVSKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSP	418
DB	349	SGKGTATVSKDDOGNITVYDVNVGDALNVQNSGNWLDKSAVAGSSGKVISGNVSP	408
QY	419	SKGKMDVTNINAGNNTIETRNKNIDIAATSMTPQFSSVSLGAGADAPTLTSDVDDKGLNV	478
DB	409	SKGKMDVTNINAGNNTIETRNKNIDIAATSMTPQFSSVSLGAGADAPTLTSDVDDKGLNV	468
QY	479	GSKANKPVRITNVAPGKEGDVTNVAQLKGVAQNANRINDVNDGNARAGTAQAIATAGL	538
DB	469	GSKANKPVRITNVAPGKEGDVTNVAQLKGVAQNANRINDVNDGNARAGTAQAIATAGL	528
QY	539	VQAYLPKSMMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYQ	598
DB	529	QAYLPKSMMAIGGGTYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGTSASVGYQ	588
QY	599	W 599	
DB	589	W 589	



## RESULT 14

US-09-669-974-19  
: Sequence 19, Application US/09669974  
: Patent No. 6333173  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: APPLICANT: JENNINGS, Michael Paul  
: APPLICANT: MOXON, E. Richard  
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
: FILE REFERENCE: 065064/0128  
: CURRENT APPLICATION NUMBER: US/09/669,974  
: PRIOR FILING DATE: 2000-09-26  
: PRIOR APPLICATION NUMBER: US 09/377,155  
: PRIOR FILING DATE: 1999-08-19  
: PRIOR APPLICATION NUMBER: PCT/AU98/01031  
: PRIOR FILING DATE: 1998-12-14  
: PRIOR APPLICATION NUMBER: GB 9726398.2  
: PRIOR FILING DATE: 1997-12-12  
: NUMBER OF SEQ ID NOS: 33  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 19  
: LENGTH: 589  
: TYPE: PRT  
: ORGANISM: Neisseria meningitidis  
US-09-669-974-19

Query Match 88.08; Score 2694; DB 4; Length 589;  
Best Local Similarity 89.78; Pred. No. 4.6e-204;  
Matches 539; Conservative 14; Mismatches 34; Indels 14; Gaps 3;  
  
Qy 1 MNKYRIIWNLSALNAWAVSELTRNHTKRASATVATLALLFATVQANATDEDEEEL 60  
Db 1 MNKYRIIWNLSALNAWVSELTRNHTKRASATVATLALLSATSQANATDEDEEL 60  
  
Qy 61 EPVVSALVLOFMIDKEGNGENESTGNGSIYDNNHTLHGATVTLKAGDNLKIKQTN 120  
Db 61 ESVARSALVLOFMIDKEGNGEISTGDIWSIYDDHNTLHGATVTLKAGDNLKIKQ--- 117  
  
Qy 121 KNTNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 180  
Db 118 -----SGKDTYSLKKELDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 170  
  
Qy 181 DTVHLNGIGSTLDTLLNTGATTNVDNDVTDKKRAASVKDVLNAGWNIKGKPGTT 240  
Db 171 DPTVHLNGIGSTLDTLLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIKGKGTST 228  
  
Qy 241 A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKONGKRTVEYKIGAKTSVKEKDKLVG 298  
Db 229 TQSENVDVFTYDTVEFLSADTKTTTVNVESKONGKRTVEYKIGAKTSVKEKDKLVG 288  
  
Qy 299 KGKGENSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKPEFTVTSCTNVTFA 358  
Db 289 KGKGENSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKPEFTVTSCTNVTFA 348  
  
Qy 359 SGKGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVSP 418  
Db 349 SGNGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVSP 408  
  
Qy 419 SKGKMDETVNIAGNNIEITRNKNIDTATSMTPQFSVSLGAGADAPTLVSDDKGALNV 478  
Db 409 SKGKMDETVNIAGNNIEITRNKNIDTATSMTPQFSVSLGAGADAPTLVSDDEGALNV 468  
  
Qy 479 GSKDANKPVRITNVAPGVKEGDTNVQALKGVAONLNRRIDNVGDNARAGTAQAATAGL 538  
Db 469 GSKDANKPVRITNVAPGVKEGDTNVQALKGVAONLNRRIDNVGDNARAGTAQAATAGL 528  
  
Qy 539 VQAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGY 598  
Db 529 AQAYLPCKSMMAIGGGTYLGEAGYAGYSSISDTCNWIIGKTASGNSRGHFGTSASVGY 588  
  
Qy 599 W 599

## Db 589 W 589

RESULT 15  
US-09-377-155-21  
: Sequence 21, Application US/09377155  
: Patent No. 6197312  
: GENERAL INFORMATION:  
: APPLICANT: PEAK, Ian Richard Anselm  
: APPLICANT: JENNINGS, Michael Paul  
: APPLICANT: MOXON, E. Richard  
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
: FILE REFERENCE: 065064/0128  
: CURRENT APPLICATION NUMBER: US/09/377,155  
: PRIOR FILING DATE: 1999-08-19  
: PRIOR APPLICATION NUMBER: PCT/AU98/01031  
: PRIOR FILING DATE: 1998-12-14  
: PRIOR APPLICATION NUMBER: GB 9726398.2  
: PRIOR FILING DATE: 1997-12-12  
: NUMBER OF SEQ ID NOS: 33  
: SOFTWARE: PatentIn Ver. 2.0  
: SEQ ID NO 21  
: LENGTH: 591  
: TYPE: PRT  
: ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 87.78; Score 2685; DB 4; Length 591;  
Best Local Similarity 89.48; Pred. No. 2.4e-203;  
Matches 538; Conservative 16; Mismatches 34; Indels 14; Gaps 4;  
  
Qy 1 MNKYRIIWNLSALNAWAVSELTRNHTKRASATVATLALLFATVQANATDEDEEEL 59  
Db 1 MNKYRIIWNLSALNAWVSELTRNHTKRASATVATLALLFATVQASANNEQEDEL 60  
  
Qy 60 -LEPVVSALVLOFMIDKEGNGENEST-GNIGWSIYDNNHTLHGATVTLKAGDNLKIKQ 117  
Db 61 YLDPQRTVAVLIVNSDKEGTGEKEVEENSDWAVYFNEKGVLTAREITTLKAGDNLKIKQ 120  
  
Qy 118 NTNKNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 177  
Db 121 -----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 170  
  
Qy 178 TNGDTTVHLNGIGSTLDTLLNTGATTNVDNDVTDKKRAASVKDVLNAGWNIKGKVP 237  
Db 171 TNGDTTVHLNGIGSTLDTLLNTGATTNVDNDVTDDEKKRAASVKDVLNAGWNIKGKVP 230  
  
Qy 238 GTTASDNVDVHTYDTVEFLSADTKTTTVNVESKONGKRTVEYKIGAKTSVKEKDKLV 297  
Db 231 GTTASDNVDVHTYDTVEFLSADTKTTTVNVESKONGKRTVEYKIGAKTSVKEKDKLV 290  
  
Qy 298 KGKGENSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKPEFTVTSCTNVT 357  
Db 291 KGKGENSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKPEFTVTSCTNVT 350  
  
Qy 358 ASGGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVS 417  
Db 351 ASGGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDKRAVAGSSGKVISGNVS 410  
  
Qy 418 PSKGMDETIVNIAGNNIEITRNKNIDTATSMTPQFSVSLGAGADAPTLVSDDKGALN 477  
Db 411 PSKGMDETIVNIAGNNIEITRNKNIDTATSMTPQFSVSLGAGADAPTLVSDG--DALN 469  
  
Qy 478 VGSRDANKPVRITNVAPGVKEGDTNVQALKGVAONLNRRIDNVGDNARAGTAQAATAG 537  
Db 470 VGSRDANKPVRITNVAPGVKEGDTNVQALKGVAONLNRRIDNVGDNARAGTAQAATAG 529  
  
Qy 538 LVQAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGY 597  
Db 530 LVQAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGY 589  
  
Qy 598 QW 599



Món Jul 8 07:47:54 2002

us-09-771-382-6.std.ra1

Page 9

Db 590 QW 591

Search completed: July 3, 2002, 08:10:21  
Job time: 533 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:12:25 ; Search time 95.27 seconds  
(without alignments)  
604.151 Million cell updates/sec

Title: US-09-771-382-6  
Perfect score: 3060  
Sequence: 1 MNKIYRIWNSALNAWAVS.....TASNSRGFGASASVGVQW 599

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	2685	87.7	591	2	G81133	adhesin NMB0992 fi
2	2587.5	84.6	592	2	A81888	probable surface p
3	601.5	19.7	298	2	I64138	adhesin homolog H
4	410.5	13.4	1190	2	A82615	surface protein XF
5	407	13.3	1107	2	AC0976	probable autotrans
6	406.5	13.3	2059	2	D82671	surface protein XF
7	369.5	12.1	1588	2	A86036	probable adhesin Z
8	369.5	12.1	1588	2	H91188	probable adhesin E
9	341	11.1	658	2	AO1110	probable surface p
10	264.5	8.6	1004	2	C82672	surface-exposed ou
11	241	7.9	2249	2	A41477	190K surface antig
12	240	7.8	1091	2	G64964	hypothetical prote
13	231	7.5	4919	2	T31105	hypothetical prote
14	228	7.5	949	2	D90803	Aida-I adhesin-li
15	228	7.5	1005	2	H85611	probable adhesin-l
16	228	7.5	1325	2	A64905	ydek protein - Esc
17	225.5	7.4	1286	2	S28634	adhesin AIDA-I pre
18	221.5	7.2	1910	2	AO3394	probable adhesin h
19	221.5	7.2	2021	2	A97859	190-Kda cell surfa
20	217.5	7.1	2551	2	B98047	hypothetical prote
21	215	7.0	3705	2	AD0123	probable autotrans
22	213.5	7.0	1487	2	AG2560	hypothetical prote
23	213	7.0	1029	2	T30852	outer membrane pro
24	213	7.0	3013	2	AO480	probable invasiv
25	211	6.9	1109	2	A56143	surface-array prot
26	210	6.9	1536	2	A43855	high-molecular-we
27	206	6.7	1477	2	B43855	high-molecular-we
28	204.5	6.7	1343	2	D85724	hypothetical prote
29	203.5	6.7	1343	2	E90893	hypothetical prote

30	203	6.6	5291	2	F90696	hypothetical prote
31	202.5	6.6	936	2	I40711	sapB protein - Cam
32	202.5	6.6	4936	2	AH2515	hypothetical prote
33	201.5	6.6	893	2	A37284	surface-array prot
34	201.5	6.6	1635	2	A10452	hemolysin [impor
35	200	6.5	1645	2	JN0896	crystalline surfac
36	199.5	6.5	1655	2	E97835	hypothetical prote
37	199.5	6.5	3029	2	S76109	hypothetical prote
38	199	6.5	961	2	AD0548	puative autotransp
39	197.5	6.5	2020	2	C48399	ABC-type transport
40	197	6.4	1366	2	S57664	Iga-specific metal
41	197	6.4	2514	2	F81045	hemagglutinin/hemo
42	196.5	6.4	585	2	F90961	flagellin [impor
43	195.5	6.4	585	2	F85809	hypothetical prote
44	194.5	6.4	5188	2	B85547	probable RTX famil
45	193.5	6.3	365	2	AB3486	cell surface prote

ALIGNMENTS

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000 #sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81133  
R:Rettlein, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: AB1000; MUID:20175755  
A:Accession: G81133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-591 <DET>  
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722 A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0992

Query Match	87.7%	Score	2685	DB	2	Length	591		
Best Local Similarity	89.4%	Pred. No.	1.9e-129						
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Qy	1	MNKYRIWNSALNAWAVSELTRNHTKRASATVKTAVALTLFLFATVOANATDDEBEE- 59							
Db	1	MNKYRIWNSALNAWVSELTRNHTKRASATVKTAVALTLFLFATVQASANNNEEQEDL 60							
Qy	60	-LEPVRSALVLOPMIDKCGNGENEST-GNIGWSIYYDNHNTLHGATVTLKAGDNLKIKQ 117							
Db	61	YLDPVQRTAVLVIVNSDKGTGKVEKVEKVEKVEKVEKVEKVEKVEKVEKVEKVEKVEK 120							
Qy	118	NTMKNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 177							
Db	121	-----NGNFTYSLKKDLTDLTSVGTPEKLSFGANGKNVITSDTKGLNFAKETAG 170							
Qy	178	TNGDTHVHLNGIGSTLDTLLNTGATTNTVNDVTDKKRAASVKDVLNAGNWKGVKP 237							
Db	171	TNGDTHVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNWKGVKP 230							
Qy	238	GTTASDNVDFVHTYDVEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSVIKEKDGKLV 297							
Db	231	GTTASDNVDFVRTYDVEFLSADTKTTTVNVESKDNCKKTEVKIGAKTSVIKEKDGKLV 290							
Qy	298	GKKGNGSGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFFETVSGTNVTF 357							
Db	291	GKDKGNGSGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGQTQADKFFETVSGTNVTF 350							
Qy	358	ASGKGTTATVSKDDQGNITVKYDVNVGDALNVNLONGSNWLDKAVAGSSGKVIISGNVS 417							

Db	351	ASGKGTATVSKDDQGNITVMDVNVGDALNVNQLGNSWNLDSKAVAGSSKVIISGNVS	410
QY	418	PSKGMDETNIINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDKGA	477
Db	411	PSKGMDETNIINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVG-DALN	469
QY	478	VGSKDANKPVRIITNVAIPGVKEGDTVNAQLKGVAQNLNRRIDNVDCNARAGTAQA	537
Db	470	VGSKDKNKPVRIITNVAIPGVKEGDTVNAQLKGVAQNLNRRIDNVDCNARAGTAQA	529
QY	538	LVQAYLPKGSMAIIGGTYRGEAGYAIGYSSISDGGNWIIKGTASNSRGHFGASASVGY	597
Db	530	LVQAYLPKGSMAIIGGTYRGEAGYAIGYSSISDGGNWIIKGTASNSRGHFGASASVGY	589
QY	598	QW 599	
Db	590	QW 591	

RESULT 2  
A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 22491  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.  
A:Reference number: A81775; MUID:2022556  
A:Accession: A81888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1200

Query Match	84.6%	Score	2587.5	DB 2	Length	592									
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DB	1	MNKYRIIWN	SALNAWAV	SELTNH	TKRASAT	VKTAV	LATLL	FATVO	ANATDEDEEEL	60					
QY	61	EPVVS	ALVLQ	FMIDK	EGNGEN	ESTGN	IGMSI	YYDVN	HNHTLHG	-ATVTLKAGDNLKIKONT	119				
DB	61	ESVQ	RS-VVGS	IQASME	GSGELET	--ISLSMT	NDSKFE	VDPIY	VVTLKAGDNLKIKQ	--	114				
QY	120	NKNTN	ENTNDS	SFFYS	LKDKDL	TLT	TSVET	EKLSFG	ANGNKVNI	ITSDPKGLNFAKETAGTN	179				
DB	115	--NTN	ENTN	ASSFF	YSLKDKDL	TG	INTG	IN	ETEKLSFG	ANGKNVNI	ITSDPKGLNFAKETAGTN	172			
QY	180	GDTTV	HLNG	IGST	LTDL	TIL	NTGAT	TNTNV	TDOKKRA	ASV	KDVLNAGWN	IKGVKPGT	239		
DB	173	GDTTV	HLNG	IGST	LTDL	TLAG	SSASHV	DAGNQST	--HYTRA	ASIKDVLNAGWN	IKGVKTGS	230			
QY	240	TA	--SDNW	DFVHT	YDTVE	FFLS	ADTK	TTTVNV	YESKDN	CKRTEVK	IGAKTSV	IKERDGLKVT	297		
DB	231	TTG	QSEN	VDVFR	YDTVE	FFLS	ADTK	TTTVNV	YESKDN	CKRTEVK	IGAKTSV	IKERDGLKVT	290		
QY	298	GK	KGNGSS	TDE	CEGL	VTAK	EV	IDAVN	KAGWR	MKTTT	TANG	QOQADK	FEVTVSGTNTVF	357	
DB	291	GK	KGNGSS	TDE	CEGL	VTAK	EV	IDAVN	KAGWR	MKTTT	TANG	QOQADK	FEVTVSGTNTVF	350	
QY	358	ASG	KGTTAT	YSK	DOQ	GNIT	TVK	YDVN	G	DALNVN	Q	LNQ	SGHWN	LDSKAVAGSSGKVISGNVS	417
DB	351	ASG	KGTTAT	YSK	DOQ	GNIT	TVK	YDVN	G	DALNVN	Q	LNQ	SGHWN	LDSKAVAGSSGKVISGNVS	410

	Qy	418	PSKGMDETVINAGNNIETRNGKNIDIATSMTPQSSVSLGAGADAPILSVDDKGAALN	477
	Dd	411	PSKGMDETVINAGNNIEISRNGKNIDIATSMAPQSSVSLGAGADAPTLSVDDECALN	470
	Qy	478	VGSKDANKPVRITNWAPGVREGDVTNVAQLKGVAQNLNNRIDNDGNARAGIAQAIIATAG	537
	Dd	471	VGSKDANKPVRITNWAPGVREGDVTNVAQLKGVAQNLNNRIDNDGNARAGIAQAIIATAG	530
	Qy	538	LVOAYLPCKSMMAIGGGTYRGEAGYAI GYSISDGGMWIIKTASGNSRGHFHASVSVG Y	597
	Dd	531	LVOAYLPCKSMMAIGGGTYRGEAGYAI GYSISDGGMWIIKTASGNSRGHFHASVSVG Y	590
	Qy	598 QW	599 ==	
	Dd	591 QW	592	
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I64138				
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)				
C:Species: Haemophilus influenzae				
C>Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997				
C:Accession: I64138				
R;R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage				
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman				
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.				
Science 269, 496-512, 1995				
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente				
A>Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.				
A:Reference number: A64000: MUID:95350630				

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RESULT 3
I64138
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)
C/Species: Haemophilus influenzae
C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 24-Oct-1997
C/Accession: I64138
R/Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Geoghagen, N.S.;
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weisburger, S.M.; Yeh, G.Y.; Roach, J.C.; Hinkle, R.; Venter, A.;
Science 269, 496-512, 1995
A/Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A.;
A/Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd
A/Reference number: A64000; MUID:95350630
A/Accession: I64138
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-298 <TIGR>
A/Cross-references: GB:U32846; GB:I42023; NID:g1574588; PID:g1574589; TIGR:HI1732

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Query Match          19.7%; Score 601.5; DB 2; Length 298;
Best local Similarity 44.2%; Pred. No. 7.8e-24;
Matches 148; Conservative 37; Mismatches 85; Indels 65; Gaps 9;

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      ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      61  STEDDIEDS-----AATKDN-----KNQALKAGDTLTLKAG 92
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      ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      93  KNLKAKL-----DOGGKSVTALAKDLVKTAKVSDTLTIGNTPAAGGATPKVKSIT 144
      ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      164  SDTKGLNPAKETAGTNGDTTTHLNGIGSLTDLTLNTGATTNVNDNTDDKKRAASVK 223
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Db      145  STADGLKLAK---GTNGDTAVHLNGLASTLPDVTNTNGASTSVT-FSPSDEKTRAAATIK 200
      ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Qy      224  DVLNAGWNIKKVPGCTTASDNVDVFHTYDTVEFLSADTKTTTVNVESKDNGKRTEVIGKA 283
      ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db      201  DVLNAGWNIKAKVAGGNTENVDLVAGVDNVEFITGDKNTLDVLVLTAKENGKTEVRETP 260
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Qy      284  KTSVIKEDGKLVGTG-----KGKNGS--STDE 310
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Db      261  KTSVIKDNNGKLLTGKOLKDKANTGTATNATEDTDE 295
      ||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

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RESULT 4  
A82615  
surface protein xF1981 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nuclear

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MUID:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82615

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 11190 <STM>

A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1

A:Experimental source: strain 9a5c

R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alves-Brites, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carriaro, D.N. as-Neto, E.; Docena, C.; El-Dorfy, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to GenBank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, J.D.; Junqueira, M.B.; Kemper, E.L.; Kitajima, J.P.; Krueger, J.E.; Kuramae, Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.

A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Neres, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, R.C.; de Oliveira, R.C.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, H.

A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A. M.; Tshakoto, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vetter

A:Reference number: A59328

A:Contents: annotation

C:Genetics:

A:Gene: XF1981

Query Match	13.4%	Score 410.5	DB 2	Length 1190
Best Local Similarity	24.8%	Pred. No. 2.4e-13		
Matches 163	Conservative 88	Mismatches 206	Indels 201	Gaps 27
Qy	84	STGNIGSIY--VDNHNTHGATVTLKAGD-NLIKIKONTNKTNTNENSSFTV--SLX	137	
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Db	592	STASKGWNLLASGANSNVPGESVDLANSOGNLLITKT-----DSNDVFNLTATLK	645	
Qy	138	KD-LTDTLSVETELKSPGAN-----	167	
		:   :   :   :   :   :   :   :   :   :   :   :   :		
Db	646	VDSLTTGNTAMTTDGVTVGSNVTLGSLVITDGPSTVSSGISAGNOKITNVAAGTADTD	705	
Qy	168	GLNFA-----KETAG-----	177	
		:    :    :    :    :    :    :    :    :    :		
Db	706	AVNFSQAOAVSSTASKGWNLLASGANSNAPGESVDLKTNDGNIVISKESGSDNVDLNL	765	
Qy	178	-----TNGDTHVLHNGIGSLTDLTLLNTGATNTYNDNVTDKKKRAASVKVDLNA	228	
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Db	766	SSSLKLDKLTGCDTVMTTNGV-----TVGSGVTLGSMGLVITDGPSTVSSGI---NA	814	
Qy	229	G-WNIKGVPKGTASDNVDF-----VHTYDTVEFFLSADTKTTVNVVESKDN	273	
		:   :   :   :   :   :   :   :   :   :   :   :   :		
Db	815	GSQKITNYAAGTADTDAYNLSQLNTAMAGSAGKSVHYIYSTYD---GGTGGNGYDGGATG	871	
Qy	274	GKRTVEVIGAKTSVIEKDGKLVTKGKGNG-SSTDEGEGLVTAKEVIDAVNKAAGRMK	332	
		:    :    :    :    :    :    :    :    :    :		
Db	872	TRSIavgvgtLAsA---EGATavGSGAAASGKGSTaIGrNavaSADGSvalGD-GAKDG	926	
Qy	333	TTTANGQTGQADKFTVTSGRNVTFASGKTTATVSKDDQGNITVKYDVNVGDAALNVQL	392	
		:    :    :    :    :    :    :    :    :    :		
Db	927	ARGAESYTGKYSGLQNNVTGVTSVGDAASKGETRTVS-----NVADAKEAT--DAVNLRL	979	
Qy	393	---QNSGWNLDLSKAVAGSSGKVIISGVNPSKGKMDENVTNINAGNNIETIRNGKNIDTAT	448	
		:    :    :    :    :    :    :    :    :    :		
Db	980	DRVAQDANRYVDNKLTESLSEGQTF-----VKVNSLNN-----SAT	1014	
Qy	449	SMTPOFSSVSLGAGADA-----PTLSVDDDKGL-----NVGSKDANK	485	
		:    :    :    :    :    :    :    :    :    :		
Db	1015	PIAAGVDATAIGVGATASGADSIAMGNKASASADNAVAIGNHSVADRANTVSVGSAGSER	1074	
Qy	486	PVRITNVAPVKEGQDVTVVQALKGVAQNLNFRIDNVGNAR-----AGTAQAATATAGLQVA	541	
		:    :    :    :    :    :    :    :    :    :		
Db	1075	--QVTVNAAGTADTDAVNVVSQLNQLGITAKQYTDGVGVSGLRRDTDGGVAAATATANLPOA	1132	
Qy	542	YLPGRSMMAIGGTVYRGEAGYAIGYSISDSDGNNTIIKTFAGSNRSRHFCSASVGYQW	599	

Db 1133 YIPGRGTVSGVSYRQGAATAVGVSSVESGRWFRFPGSANTSRQVGIGAGVGIO 1190  
|::|| |::| :||::| |::| |::| |::| |::| |::| |::| |::| |::|  
RESULT 5  
AC0976  
C:Species: Salmonella enterica subsp. [imported] - Salmonella enterica subsp. ent.  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: This species has also been called Salmonella typhi  
C>Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AC0976  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; Whitt  
am, S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.  
A>Title: Complete genome sequence of a multiple drug resistant Salmonella  
A:Reference number: AB0502; PMID:11677608  
A:Accession: AC0976  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1107 <PAR>  
A:Cross-references: GB:ALJ513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GNB  
C:Genetics:  
A:Gene: sapB

Query Match	13.3%	Score	407;	DB	2;	Length	1107;		
Best Local Similarity	22.1%	Pred.	No.3.3e-13;						
Matches	188;	Conservative	116;	Mismatches	255;	Indels	290;	Gaps	32;
QY	27	TKRASATVKTAVLATLLFATYQANATDEBEEL----	EPVVSALVLFQMDKGENGEN	82					
Db	273	TFSASRNGSASKITNLAAGTAAADSTDAVNGSOLYETNQKVDQNTSAI----	ADINTSITN	329					
QY	83	ESTGNIGWSIIYDHNHTLHGATVTILK----	AGD----	120					
Db	330	LSSDNLSNWNETTNSFSASHGSSSTTKITNVAAGELSEESTDAVNGSOLFETNEKVDQNT	389						
QY	121	---KNTNENTWDSSTYSILKKDLIDL-TSV-----	ETEKLSFGAN--GNKVNTS	164					
Db	330	DIAAONTTITONSTAIENLTSVSDINTSITGLDNLALWDEDGAFSANHGGSTSKTIN	449						
QY	165	DTKGLNFAKETAGTNG-----DTVHLNGIGSTPLTLLNTGATTNVTNDVTDKKRAA	220						
Db	450	VAAGALSSEDSTDAVNGSOLYETNQKVDQNTSAID--INT-SITNLGTDALSDDDEGAF	506						
QY	221	SVKDYVLNAGWNIKGVKPGTTASNDVDFVH---TYDT-----	VFLSADTKTTVIN	267					
Db	507	SASHGTSCTNKITNVAAGELASDSDAINGSOLYETNMLISQYNPSISQLAGDTSETYIT	566						
QY	268	-----VESKDNGKRTVEVIGAKTSVIKEKDLVTKG--	KGENGSSDTEG----	311					
Db	567	ENGTGVKYRTNDNLEGQDAYATNGCATAVGYDAVASAGCLALQGNSSSIEGSIALG	626						
QY	312	-----EGLV-----TAKEVIDAYNKA-----	GWRMKTITANGQTQ	342					
Db	627	SGSTSNRAITTCIRTSATSQGVVIGYNTDRELLGALSGLTGDGSGRYOITNVADG--SE	684						
QY	343	ADKFETVTSNTVTPASGKGTATVSKDDQGNIT-----	VKYDVNV	383					
Db	685	AQDAVTVRQLQNAIGA---VTTTTPKYHANSTEEDSLAVGCTDSLAMGAKTIVNADAGI	740						
QY	384	GDALNVNQLON--SGWNLDKAVAGSSGKVISGNNVSP-----	-----	418					
Db	741	GIGLNTLYMADAIGIAGSNARANHANSIANGSGQSTRGAGTDYTYAINDMTPONSUGE	800						
QY	419	--SKGKMD---EPTVNIAGN-----NIEITRNKNI-----	-----	444					
Db	801	FVSGSEDDGQRQITNVAAGSADTDVYNGQLKYTDAQVSRNTQSITNLNTOVSNLDRVTN	860						
QY	445	-----DIATSMTPOF-----SSVSLGAGADAP-----	TLSV-DKGG	474					

Nature 406, 151-157, 2000

A:Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.

A:Reference number: A82515; MIDJ:20365717

A:Note: for a complete list of authors see reference number A59328 below

A:Accession: A82615

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1190 <SIM>

A:Cross-references: GB:AE004017; GB:AE003849; NID:99107083; PIDN:AAF84783.1; GSPDB:GN0001

A:Experimental source: strain 9a5c

R:Simpton, A.J.G.; Reinach, F.C.; Artuda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Azeiteiro, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H.; Casanova, J.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S. submitted to Genbank, June 2000

A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fromberger, J.D.; Junqueira, M.L.; Kemper, E.L.; Kitaajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigret, C.; Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.; Azeiteiro, R.; F.G.; Nunes, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.; Rodrigues, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmeri, D.A.; Palmeri, D.A.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasakimura, M.; Tshakoe, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Zamboni, A.; Zamboni, A.

A:Reference number: A59328

A:Contents: annotation

A:Genetics:

A:Gene: XF1981

Query Match	13.4%	Score 410.5	DB 2	Length 1190
Best Local Similarity	24.8%	Pred. No. 2.4e-13		
Matches 163	Conservative	86	Mismatches 206	Indels 201
Gaps	27			
Qy	84	STGNIGSIY--YDNHNTLHGATVTLKAGD-NLKIKONTNKNNTNENTNDSSEFY--SLK	137	
Db	592	STASKGNWLLASGANSNVVPCESVDLKNSDGNLLIYTT-----DSNDVTFNLATALK	645	
Qy	138	KD-LTDLTSYETEKLFSGAN-----GNK--VNI-----TSDTK	167	
Db	646	VDSLTTGNTAMTTDGVTVGSNWTLTGSTGLVITDGPSVTSSTGISAGNOKITNVAAGTADTD	705	
Qy	168	GLNEA-----KETAG-----	177	
Db	706	AVNFSQQAQVSSASKGNWLLASGANSNVAPGESVDLKNTDGNIVISKESGNDVLFNL	765	
Qy	178	-----TNGDTHVLHNGIGSTLDTPLLTGATTNTVNDVNTDDKKKRAASVKVDLNA	228	
Db	766	SSSLKDLKLTGCDVMTTNGV-----TVSGSVTLGSMGLVITDGPSTSSGI-----NA	814	
Qy	229	G-WNIKGVKPGTTASDNVDF-----VHYIDTVEFLSADTKTITTVNVESKDN	273	
Db	815	GSQKITNVAAGTADTDVNLSQLNTAMAGSGAKSVHYIYSTYD---GGTQGGNYNGDGGATG	871	
Qy	274	GKRTVEKIGAKTSVIKEKDGKLVTKGKGNG-SSTDEGEGLVTAKEVIDAVNKAGWRMK	332	
Db	872	TRSIAGVGVTLASA-----EGATAVSGSAAASCKGSTAIGRNAVASADGSAVGLD-GAKDG	926	
Qy	333	TTTANGQTQADKETVTSYSGNTVTFASGKTTATVSKDDQGNITVKYDVNVGDLNVQL	392	
Db	927	ARGAESYTGKYSGLQNNNTVGVTSVSGDASKGTRTVS-----NVADAKEAT--DAVNLROL	979	
Qy	393	---QNSGNWLLDSKAVAGSSGKVIISGNVSPSKGMDETVNINAGNNIETRNGKNIDTAT	448	
Db	980	DRVAQDANRYVDNKIESLSEGTTF-----VKVNSLNN-----SAT	1014	
Qy	449	SMTQFSSVSLGAGADA-----PTLSVDKKGAL-----NVGSKDANK	485	
Db	1015	PIAAGVDATAIGVGATASGADSIAMGNKASASADNAVAIGNHVSADRANTVSVGSAGSER	1074	
Qy	486	PVRLTNAPGVKEGDTVNVQALKGVAQNLNRRINDVGNAR-----AGTAQAIATAGLVQA	541	
Db	1075	---QVTNVAAGTADTDVNVSQLNGLITAKOYTDGVVGSLLRRDTGGVAAAIATANLUPQA	1132	
Qy	542	YLPKSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW	599	

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Qy 475 ALNYSKDKANPVRITNVAPGKEDGTVNVAOLK-----GSSTDEGEGLVTAKEVIDAVNKA 327  
Db 921 TVSVGSSTQOR--RITNVAAGVNNNTDAVNVAQLKASEAGSVRYETNADGSVNYSVLNLGD 978  
Qy 509 -----GVAQ-----NLNRRIDNVDGNARAGIA 530  
Db 979 GSGGTTTRIGNVSAAVNDTDAVNVAQLKRSVEANTYTDQKMGEMNSKIKGIENKMSGGIA 1038  
Qy 531 QAIATAGLVQAYLPCKSMALGGTYRCEAGYAGYSSISDGWNWIKGTASGNSRGHFG 590  
Db 1039 SAMAWGLPQAYAPGANNTSTAGTTFNGESAIVAGVSMVSESGGWYKLOGTSNSQGDYS 1098  
Qy 591 ASASVGYQW 599  
Db 1099 AAAGAGFQW 1107  
RESULT 6  
D82671  
surface protein xfl529 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: D82671  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2059 <SIM>  
A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H  
da-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From  
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, B  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XFL529

Query Match 13.3%; Score 406.5; DB 2; Length 2059;  
Best Local Similarity 25.5%; Pred. No. 7.8e-13;  
Matches 170; Conservative 93; Mismatches 219; Indels 185; Gaps 32;  
Qy 89 GWSIYYDNH--TLHGATVTLKAGD-NLKIKQNTNK-----NTNENTNDSSFTY----SL 136  
Db 1422 GWTLTGANGSKVAGSGTVDLKNLTGNTLTKSGSDNDVVFNLSDELKESITVGNLTQ 1481  
Qy 137 KDLTDLTTS---VTEKLSFGANGKNVITSDTKGLNFAKETA---GTNGDTTVHLNGI 189  
Db 1482 DKDGVKSSNVLNDSNELVITSHSSTSSVKTLANGESVNVRTVVVNGDVNIDVVVNDL 1541  
Qy 190 -----GSTTDLTLLNTGA---TTNVT-----NDNVTDDKKRAASVKDVLNAGWNI----- 232  
Db 1542 GLSIVGASITLGSINAGSHKITNVTAGTEDTDAVNFSQLK---SVSEAVDKGWTLTASG 1598  
Qy 233 ----KGKPGCTTASDNDV-----FVHTYDTVEFLSADTK-----TTTVNVESKDNG 274  
Db 1599 ANGSKVYSGGTVDLKNLTGNTLTKSGSDNDVVFNLSKDFKDVETAGNTVWNTDGVKVG 1658

Qy 275 KRTEVKIGAKTSVIERKDGKLVTKGKGEN-----GSSTDEGEGLVTAKEVIDAVNKA 327  
Db 1659 --SDVSLGAMCLFTANGPSVYATSGFNAGDKVISHVAVGMADTDAVNVSQLKQAVQSVTVK 1716  
Qy 328 GWRMKTTT-----ANGQTGQ---ADKFETVTSCTNV-----TFASGKGT--- 364  
Db 1717 ATRYSTNDGQTGGNTDGDGATGSKAIAAGVGTQASGEAAAVGSGAAASGKSTALGR 1776  
Qy 365 -ATVSKD-----DOG-----NITVKYD-----VNVG----- 384  
Db 1777 NATASDGSVALGDKAGGGRGAEYTGKYSGVQNNVTGTVSVGDAAKAGETRSTSNVADA 1836  
Qy 385 ----DALNVNQL-----QNSGNWLDL-----KAVAGSSGKVISGNSPSKGMKD 424  
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Qy 425 ETVNINA---GNNTIEITRN-----GKNIDITATSMTPQFSSVSLGAGADAPLTSVDDKAL 476  
Db 1887 --MGVNAIAGTNAAVSGTESVALGKNTNVSAD-----NAVAIGNGSA-----DRANSV 1934  
Qy 477 NVGSKDANKPVRITNVAPGVKEGDTVNVQOLKGVQAOVLNNRIDNVGNAR-----AGTAA 532  
Db 1935 SVSGGSGSER--QVTNVAAGTADTDAVNVSQNLQGLITAKQYTDGMVGNLRRETSGGVAAA 1992  
Qy 533 IATAGLVQAYLPCKSMALGGTYRCEAGYAGYSSISDGWNWIKGTASGNSRGHFGAS 592  
Db 1993 IATANLPQAYVQGRGTMVSGVSSVQGGOSATAVGVSASESHWVFKFSGSANTSHVGVG 2052  
Qy 593 ASVGYQW 599  
Db 2053 AGVGYQW 2059  
RESULT 7  
A86036  
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: A86036  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A86036  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <STO>  
A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5029  
Query Match 12.1%; Score 369.5; DB 2; Length 1588;  
Best Local Similarity 24.7%; Pred. No. 4.2e-11;  
Matches 164; Conservative 97; Mismatches 259; Indels 143; Gaps 26;  
Qy 49 ANATDEDEEELPVRSAVLQFMIDKEGNG-----ENES-----TGNIGWSIYYDN 96  
Db 957 ANAEYNNVGDAIDALDDNAL-----LWDETANGAGAYNASHDGKASITITNVANGSISDS 1012  
Qy 97 HNTLHGATVTLKAGDNLKIKONTNKNENTNDSSFTYSLKDLTDLTSET--EKLSE- 153  
Db 1013 TDAVNGSQLN---ATNMIEQNT--QIINQLAGNTDAHY--IQENGAGINRYRTNDGDLAFN 1067  
Qy 154 -----GANGKNVITSDTKGLNFAKETAAGTNGDTTVHLNGITGLTDLTLLNTGA--TTNVT 207  
Db 1068 DASAQGVGATAIGYNSVAKGDSVAIGOGSVSDVDTGIALGSSSVSRVIAKGRDTSIT 1127  
Qy 208 NDNY-----TDDKKRAASVKD-----VLNAGWNTKGVKPGTASDNDVDF----- 247

Db 1128 ENCWWGYDITDGGELGALSIGDDGKYROIIN-----VADGSEAHDAVTVRQLQNAIG 1180  
QY 248 -VHTYDTVEFLSADTKTTTNNVESKNGKRTVEKIGAKTSVIEK-----DGKLV 296  
Db 1181 AVATPTKTFHANSTEEDSLAVGT-----DSLAMGAKTIVNGDKIGIGYGAYVDANAL 1234  
QY 297 TKGKGE-----NGSSTDEGGLVTAKEVIDAVNKGWRMKTITANGQ-----339  
Db 1235 NGIAIGSNAQVIHVNSIAIGNGSTTTTGAQNTYNTAYMDAPQNSVGEFSVGSADGQRIIT 1294  
QY 340 ---TGQADKFEVTSNTNVTFSAGKGTATTATVSKDDGNIT-----VKYDVNV 383  
Db 1295 NVAAGSAD-----TDAVNV--GOLKVTDAQVSONTO--SITNLDNRVTNLDSTRVTNIENGI 1346  
QY 384 GDAL-----NVNQLNSGNWLDKAVAGSSKVISGNVSPSKGK-----DETVIN 430  
Db 1347 GDIVTTGSKYKFTNTDGDVDSAQGKDSVAIGSGSIAAADNSVALGTGVSATTEENTISVG 1406  
QY 431 AGNIEITRN---GKNIDTATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGSKDANKPV 487  
Db 1407 SSTNQRRIITNVAAGKKNATDAVNVNVAQLKSEAGGVRYDTRADGSIDYSNITLGGNGG-TT 1465  
QY 488 RTNVAPGKGVGDTNVNVAQLKGVQA-----NLNRRIDNVGDNARAGIAQAIATA 536  
Db 1466 RISNVSAGVNNNDVNVNVAQLKQSVQETKQYTDQRMVEMDNKLSKTESKLSGGIASAMWT 1525  
QY 537 GLVQAYLPCKSMMAIGGGTYRGAGYAIGYSSISDGGNIIKCTAGSNRGRHFGASASVG 596  
Db 1526 GLPQAVTPGASMASIGGGTYNGESAVALGSMVSNRGRVYKLOGSTNSQGEYSAAALGAG 1585  
QY 597 YQW 599  
Db 1586 IQW 1588

RESULT 8  
H91188  
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shingawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: H91188  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA037903.1; PID:g13363955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs4480

Query Match 12.1%; Score 369.5; DB 2; Length 1588;  
Best Local Similarity 24.7%; Pred. No. 4.2e-11;  
Matches 164; Conservative 97; Mismatches 259; Indels 143; Gaps 26;  
QY 49 ANATDEEEELPEPVRSALVQFMIDKEGNG-----ENES-----TCNIGWSIYYDN 96  
Db 957 ANAEYNVGDALDLDNAL----LWDETANGAGAYNASHDGKASIIINVANGSISEDS 1012  
QY 97 HWYTLGATVTLKAGDNLKIQTNNKNTNENTNDSSFTYSLKKDLTLTSVET--EKLSP- 153  
Db 1013 TDAVNGSQLN--ATNMTEQNT-QIINQLAGNTDATY-IQENGAGINVTNDDGLAEN 1067  
QY 154 ----GANGKNYITSDTKGLNFAKETAGTNGDTTVHLNIGIGSLTDLTLNTGA--TTNVT 207  
Db 1068 DASAQGVGATAGYNSVANGDSVAIGQGSYSDVTGIALGSSSVSRVIAKGRDTSIT 1127  
QY 208 NDNV-----TDDKKRAASVKD-----VLNAGWNIGKVPKGTITASDNVDF-----247

Db 1128 ENCWWGYDITDGGELGALSIGDDGKYROIIN-----VADGSEAHDAVTVRQLQNAIG 1180  
QY 248 -VHTYDTVEFLSADTKTTTNNVESKNGKRTVEKIGAKTSVIEK-----DGKLV 296  
Db 1181 AVATPTKTFHANSTEEDSLAVGT-----DSLAMGAKTIVNGDKIGIGYGAYVDANAL 1234  
QY 297 TKGKGE-----NGSSTDEGGLVTAKEVIDAVNKGWRMKTITANGQ-----339  
Db 1235 NGIAIGSNAQVIHVNSIAIGNGSTTTTGAQNTYNTAYMDAPQNSVGEFSVGSADGQRIIT 1294  
QY 340 ---TGQADKFEVTSNTNVTFSAGKGTATTATVSKDDGNIT-----VKYDVNV 383  
Db 1295 NVAAGSAD-----TDAVNV--GOLKVTDAQVSONTO--SITNLDNRVTNLDSTRVTNIENGI 1346  
QY 384 GDAL-----NVNQLNSGNWLDKAVAGSSKVISGNVSPSKGK-----DETVIN 430  
Db 1347 GDIVTTGSKYKFTNTDGDVDSAQGKDSVAIGSGSIAAADNSVALGTGVSATTEENTISVG 1406  
QY 431 AGNIEITRN---GKNIDTATSMTPQFSSVSLGAGADAPTLSVDDKGALNVGSKDANKPV 487  
Db 1407 SSTNQRRIITNVAAGKKNATDAVNVNVAQLKSEAGGVRYDTRADGSIDYSNITLGGNGG-TT 1465  
QY 488 RTNVAPGKGVGDTNVNVAQLKGVQA-----NLNRRIDNVGDNARAGIAQAIATA 536  
Db 1466 RISNVSAGVNNNDVNVNVAQLKQSVQETKQYTDQRMVEMDNKLSKTESKLSGGIASAMWT 1525  
QY 537 GLVQAYLPCKSMMAIGGGTYRGAGYAIGYSSISDGGNIIKCTAGSNRGRHFGASASVG 596  
Db 1526 GLPQAVTPGASMASIGGGTYNGESAVALGSMVSNRGRVYKLOGSTNSQGEYSAAALGAG 1585  
QY 597 YQW 599  
Db 1586 IQW 1588

RESULT 9  
AH0110  
probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
geno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Bartel  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0902

Query Match 11.1%; Score 341; DB 2; Length 658;  
Best Local Similarity 24.7%; Pred. No. 3.8e-10;  
Matches 124; Conservative 70; Mismatches 204; Indels 104; Gaps 17;  
QY 149 EKLSPGANGKNYITSDTKGLNFAKETAGTNG-----DTTVHLNIGTSLTD 195  
Db 210 QSLALGAGA---VTQANSIALGAASINTVGAQSSYSAYALTAPQASVCELIGITAGLN 265  
QY 196 TLLNTGATTNVTNDNYT-----DDKKRAASVKDVLNAGWNIGKVPKGTITASDNVDF 247  
Db 266 RKITGVAAGSASSDAVNVAQLTAVGQVQONTANITSLGGRVTTIEGSMASIANGGVKY 325  
QY 248 VHTYDT-VEFLSADTKTTTNNVESKNGKRT-----EVKIGAKTSVIEKDKLVTGKG 300  
Db 326 FHANSTQPSVASGTSNVAIGPASLASGNAALASGAGAVAIG--DGAASADSGVAIGOG 383

**QY**    301 KGENSGSTDEGLVTAKEVIDAVNKAQRPMKTTTANGQTGOADKETVTSGTNVFASC 360  
               : |::| : |::| : |::| :  
**Dg**    384 SGGNGRGEVNIIG-----KYSNASNTSSG-----TVSVGNAT- --- 416  
                        :  
**QY**    361 KGFTATVSXDDQCQNITVKYDVNVGDALVNQLNSCWNLDSKAVAGSCKGVISGNVSPSK 420  
               : ||||| : ||||| : ||||| :  
**Dg**    417 -GETRTVSNVADG-----LQATDAVLRLDQG-----IAASIVVENNYSLGLO 458  
                        :  
**QY**    421 GKMDETVINIAGNNI-EITRNKGKNIDI--ATSMTPOFSSVSLGAGADAPTLS----- 469  
               : |::| : |::| : |::| :  
**Dg**    459 NGTDGMFOVNSSGLAKPSATGSATGAGSVASNNSSTAFAKGAATAANSAAALCANS 518  
                        :  
**QY**    470 -VDOKALNVGSDKANPKVRITINVAQPVKEEDYTIVAQLKGYAQN---LNNRIDNVDCN 524  
               : :::::: : :::::: : :::::: :  
**Dg**    519 VADRANSVSYGVSENER--OITWPAOTGTDAVNFDLQSISNOTNAYNTRYSELKOD 576  
                        :  
**QY**    525 AR-----AGIAQAATACLAGLVAYLPKGSMAAIHGCTYRGEGYAIGYSISDGWNII 577  
               : ||||| : ||||| : ||||| :  
**Dg**    577 LRKQNSVLSAGIASAMSMASLTOPYTGSSMWTIGAASYRGQSALSILGVSSISDSGRHWS 636  
                        :  
**QY**    578 KGTASGNSRHFGCASVSGYW 599  
               : |::| : |::| : |::| :  
**Dg**    637 KLQASSNTQDFGIGVGCVGW 658 .  
                        :

RESULT 10  
C82672  
surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a)  
C;Species: Xylella fastidiosa  
C;Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C;Accession: C82672  
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences  
Nature 406, 151-157, 2000  
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A;Reference number: AB2515; MUID:20365717  
A;Note: for a complete list of authors see reference number A59328 below  
A;Accession: C82672  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1004 <SIM>  
A;Cross-references: GB:AEO03981; GB:AEO03849; MID:g9106543; PIDN:AAF84325.1; GSPDB:CNO001  
A;Experimental source: strain 9aSC  
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H  
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fromh  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krueger, J.E.; Kuranae, E.E.; Laig  
chado, M.A.; Madeira, A.M.B.N.; Madeiral, H.M.F.; Marino, C.L.; Marques, M.V.; Martins E  
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;  
. F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, C.A.;  
Rodrigues, V.; Rosa, A.J. de M.; de Sa, R.G.; Santelli, R.V.; Sawasaki  
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silveira Jr., W.A.; da Silveir  
M.; Tshakoto, M.H.; Vallada, H.; Van Sluis, M.A.; Verjovski-Almeida, S.; Vittore, A.L.; Z  
A;Reference number: A59328  
A;Contents: annotation  
C;Genetics:  
A;Gene: XF1516

Db	120	FSKAFAPNALALGYNSSVTSQANNVALGSNST	-----VSGVNSVALGAGSMA	167
QY	158	NKVNIITSDTKGLMFAKETAGTNGDITVHLNGIGSTLTDLILLNTGATTNTVNDVTDKKK	217	
Db	168	SELNVIISVGGG-----DGVTPAVRRIRVNVG-----DGIGNDNAVKNKSLDGVTSVND	216	
QY	218	RAASVKDVL-----NAGWNIKGVKPGTTA--SDNVFVHTVDTVEF-----	256	
Db	217	VAASVKTIALTNQVTGSSVASASGKKESTAIGSAQAQAVDN-----TVAFGGRALANA	268	
QY	257	-----LSADT-----KTTTVNVESKD-----NGKRTEVKTGAKTSVIEK	291	
Db	269	VGASALGFDSHAKGINSTTVGTQTSVLGQGVSLGYNFSFVGESEFNGALGSNSLVLLQG	328	
QY	292	DGKLVTGK---KGENGSSTDEEGL--VTAKEVI-----DAVNKAGWRMKTITAN	337	
Db	329	VDSVALGSGSMASEPNVSVSGDGLRGPAVRIRVNVGDGIGNNDNAVKNKSOLDGVTTASVN	388	
QY	338	GQTQGAQKFTV--TSGTNTVFASGKGTAT--VSKDDQGNITVKYDVNVGDALNVNOLON	394	
Db	389	DVTASVKNIATGAIQTIGSGVASVSGDSTAAGASQAAGDSSIA---LGAERSANAIGS	444	
QY	395	SGWNLD-----SKAVAGSSGKVISGNVSPSKKMDETVINAGNMIETRNCKNIDIA	447	
Db	445	SALGVCHALGANSTALGGQSTAISEGGTSLG---YNSFVGOSATNGIALGSN-----	494	
QY	448	TSMTPTQFSSVSLGAGADAPTLSVDKDALNVGSKD--ANKPV--RITNVAPGVKEGDTVNV	504	
Db	495	-AIVSGVNSVALGAGSVASELNV-----ISVGGDGYTGPVRRIVNVGDGIGNNDAVNK	548	
QY	505	AQLKGVAQNLN---RIDNVDGNAR---AGIAQAI-----ATAGLVOAYLPKSKMAIG---	552	
Db	549	SOLDGVTTASVNDVAASVKKIVGTIQTIGSGVASAIGKDSSTATGASQAQAVGDSVALGTGA	608	
QY	553	-----CGTYRGEAGYALGYSSISDGGNWIK-----CTASGNSRGH	588	
Db	609	TANAIGSSVLGVDSRARGINSTALGROSNAGIDGVSILGFSFVRQSGEHGVALGTDAVG	668	
QY	589	FGA--SASVGY	597	
Db	669	SGKDSIALGY	678	

RESULT 11  
 A14177  
 190K surface antigen precursor - Rickettsia rickettsii  
 C:Species: Rickettsia rickettsii  
 C:Date: 16-Sep-1992 #sequence\_revision 16-Sep-1992 #text\_change 08-Oct-1999  
 C:Accession: A14177  
 R:Anderson, B.E.; McDonald, G.A.; Jones, D.C.; Regnery, R.L.  
 Infect. Immun. 58, 2760-2769, 1990  
 A:Title: A protective protein antigen of Rickettsia rickettsii has tandemly repeated,  
 C:Keywords: surface antigen; tandem repeat  
 F:1-20/domain; signal sequence (uncleaved) #status predicted <SIQUP>  
 A:Reference number: A14177; MUID: 90354033  
 A:Accession: A14177  
 A:Molecule type: DNA  
 A:Residues: 1-2249 <AND>  
 A:Cross-references: GB:M31227; NID:gl52465; PIDN:AAA26380.1; PID:gl52466  
 A:Note: the authors translated the codon GAT for residue 430 as Gly, and CAA for resi

F:1-20/Domain: signal sequence (uncleaved) #status predicted <SIGU>



Db 763 TLTNANAVITGAIIDNTGDNVGVNLNGLSQTVDIG-----NTNSL--ATISVGAG 814  
QY 111 ----DNLIKIQNTKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDT 166  
Db 815 TATLGAVIKATTKLTNA-----ASVLT-----LTNANAVLTGAVDNTTGGDNVGV--- 861  
QY 167 KGLNFAKETAGNGDTTVDHLNGIGSTPLDTLNTGATTNNTDNNV---TDDKKKRAASVYK 223  
Db 862 --LNLNGLSQTVDG-----IGNTSLATISVGAGTATLGGAIVKATTKLTNAASVL 912  
QY 224 DVNLNAGNNIKGVPKGTASDNDVDFVHTYDVEFLSADTKTT---TVNVESKD---NG-- 274  
Db 913 TLTNANAVITGAIIDNTGDNVGVNLNGLSQTVDIGNTGNTSLATISVGAGTATLGGA 972  
QY 275 -RTEVKIGAKTSVKEGKGLVTG---KKGKNGSSSDEGEGLVTAK-----EVIDAVN 325  
Db 973 IKATTKLTDAASAVKFTNPVVVGTGAIIDNTGNANNGIVTFTGNSTVTVGNVNTNALATVN 1032  
QY 326 KA-----GWRMKTFTAN-----GOTGQADKFETVTSNTVTFASGKGT 364  
Db 1033 VGAGLLQVGGVGVKANTINLTDNASAVTFTNPVVVGTGAIIDNTGNANNGI-VTFTGNSTVT 1091  
QY 365 ATVSKDDQGNITVKYDVNVGDAL-----NVN-----QLQNS 395  
Db 1092 GNV-----GNTNALATPVNVGAGLLQVGGVVKANTINLTDNASAVTFTNPVVVGTGAI 1146  
QY 396 GWNLDKAVAGSGGKVISGNVSPSKGMDETVNNAGNIEITRNG-----KNIDIATSM 451  
Db 1147 G-NANNGIVTFTGNSTVTDI-----GNTNALATVNVGAGITLQAGGSLAANNIDFGARST 1201  
QY 452 POFSSVSLGAGADAP-----TISVDKGLNGLVSKDANK-----PVRITNVAPG----- 495  
Db 1202 LEFNGPLDGGRAIPYFKGAIANGNAILNVTNKLTLTASHLTIGTVAEINIGAGNLF 1261  
QY 496 -VKEGDTVNVQALGVQANLNR-----INDVDGNARAGIAQAATAGLVQVQALPG--- 545  
Db 1262 DASVGDVITLN-----AQINFRARDSVLVLSNLTG---VGVNILLAADLV---APGAD 1310  
QY 546 KSMATGGCTYRGEAGYATGYS--SISDGG 573  
Db 1311 EGTVPFNGVGNLNVGNSVAGTARNIGDGG 1340

## RESULT 12

G64964  
hypothetical protein b2000 - Escherichia coli  
C:Species: Escherichia coli  
C>Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 02-Feb-2001  
C:Accession: G64964  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: G64964  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-1091 <BLAT>  
A:Cross-references: GB:AE000291; GB:U00096; NID:g1788298; PIDN:AAC75061.1; PID:g1788309;  
A:Experimental source: strain K-12, substrain MG1655  
A:Keywords: nucleotide binding; p-loop  
F:683-690/Region: nucleotide-binding motif A (p-loop)

Query Match 7.8%; Score 240; DB 2; Length 1091;  
Best Local Similarity 21.9%; Pred. No. 0.0001;  
Matches 148; Conservative 80; Mismatches 249; Indels 200; Gaps 33;  
QY 1 MNKIYRIWNSALNANVAVSELTRNTHKRASATVKTAVLATLLFAIVQANATDEDEEEL 60  
Db 57 LNTCYRLVNMHTGAFVAVASELARARGGVAVLSLAATVSL----- 100  
QY 61 EPVRSALVQLQFMIDKEGNESTGICWSIYDNNHNT--LHGATVTLKAGDNLKIKON 118

Db 101 -PVLAADIVVH-----PCETVNGGTLA-----NHDNQIVFEGTNGMTISTGLEYPD 146  
QY 119 TNKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTGLNFAKETAGT 178  
Db 147 NEANTG-----GQVQDGGTANKTTVTSG--GLQ-RVNPGG 180  
QY 179 NGDVTTVHLNGIGSTL-----TDTLLNTG-----ATTNVTNDVNTDDKKRAASVKDV 225  
Db 181 VSDTVISAGS-GQSLQGRAVNTTLNGEQMHGAIATGTVINDK----- 224  
QY 226 LNAGNNIKGVPKGTASDNDVDFVHT---YDTEFLSADTKTTVN-----VE 269  
Db 225 --GMOV--VKPGTAVATDV--VNTGAEGGPDAGNDTQGVFRGDAVFTTINKNGRQIVR 277  
QY 270 SKDNGKRTVEKIGAKTSV-----IKEKDGKLVTKGCKGEN 304  
Db 278 AEGTANTTVVYAGGDDTVHGHALDITLNGGYQVHNGGTASDTVNVNSDGMQIVKNG-GVA 336  
QY 305 GSSTDEGEGLVTAKEVIDAVN---KAGWRMKTFTTANGOTG--QADKFETVT-SCTNVVTF 358  
Db 337 GNTTVNQKGRLOVDAGGTATNVTLKOGGALVTSTAATVTGINELGAFSVVVEGRADNVVLE 396  
QY 359 SG-----KGTATVSK-DDQGNITVKYDVNVGDALNVNQLONGSNLDSKAVAGSSGV 411  
Db 397 NGRRLDVLGTGHTATNTRVDDGGTLDVR--NGGTATTVS-MGNGG-----VLLADSGAA 446  
QY 412 ISGNVSPSK-----GKMDETVNNAGNIEITRNGKNIDIATSMTPQFSSVSLGAGADAP 466  
Db 447 VSTRSDGKAFSTGGQADALMLEKSSFTLNAG-----DTATDTTVNGGLFTARGGTLAG 502  
QY 467 TISVDKGLNGLVSKDANKPVRITNVAPGVKEGDTVNVQALGVQANLNRINDVDGNAR 526  
Db 503 TITLNNGALITLSGKTVN-----NDTLIREGD-----ALQGGSLTNGSVSK-SGSGT 551  
QY 527 AGIAQAIAATAGLVQVQALPGKSMMAIGGT-----YRGEAGYATGYS-----S 568  
Db 552 LTVSNTTLTKQKAVNL--NEGTLTNDSTVTDVIAORGFTALKLTGTVLNGAIDPTNVT 608  
QY 569 ISDGGNWIIGKTASGNS 585  
Db 609 LASGATWNPIDNATVQS 625

## RESULT 13

T31105  
hypothetical protein 2 - Haemophilus ducreyi  
C:Species: Haemophilus ducreyi  
C>Date: 22-Oct-1999 #sequence\_revision 22-Oct-1999 #text\_change 22-Oct-1999  
C:Accession: T31105  
R:Ward, C.K.; Lumbley, S.R.; Latimer, J.L.; Cope, L.D.; Hansen, E.J.  
J. Bacteriol. 180, 6013-6022, 1998  
A:Title: Haemophilus ducreyi secretes a filamentous hemagglutinin-like protein.  
A:Reference number: Z20984; MUID:99030326  
A:Accession: T31105  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: DNA  
A:Residues: 1-4919 <WAS>  
A:Cross-references: EMBL:AF057696; NID:g3929021; PID:g3929023; PIDN:AAC79761.1  
C:Genetics:  
A:Gene: lspA2

Query Match 7.5%; Score 231; DB 2; Length 4919;  
Best Local Similarity 22.4%; Pred. No. 0.002;  
Matches 173; Conservative 91; Mismatches 268; Indels 240; Gaps 37;  
QY 1 MNKIY----RIWNS---ALNANV-AVSELTRNTHKRASATVKTAVLA-----T 41  
Db 376 LNKVYADYVRVVGKDELANNGQIHADQQQLILNATGHVKLNDGSSVSNLNLGIALNLT 435  
QY 42 LFPATVQAN-----ATDEDEEELEPVRVSALVLQ---FMIDKEGNESTGICWSIY 93

Db 436 LENTVSNANLSFRVNTDKLNNLSKVSARAADLQSGNLDKASVLAKHKLTLNISNDVS 495  
Qy 94 YDNHTLHGATVTLKAGDNLIKQ-----NTNKNNTNNDSSFTYSLKDLTDLTSV 146  
Db 496 LNNOSKL-----SANNLAKKKVRLDNLNSELNANLTLNNTLTK-----538  
Qy 147 ETEKLSFGANGKVNITSDTKGLNFAKETAGTNGDITVHLN---GIGSTLDTLLNTGAT 203  
Db 539 --NKSKEFTAGNNTLVNTVNNVT--LNNDSELAANNLTLVNTKVNLTNDASKLSANKLDELNVT 595  
Qy 204 TNYTND-----NVTDDKKRAASVKDVLNAGWNKIKGVKPTTASDNVDF 247  
Db 596 DNVTLNKSSTLSAGELFKVKYKNVTLNNDSELANNSLNASHNVTLNKSKLSAQAKADI 655  
Qy 248 ----VHTYDVTVEFL--SADFTKVTNVNVEKONGKRTVEKIGAKTSVKEKGLVTG---298  
Db 656 KAVNLTLDNHTTAKNLDINSTIIT-----NNGTIAGIFANITTEKLNKKEKALILABON 711  
Qy 299 -----RKGE-----NGSSTDEGEGLVTAKEVIDAVNKAQWRMKTIT 335  
Db 712 LNFVNGSHYENKGDIVSKDKATVTFESKNSDFTSNGSKLVNAQN-----QLKYNV 761  
Qy 336 ANQOTQOAKFE---TVTSGTNVTF--SGKGTTA--TVSKDDQGNITVKYDVNVDALNV--389  
Db 762 NNTISQDDITLIGNVTLNASGFTNNGNLTITVKTLVDVGDIQNFNTKGNLTVGEDLHIK 821  
Qy 390 --NOLNSG-----WNLDSKAVAGSSGKVI-----SGN-----415  
Db 822 SKTKITNDGKLISLKNLISEADFINNGTULGIEALKIATGNFTNKEKAILASNSLLD 881  
Qy 416 VPSKGRKMDVTN---INAGNIEITRNGK--NIDIATSMTPQFSSVSLGAGADAPTLVS 470  
Db 882 LSVABGK--KTFNCTIESGRNLNITNIGAFNLVDNATIR-----SFGVLNITSTGNV 932  
Qy 471 DDGALNVGSK--DANKPVRIINVAPG-----VKEGDVTN-----VAQLKGV 510  
Db 933 SNNGTLISNERLNITSAANFTNESNGTVMSNGLNIIITAKOGNITMKNLIASROQLNLTAV 992  
Qy 511 AONLNNRIDNVDGNARAGIAQAIATAGIV-----QAYLPG-----545  
Db 993 ADNITN-----DSNISNKIA-VLHSLGNLSLNSKDDQVYNLGEIYAGNINSVKAHQLKNDV 1046  
Qy 546 KSMMAIGGTYRGEAGYAIYSSIDSGNWIITKTASGNSRHFPCASASVGY 597  
Db 1047 KLMDGTTTKTEGQASQKLYQAS-----NGHEGNDGSSGY 1082

RESULT 14  
D90803  
Aida-I adhesin-like protein [imported] - Escherichia coli (strain O157:H7, substrain RIM  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: D90803  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: D90803  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-949 <HAY>  
A:Cross-references: PIDN:BA834819.1; PID:q13360856; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
A:Gene: ECs1396

Query Match 7.5% Score 228 DB 2 Length 949;  
Best Local Similarity 22.0% Pred. No. 0.00034;  
Matches 180; Conservative 102; Mismatches 270; Indels 268; Gaps 42;  
Qy 1 MNKYRIIWSALNANWAVSELNRHTNKRASATVKRTAVLATLFLFATVQANATDEDEBEL 60

Db 5 LNTSYRLVWNHITGLTVVASELARSGRKAGVAVALSAAV---TSVPALAAK-----55  
Qy 61 EPVYRSALVLOFMIDKEGNGENESTGNIGWIIYYDNH---NTLHCATVT--LKAGDNLKI 115  
Db 56 --VVOA-----GE---TVNDGTLTNHDNQIVFGTANGMTISTGLELGPD--S 95  
Qy 116 KQNTN-----KNTNENTNDSSTFYSLKDLTDLTSVETEKLSFGA---NGKNYNI 162  
Db 96 EENTGGQIIONGGIAGNTVTTNGRVV-----LEGCTASDVTIROGGGOSLGLAVNT 149  
Qy 163 TSDTKGLNFAKETAGTNGDITVHLNGI-----GSTLDTLLNTGATNVTNDVTDKKK 217  
Db 150 TLNRRGEQWHE--GGVATGTIINRDYQSVKSGGLATGTIINTGAEGGPDSDNSYTGQV 208  
Qy 218 RAASVKDVLN-----AG---WNKGVKPGTTASDNVDVH---TYD 252  
Db 209 QGTAESTTINKNQRIILFSGGLARDTLIYAGDQSVHGRALNTLNGGYQVYHRDGLALN 268  
Qy 253 TV-----EFLSAD--TKTTVNVEKDNKRTVEKIGAKTSVKEKDKLVT-----297  
Db 269 TVINEGGQVVKAGGAAGNTIN---QNGELRVHAGGEATVQNTGGALVTSTAATVI 324  
Qy 298 -----GRGKG---ENGSTDEGEGLVTAKEVID-----AVNKAQWRMKTITAN 337  
Db 325 GTNRLGNFTVENGKADGVVLESGRGLDVLESHSAQNTLIVDDGTLAVSAGKATSVTTS 384  
Qy 338 QOTQOAKFEIVTSGTNVTFASGK-----GTTATYSKDDQ--GNITVKY 379  
Db 385 GGALIASGATV--EGTN---ASGKFSIDGTSGQASGLLENGSGFTVNAGGQAGNTTVGH 440  
Qy 380 D-----VNVGDALNVNOLNSQWNLD-----SKAVAG 406  
Db 441 RGTTLAAGSGLSGRTQLSKCASVNLGCVVSTGDIVNAGEIRFDNQTPPNAALSRAVAK 500  
Qy 407 SSG-----KVISGNVSPSKGMDVTNI-----NAGN--NI 435  
Db 501 SNSPVTFHKLTTNLTGQGTINMRVLDDGSNASDQLVINGQATGKTWLAFTNVGNSNL 560  
Qy 436 EITRNGKNIDI-----ATSMTPQFS--SVSLGACADAPTLSDDKGALNVSKDANK---485  
Db 561 GVATTGQIRVVDQNGATTEEGAFALSRPLOAGAFNYTLNRDDEDEWYLRSENAIRAEV 620  
Qy 486 PVRTINVAPG-----VKEGDVTNVAQLKGAQNLNNRI-----DNVDGNARAGIAQAI 533  
Db 621 PLYTSMLTQAMDYDRILLAGSRSHQTVNGENNSVRLSIQGGHLGHDNNGGIARGATPSS 680  
Qy 534 ATAG-----LVQAYLPKSKMM-----AIG-----GGTYRGEAGYAIYGVSS 568  
Db 681 GSYGFVRLEGDLRLTEVAGMSLTGTGYGAAGHSSVDVKDDGSRAGTVRDDAGSLGGYLN 740  
Qy 569 I--SDGGNW---ILKGT-----ASGNSRCHFCASASVGYQW 599  
Db 741 LVHTSSGLMADIVAQGRTHSMKASSDNNDFRFR---GNGW 777

RESULT 15  
H85611  
probable adhesin Z1211 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: H85611; B85663  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: H85611  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1005 <STO>  
A:Cross-references: GB:AE005174; NID:g12514025; PIDN:AAG55356.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933

A, Cross-references: GB: A8005174; NID: g12514546; PIDN: AAG55766.L; GSPDB: GN00145; UWGP: Z16  
A, Experimental source: strain O157:H7, substrain EDL933

Query Match 7.5%; Score 228; DB 2; Length 1005;

Search completed: July 3, 2002, 08:12:32

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:30:09 ; Search time 48.34 Seconds  
(without alignments)  
479.789 Million cell updates/sec

Title: US-09-771-382-6  
Perfect score: 3060  
Sequence: 1 MNKIYRIINWALSNAWAVS.....TASGNSRGFGASASVGYQW 599

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 3871950 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match %	Length	DB ID	Description
1	241	7.9	2249	1 OMPA_RICRI	P15921 rickettsia
2	240	7.8	1039	1 AG43_ECOLI	P39180 escherichia
3	228	7.5	1325	1 YDBK_ECOLI	P32051 escherichia
4	225.5	7.4	1286	1 AIDA_ECOLI	Q03155 escherichia
5	221.5	7.2	2021	1 OMPA_RICCN	Q52657 rickettsia
6	200	6.5	1645	1 OMPB_RICTY	P96989 r outer mem
7	199.5	6.5	1655	1 OMPB_RICCN	Q9KXK3 r outer mem
8	197.5	6.5	2003	1 YDBA_ECOLI	P33666 escherichia
9	196.5	6.4	933	1 SLAP_CAMPE	P35827 campylobact
10	189.5	6.2	1608	1 HLYA_SERWA	P15320 serratia ma
11	187.5	6.1	1577	1 HLYA_PROMI	P16466 proteus mir
12	185.5	6.1	1567	1 ICEN_XANCT	P18127 xanthomonas
13	185.5	6.1	1654	1 OMPB_RICRI	Q53047 r outer mem
14	180.5	5.9	918	1 YWJB_CAEEL	P34487 caenorhabdi
15	180	5.9	1569	1 YRJA_ECOLI	P52143 escherichia
16	179	5.8	1953	1 BIGA_SALTY	P25927 salmonella
17	178.5	5.8	1300	1 120K_RICRI	P14914 rickettsia
18	177.5	5.8	1643	1 OMPB_RICPR	Q53020 r outer mem
19	177.5	5.8	1656	1 OMPB_RICJA	Q06653 r outer mem
20	176.5	5.8	550	1 FLIC_SHIFL	Q08860 shigella fl
21	176	5.8	1861	1 APU_THETU	P38536 t amylopull
22	174.5	5.7	2329	1 YS89_CAEEL	Q09624 caenorhabdi
23	174	5.7	2334	1 WAPA_BACSU	Q07833 bacillus su
24	171	5.6	523	1 P60_LISSE	Q01838 listeria se
25	171	5.6	787	1 SPI_RAT	Q01714 rattus norv
26	170.5	5.6	497	1 FLIC_ECOLI	P04949 escherichia
27	168.5	5.5	1694	1 IGA0_HAEIN	P44969 haemophilus
28	168.5	5.5	1702	1 IGA2_HAEIN	P45384 haemophilus
29	167.5	5.5	1396	1 VLTF_BPT5	P13390 bacterioph
30	167	5.5	1025	1 SLAP_CAUCR	P35828 caulobacter
31	166	5.4	1148	1 ICEK_PSEXX	Q30611 pseudomonas
32	166	5.4	1196	1 ICEV_PSEXX	Q33479 pseudomonas
33	164.5	5.4	928	1 HXA2_HAEIN	P45354 haemophilus

RESULT 1  
OMPA\_RICRI  
ID OMPA\_RICRI STANDARD; PRT: 2249 AA.  
AC P15921:  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
DE antigen) (rOmpA) (rOmp A).  
GN OMPA.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=90354033; PubMed=2117568;  
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
RT "A protective protein antigen of Rickettsia rickettsii has tandemly  
RT repeated, near-identical sequences.";  
RL Infect. Immun. 58:2760-2769(1990)  
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC -!- PTM: GLYCOSYLATED (PROBABLE).  
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
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CC -----  
CC EMBL; M31227; AAA26380.1; -  
DR PIR; A14777; A14777.  
DR InterPro; IPR003858; rOmpA\_rOmpB.  
DR Pfam; PF02708; rOmpA\_rOmpB; 1.  
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
FT SIGNAL 1 28 POTENTIAL.  
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.  
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.  
FT REPEAT 212 286 A (TYPE I).  
FT REPEAT 287 358 B (TYPE II).  
FT REPEAT 359 430 C (TYPE II).  
FT REPEAT 431 505 D (TYPE I).  
FT REPEAT 506 577 E (TYPE II).  
FT REPEAT 578 652 F (TYPE I).  
FT REPEAT 653 724 G (TYPE II).  
FT REPEAT 725 799 H (TYPE I).  
FT REPEAT 800 874 I (TYPE I).  
FT REPEAT 875 949 J (TYPE I).  
FT REPEAT 950 1021 K (TYPE II).  
FT REPEAT 1022 1093 L (TYPE II).

34 164 5.4 1007 1 Y741\_CHLMU Q9pit6 chlamydia m  
35 162.5 5.3 1005 1 Y456\_CHLTR O84462 chlamydia t  
36 161 5.3 1200 1 ICEN\_PSEXY P06620 pseudomonas  
37 160.5 5.2 671 1 ALYS\_ENTFA P37710 enterococcu  
38 160 5.2 928 1 PM10\_CHLPN Q9rb65 chlamydia p  
39 160 5.2 948 1 HPI1\_DEIRA P56867 deinococcu  
40 160 5.2 959 1 N100\_YEAST Q02629 saccharomyc  
41 159.5 5.2 1036 1 HPI2\_DEIRA P13126 deinococcu  
42 159 5.2 1210 1 ICEN\_PSEFL P09815 pseudomonas  
43 158.5 5.2 575 1 FLA2\_CAMJE P22251 campylobact  
44 158.5 5.2 1770 1 PMPC\_CHLTR O84419 chlamydia t  
45 158 5.2 1322 1 ICEA\_PANAN P20469 pantoea ana

ALIGNMENTS



```
FT SIGNAL 1 52
FT CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.
FT VARIANT 552 1039 ANTIGEN 43 BETA CHAIN.
FT VARIANT 2 2 K -> N (IN STRAIN ML 308-225).
FT VARIANT 41 42 SL -> FF (IN STRAIN ML 308-225).
FT VARIANT 46 46 T -> K (IN STRAIN ML 308-225).
FT VARIANT 157 157 W -> L (IN STRAIN ML 308-225).
FT VARIANT 188 188 V -> F (IN STRAIN ML 308-225).
FT VARIANT 303 305 ATN -> STI (IN STRAIN ML 308-225).
FT VARIANT 320 320 A -> T (IN STRAIN ML 308-225).
FT VARIANT 372 372 N -> Q (IN STRAIN ML 308-225).
FT VARIANT 493 493 E -> V (IN STRAIN ML 308-225).
FT VARIANT 497 497 S -> N (IN STRAIN ML 308-225).
FT VARIANT 585 585 H -> Y (IN STRAIN ML 308-225).
FT VARIANT 709 709 E -> K (IN STRAIN ML 308-225).
FT VARIANT 721 721 M -> T (IN STRAIN ML 308-225).
FT VARIANT 751 753 GHL -> SHF (IN STRAIN ML 308-225).
FT VARIANT 803 803 S -> P (IN STRAIN ML 308-225).
FT VARIANT 815 815 A -> V (IN STRAIN ML 308-225).
FT VARIANT 824 824 C -> S (IN STRAIN ML 308-225).
FT VARIANT 829 835 LNLVHTS -> MNLYNA (IN STRAIN ML 308-225).
FT VARIANT 845 847 QGT -> LGA (IN STRAIN ML 308-225).
FT VARIANT 855 855 S -> T (IN STRAIN ML 308-225).
FT VARIANT 888 888 Q -> L (IN STRAIN ML 308-225).
FT VARIANT 1025 1025 S -> I (IN STRAIN ML 308-225).
FT CONFLICT 61 63 ETV -> TTT (IN REF. 5).
SQ SEQUENCE 1039 AA; 106841 MW; 51700647C8DEBE0 CRC64;

Query Match 7.8%; Score 240; DB 1; Length 1039;
Best Local Similarity 21.9%; Pred. No. 6.4e-05;
Matches 148; Conservative 80; Mismatches 249; Indels 200; Gaps 33;

QY 1 MKKIYRIINWALNAWVSELTNRHTRKASATVKTAVLATLLFATVQANATDEDEEEL 60
DB 5 LNTCYRLVNHMTGAFVVASSELARARGRGVAVALSLAATVSL----- 48
QY 61 EPVRSALVQFMIDKEGCNESTNIGWSIYYDNHNT--LHGATVTLKAGDNLKIKON 118
DB 49 -PVLAAIDIVVH-----PGETVNGGTLA-----NHDNQIVFGTTNGMTISTGLEYPD 94
QY 119 TNKNTNENTNDSTFYSLKKDLTDSVETKLSFGANGKNYITSDTKLFAKETAQT 178
DB 95 NEANTG-----GQWVDGCTANKTIVTSG--GLQ-RVNPGRS 128
QY 179 NGDITVHLNGIGSTL---TDILLNG-----ATTNTVDNNTDDKKRAASVKDV 225
DB 129 VSDTVISAGG-GQSLOGRAVNTTLNGGEQWHEGATATGTVINDK----- 172
QY 226 LNAWNKIKGPKTASDNVDFVHT-----YDTVEFLSADTKTTVN-----VE 269
DB 173 ---GQWQ--VKPGTATDVT--VNTGAEQDPAEDGTCQFVRGDAVRTTINKNGRQIVR 225
QY 270 SKDNKRTRTEVKIGAKTSV-----IREKDKLVTGKGKGEN 304
DB 226 AEGTANTTVYAGGQTVHGHALDTTLNGGYQYVHNGGTASTVYNSDQWQIVKNG-GVA 284
QY 305 GSSTDEGELVTAKEVIDAVN---KAGWRMKTMTTANGQTG---QADKFETVT-SGTNVTEFA 358
DB 285 GNTTVNKGRLQVDAGGTATNTLQGGALVTSTAATVTGINRLGAFSVVEGKADNVILE 344
QY 359 SG-----KGTATVSK-DDQGNITVKYDVNVGDALNVQLNSGNLNSKAVAGSSGVK 411
DB 345 NGRRLDVLVGHATATNRVDGGLDVR---NGGTATTVS-MGNGG-----VLLADSGAA 394
QY 412 ISGNVSPSK-----KMGDETVINAGNNITEITRNKNIDIAATSMTPQFSSVSLGACADAP 466
DB 395 VSGTRSDGKAFSIGGGQADALMLEKSSFTLNAG-----DTATDTTVNGGLFTARGGTLAG 450
QY 467 TLSVDKGAALNKGSKDANKPVRITNVAPGVKEGDVTNVQALKGVAQNLNNRIDNVDGNAR 526
DB 451 TTTLNNGAILTSLGKTVN-----NDTLTIREG-----ALLOGGSLTGNGSVEK-SGSCT 499
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QY 527 AGTAAIATAGLVQAVLPCKSMMAIGGGT-----YRGEAGVAGVYS-----S 568
DB 500 LRVNTTTLTKAVNL---NEGTLTLDNSTVTTVDVIAQRGALKLGTGVLNGAIDPTNVT 556
QY 569 ISDGGNWIIGKTSAGNS 585
DB 557 LASGATWNIPDNATVQS 573

RESULT 3
YDEK_ECOLI
ID YDEK_ECOLI STANDARD; PRT: 1325 AA.
AC P32051: P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORET).
GN YDEK OR ORFT OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC MEDLINE=97251357; PubMed=9097039;
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Sampaio G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
(Potential).
CC -!- SIMILARITY: TO E-COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
FRAMESHIFT IN POSITION 653.
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CC -----
DR EMBL; AE000248; AAC74583.1; -
DR EMBL; D90793; BAA15190.1; ALT_INIT.
DR EMBL; D90794; BAA15197.1; ALT_INIT.
```





Db	437	IVNTSGFORINSGGTAPVQNSVVVTRTVSSAAKPFDAEIVSGGKQVYVLRGIIWYSNFUT	496
Qy	449	SMTPQFSVSLGAGADAPTLVSDVDKGNL	480
Db	497	AVSMFPCTASG-----NVNLSGRLLNAPAGNVVGTILNQGROVYVSGATAITVGN	549
Qy	481	KDANKPVRIITNPAPVKEGVDVITVAOLKGVAQNLNNRIDNVGNARA-----GIAQAIAT	535
Db	550	NEGREYV-----LSGGITDGTVNLGSLQAVSSG-----GKASATVINEGGAFFVD	596
Qy	536	AGLVQAYLPCKSMMA TGGGTGYRGEAGYATGYSSISDGN	574
Db	597	GGQV-----TCTNIK--NGGTRVDSGASALINIALSSGNN	629

## RESULT

OMPA\_RICCN  
ID OMPA\_RICCN STANDARD; PRT: 2021 AA.  
AC Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;  
AD Q52670; Q52674;  
AT 16-OCT-2001 (Rel. 40, Created)  
DT 01-MAR-2002 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
antigen) (rOmpA) (rOmp A).  
GN OMPA OR RC1273.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RC MEDLINE=94171067; PubMed=8125327;  
RA Crocquet-Valdes P.A., Weiss K., Walker D.H.;  
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia  
conorii (Malish 7 strain).";  
RL Gene 140:1115-1119(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Malish 7;  
RC MEDLINE=21442074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
RA Raoult D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";  
RL Science 293:2093-2098(2001).  
RN [3]  
RP SEQUENCE OF 8-204 FROM N.A.  
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;  
RX MEDLINE=97015921; PubMed=8862558;  
RA Roux V., Fournier P.E., Raoult D.;  
RT "Differentiation of spotted fever group rickettsiae by sequencing and  
analysis of restriction fragment length polymorphism of PCR-amplified  
DNA of the gene encoding the protein rOmpA";  
RL J. Clin. Microbiol. 34:2058-2065(1996).  
RN [4]  
RP SEQUENCE OF 953-1012 FROM N.A.  
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;  
RA Raoult D., Fournier P.E., Roux V.;  
RT "Phylogenetic analysis of spotted fever group rickettsiae by study  
of the outer surface protein rOmpA";  
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).  
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC -1- S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -1- PTM: GLYCOSYLATED (BY SIMILARITY).  
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
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```
QY 64 VRSALVQLQFMIDKEGN-----GENESTGNGWISYIDNHNTHLHGATVTLKAG----- 110
Db 111 DNLKIKONTNKNNTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLN 170
QY 594 GGAIKATTKTKLT-DNASAVTFTNPV-----VVTGADNTGNANN-GIVTFTGNST 642
Db 171 FAKETAGTNGTTHLNGIGSTLDTLLNTGATTNNTVNTDDKKRAASVKDVLNAGW 230
Db 643 VTGIGNTNALATVNV-GAGIATLEGAVIKATTKLTN-----AASVLTLTNVA 691
QY 231 NIKGVKGTASDNVDFVHTYDTVEFLSADTKTT-----TNVNV-----ESKDNG---KRTEVK 280
Db 692 VLTGAIDNTTGVNDVGNVLNGLALSQVGTGNTGNATLISVGAKGATLGGAVIKATTK 751
QY 281 IGAKTSVIKEKDKGLVYG-----KKGKENGSSSTDEGEGLVTKA-----EVIDAVNKA----- 327
Db 752 LTDNASAVTFTNPVVTGADNTGNANNGIATFTGDSVTGTGNTGNATLATVNVYAGALLR 811
QY 328 --GWRMKTTTAN-----GOTGOADK-----FETVT---SGTN- 354
Db 812 VOGGVVKSNTINLTDNASAVTFTNPVVTGADNTGNANNGIATFTGDSVTGTGNTGN 871
QY 355 ---VTFASGKGT-----TATVSKDDQGNITVKYDVNVGDALNVNOLQNGWNLDSKA 403
Db 872 LATISVGAGKATLGAIIKATTKLTLDNASAVTFTNPVVTGAID-----NTG-NANNGI 925
QY 404 VAGSSGKVISGNVSPSKGMDVETNINAGNNIEI--TRNGKNIDIAIATSMTPQFSSVSLGA 461
Db 926 VTFTGDSVTGTGNTGNAL--ATVNVGAGVTLQAGSLDANNIDFGARSTLTFNGPLDGG 983
QY 462 GADAP-----TLSVDDK-----GALNVGSKDANK-PVRI 490
Db 984 GNAIPYFKGAIANGNNAIINVTNKLTYHLTGTVAEINIGAGNLPADASAGDVTIL 1043
QY 491 N-----VAPGYKEGDV-----TNVAQ 506
Db 1044 NAOQDIFRALDSALVLSNLGTGVGNVILLAADLVAPGVDEGTVPVFDGCVGNLIGSNVA- 1102
QY 507 LKGAQNLLNN-----RIDNVGNARAGTAQATA-TAGLVQA 541
Db 1103 --GAARNIGDVGKFNFTLLIYNAVTTDDVNLEGIONVLLNNNADEFTSTAFNAGTIQ- 1159
QY 542 YLPCKSMMAIGGTY-----RGEAGYAGYSSISDGGWIIKGTASGNSR 586
Db 1160 -----INDATYTTDANNGLNIPAGNIKFAHADRAQLILQNLSSGND 1200
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## RESULT 6

```
OMP_RICTY
ID OMP_RICTY STANDARD; PRT; 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
DE OMPB OR SLP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxId=785;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=WILMINGTON; PubMed=8224886;
RX Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;
RT "Cloning and sequence analysis of the gene encoding the crystalline
RL surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1993).
```

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RN [2]
RP PARTIAL SEQUENCE.
RC STRAIN=WILMINGTON;
RX MEDLINE=92114896; PubMed=1370573;
RX Ching W.M., Carl M., Dasch G.A.;
RT "Mapping of monoclonal antibody binding sites on CNR fragments of
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
RT prowazekii.";
RL Mol. Immunol. 29:95-105(1992).
RN [3]
RP IDENTIFICATION OF CLEAVAGE SITE.
RX MEDLINE=92104668; PubMed=1729180;
RX Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
RT membrane protein of rickettsiae: identification of an avirulent
RT mutant deficient in processing.";
RL Infect. Immun. 60:159-165(1992).
CC -1- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC
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CC
CC EMBL: L04661; AAB48987.1; -
CC InterPro: IPR003858; rOmpA_rOmpB.
CC Pfam: PF02708; rOmpA_rOmpB; 1.
CC Antigen; S-layer; Transmembrane; Cell wall.
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.
FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).
FT TRANSMEM 657 657 H -> N (IN REF. 2).
FT CONFLICT 842 842 V -> I (IN REF. 2).
FT CONFLICT 1071 1071 G -> A (IN REF. 2).
FT CONFLICT 1306 1306 G -> S (IN REF. 2).
SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;
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Query Match 6.5%; Score 200; DB 1; Length 1645;  
Best Local Similarity 21.1%; Pred. No. 0.01;  
Matches 158; Conservative 86; Mismatches 256; Indels 248; Gaps 37;

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QY 25 NHTKRASATV-----KTAVLATLLFAT---VQANATDE-----DEEEE 59
Db 40 NRTTNAATTVDGAGFDGTGAGVNLVPATNSVITANSNNNAITFTNPNGNLSLFDNTANT 99
QY 60 LEPVVSALVQLQFM--IDKEGNGENESTGNGWISYIDNHNTHLHGATVTLKAGDNLKIQ 117
Db 100 LAVTINENTTLGFTVNTVKQGNFFNTIG-AGKSLTITGHGITAQAATTKSAQNVVSKV 158
QY 118 NTKNTNENTNDSFTYSLKDKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG 177
Db 159 NAGAAINDN-----DLSGVGSIDFTAAPSVLFEFLNIPTT-----QEAPL 198
QY 178 TNGDTTHLNGICIGSTLDTLLNTGATTNVTND--NVTDKKKRAASVKDVLNAGWNKGV 235
Db 199 TLGDNNAKIVNGANGIL-----NITNGFVKVSD---KTFAGIK-TINIGDN-OGL 242
QY 236 KPGTTASDNVDVHTYDTVEFLSADTKTTTVNVESKD-----NGKTEVKI----- 281
Db 243 MFNTTP-----DAANALNLOGGNTINFNGRGTGKLVLSKNGNATEFNVTGSL 292
QY 282 GAKTSVIKEKD-----GKLVTKGKG-----ENGSG-----STDEG-----EGLVTA 317
RL Gene 133:129-133(1993).
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Db 293 GGNLKVIEFTTAAAGKLIANGAANAVIGTDNGAGRAAGFIIVSDNGNAATISQGVYA 352  
 QY 318 KEVIDAVNAGWRKTTTANGOT-----GQADKETVTSCINVTFFASCKGTATV 367  
 Db 353 KDIV-----IQSANAGQVTFEHLVDVGLGGKTNFKTADSKVITITENASFGST--- 400  
 QY 368 SKDDOGNITVYDVN-----VGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSP 418  
 Db 401 ---DFGNLAVQIVPNKILITGFIDG-----KNGG-NTAGVIITFNANGTLVSGNTDP 450  
 QY 419 S-----KGKMDTVNI-----NAGNIEITRNKNIDIAITSMTPQSSVS 458  
 Db 451 NIIVVTNIKATEVEGAGIVQLSGIHGAELRLGNAGSIFKLA-DGTVINGPVPNQPLVNNNA 509  
 QY 459 LGAGA---DAPTLSDVD---KGALNVGSKD---ANKPVRITNVAP-----GVKEG----- 499  
 Db 510 LAAGSITDGSATITGDIGNGAVNAALQDITLANDASKILITLGSANIIGANAGGAIHFQA 569  
 QY 500 -----DVTNVAQLKGVAQN-----LNNRIDNVDGNAR----- 526  
 Db 570 NGCTIQLTSPONNLLVDFDLVDITDQGVVDASSLLNNQTLTNGSIGTIGANTKILGRF 629  
 QY 527 -AGIAQAIATAGLV-----QAYLPKSMMAITGGGTGTYRGEAGYAIYSS 568  
 Db 630 NVGSSKTIILNAGDVAINELVWENDGSVHLTHNTYLTITKTINAANQGIIVAAADPINTDTA 689  
 QY 569 ISDGGNWLKGTASGNSRGHFGASASVG 596  
 Db 690 LADGTN--LGSAESPLSNTHFATKAANG 715

RESULT 7

OMP\_RICCN STANDARD; PRT; 1655 AA.  
 AC QPKRA3; Q9XK98; Q9XC45;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (rel. 41, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Scs5) (rOmpB)  
 DE antigen] (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB OR RC1085.  
 OS Rickettsia conorii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_Taxid=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Malish 7;  
 RX MEDLINE=21442074; PubMed=11557893;  
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";  
 RL Science 293:2093-2098(2001).  
 RN [2]  
 RP SEQUENCE OF 33-1649 FROM N.A.  
 RC STRAIN=Indian tick typhus, and Malish 7;  
 RX MEDLINE=20393643; PubMed=10939649;  
 RA Roux V., Raoult D.;  
 RT "Phylogenetic analysis of members of the genus Rickettsia using the  
 RT gene coding the outer-membrane protein rOmpB (ompB).";  
 RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).  
 RN [3]  
 RP SEQUENCE OF 353-1655 FROM N.A.  
 RC STRAIN=Malish 7;  
 RA Stenos J., Walker D.;  
 RT "The rickettsial outer membrane protein A and B genes of Rickettsia  
 RT australis, the most divergent rickettsia of the spotted fever group.";  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL

CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
 CC SIMILARITY).  
 CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
 CC (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
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 CC  
 CC EMBL; AE008659; AAL03623.1; -  
 DR EMBL; AF123721; AAF34124.1; -  
 DR EMBL; AF123726; AAF34129.1; -  
 DR EMBL; AF149110; AAD39533.1; -  
 DR InterPro: IPR003858; rOmpA\_rOmpB.  
 DR Pfam: PF02708; rOmpA\_rOmpB; 1.  
 KW Antigen; S-layer; Cell wall; Complete proteome.  
 FT CHAIN 1 1334  
 FT CHAIN 1335 1655  
 FT VARIANT 61 61  
 FT VARIANT 75 75  
 FT VARIANT 78 78  
 FT VARIANT 251 251  
 FT VARIANT 413 413  
 FT VARIANT 959 959  
 FT VARIANT 988 988  
 FT VARIANT 1139 1139  
 FT CONFLICT 353 354  
 FT CONFLICT 776 776  
 FT CONFLICT 1159 1159  
 FT CONFLICT 1177 1177  
 FT CONFLICT 1492 1492  
 FT SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;  
 SQ

Query Match 6.5%; Score 199.5; DB 1; Length 1655;  
 Best Local Similarity 23.6%; Pred. No. 0.011;  
 Matches 141; Conservative 66; Mismatches 253; Indels 137; Gaps 29;  
 QY 95 DNHTL-----HGATVTLKAGDNLKIKONTNK-----NTNMENTNDSSFTYSLKKDLTDTSV 146  
 Db 249 DNVNTLNQANGATITFNGTD-----GTGRLVLLSKNAATDFNVTGSLGGLKGIIEF 302  
 QY 147 ETE-----KLSTGA-----NGNKVNITSDTKGLNFAKETAGT 178  
 Db 303 NTVAVNGQLKANAGANAIVGTNGAGRAAGFVVDNGKVATIDGOVYAKDMVIOQANA 362  
 QY 179 NGDTT-----VHLNGIGSTLTDLTLLNTGATTNVTNDVNTDDKKRAASVKD---VLNAGWN 231  
 Db 363 VGQVNEPHIVDVGTDGTTAFKTAASKVAITQNSNFGTDFGNLAQAQIIVFTWTLNGNFT 422  
 QY 232 IKGVKPGTTASDNVDFVHTYD---TVEFLSADTKTTTVN-----VESKDNG-----KRT 277  
 Db 423 GDASNPGNTAG-----VITFDANGTLASADANAVTNNTITAEASGAGVQVLSGTHAA 477  
 QY 278 EVKIGAKTSVIKEDGKLVTK-----GKGENSSTDEGEGLVTAKEVIDAVNKGW 329  
 Db 478 ELRLGNAGSVFKLADGTVINGKVNQOTALVGAALAAQITLDGSATITG-----DIGNAGG- 532  
 QY 330 RMTTNTANGOTQADKFTVT-----SGTNVTFASGKGTATTATVSKDDOGNITVKYD 380  
 Db 533 ---AALQGITLANDATKTLTFLGANIIGANGGTINFQANGGTIKLTS---TQNNIVVDFD 587  
 QY 381 V-----NYGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGM-DETNTIN-- 430  
 Db 588 LAIATDQTVGVVDASSLTNAQTTLINGKIGTVGANNTKLTGQFNIGSSKTVLSDGVDVAINEL 647

Qy 431 -AGNN--IEITRNGKNIDIASTMTQ-----FSSV-----SLGAGADAPTSLVDDKALNV 478  
Db 648 VIGNGAVQFAHVTYLIIRTTNAAGQKIIIPNVVNNNTTILATGTLNLS-ATNPLAEINE 706  
Qy 479 GSKDANKPVRTITNVPAGVKEGVDNVAQLKGAQNALNNRIDNVDG-NARAGIAQAIAATAG 537  
Db 707 GSKGANVDTVLNKGKGNVL-YANITTTDA---NVGSFIFNAGTNIVSG-----TVG 756  
Qy 538 LVQ-----AYLPKSKMAIGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRG 587  
Db 757 GQGNKNTVALDNGTTVKELGNATFNNGTITIAAN-STLQIGGNVTADEVASADGTG 812

RESULT 8  
YDBA\_ECOLI  
ID YDBA\_ECOLI STANDARD; PRT: 2003 AA.  
AC P33666; P76087; P76856; P76857; P76859;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein ydba.  
GN YDBA OR B1401/B1405.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blatner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.P.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Alba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sempel G., Seki Y., Siwasundaram S., Tagami H., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
RA "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 464-2003 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=92190338; PubMed=1665988;  
RA Moszer I., Glaser P., Danchin A.;  
RT "Multiple IS insertion sequences near the replication terminus in  
RT Escherichia coli K-12.";  
RL Biochimie 73:1361-1374(1991).  
CC -!- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYSG (AC P25928).  
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: THE GENE CODING FOR  
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT  
CC BETWEEN AMINO ACIDS 839 AND 840.  
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CC -----  
DR EMBL; AE000237; AAC74483.1; ALT\_SEQ.  
DR EMBL; AE000237; AAC74487.1; ALT\_SEQ.  
DR EMBL; D90778; BAA15009.1; ALT\_SEQ.

DR EMBL; D90778; BAA18880.1; ALT\_SEQ.  
DR EMBL; D90779; BAA18881.1; ALT\_SEQ.  
DR EMBL; X62680; -, NOT\_ANNOTATED\_CDS.  
DR EcoGene; EG11307; ydba.  
KW Hypothetical protein; Complete proteome.  
FT CONFLICT 489 489 I -> V (IN REF. 2).  
FT CONFLICT 495 495 I -> V (IN REF. 2).  
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;  
  
Query Match 6.5%; Score 197.5; DB 1; Length 2003;  
Best Local Similarity 24.2%; Pred. No. 0.017;  
Matches 167; Conservative 89; Mismatches 249; Indels 185; Gaps 42;  
  
Qy 33 TVKTAVLATLLFA-TVQANATDEDEEELEPVRVSALVLPQFMIDKEGNG-ENESTGNIGW 90  
Db 151 TEKTLTIRDSVFTYTENADGTFISLQDSN---GRKATINLWQIDEANNVALEGSADGA 206  
Qy 91 SIYYDNINHTLHGATVTLKAGDNLIKONTNKNNTNNTNDSFTYSLKDLTDLTSVETEK 150  
Db 207 TKWOYNHN--GELVI--TGDNATV--NNNGKTTVDGKDSGTCT--EINGNNGKVIQDGD 256  
Qy 151 LSPGANGKNVNTSDT-----KG-----LNFAKETAGTNGDITVH 185  
Db 257 LDVSGGGHGDITGDSATVDNKGKMTVTVDPESMGIDGDKAIVNNEGESITITNGGTGTQ 316  
Qy 186 LNG-----IGSTLTDTLLNTGATTN-----VTNDNVNDDKK 216  
Db 317 INGDDATANNKKTVDGKDSGTGTEINGNNGKVIQDGLDVSGGHGDITGDSATVD-N 375  
Qy 217 KRAASVDKVLNAGNINIKVPGTGVDFVHYDVFVFLSADTKTTTVNVSCKDNKG- 275  
Db 376 KGTMTVTPDESIGIQVDG-DQAVVNNEGESAITNGGTGTQINGDDATANNKKTVDGKD 434  
Qy 276 --RTEVKIGAKTSVKEKDKL-VTGKCKG---ENGSTDEGEGLVTAKE-----VIDA 323  
Db 435 STGTEI-AGNNGKVI--QDGLDVSGGHGDITGDSATVDNKGKMTVTVDPESIGIQIDG 491  
Qy 324 ---VNKAGRMKTTTANGQTGQADKPFVTSGTNVTFASGKGTATVSKDD-----QGN 374  
Db 492 DQAVNNEG---ESTITNGGTG-----TOINGNDAT-ANNSGKTTVDGKDSGTGKIAGN 541  
Qy 375 ITVYDVNVGDALNV-----NQLQSGNWN--LDSC-----AVAGSSGKVISGNVSPSKGM 423  
Db 542 IGI---VNLDSLAVTGGAHGVENIGDNGTVNNKGDIVVSDTSGTGLVINGEGATVSN TG 598  
Qy 424 DETVINAGNNIETRNCKNIDIAISM-TPOFSS-VSLGAGADAPTSLVDD-----KG 474  
Db 599 DVNVS-NEATGFSITTSNGKVSAGSMQVGFSTGVDLNGNNSVTLAOKLKVVGQKAT 657  
Qy 475 ALNVGSKDANKPVRIT-----NVA-----PGV-----KEGDVTNVAQLKGA 511  
Db 658 GINV-SGDAN-TVNITGNVLVDKDTADNAAEFYDPSGVGINVYSDNNVTLDGKLTVVS 715  
Qy 512 QN-LNNRIDNV-DGNARAGIAQAIAATAGLV-----QAYLPCKSKMAIGGTTY 556  
Db 716 DSEVTSRQSNLFDGSAE-----KTSGLVIVIGDNTVNMNGGLELIGEKNALADGSQVT 768  
Qy 557 RGEAGYAI-----GYSSISDGGNWIIGK 579  
Db 769 SLRTGYSTYSVIVVSGESSVYLVNGDITISG 798  
  
RESULT 9  
SLAP\_CAMEE  
ID SLAP\_CAMEE STANDARD; PRT: 933 AA.  
AC P35827;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 01-OCT-1994 (Rel. 30, Last annotation update)  
DE S-layer protein (Surface array protein) (SAP).  
GN SAPA.  
OS Campylobacter fetus.

OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;  
OC Campylobacter.  
OX NCBI\_TaxID=196;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.  
RC STRAIN=84-32 / 23D;  
RX MEDLINE=90354448; PubMed=2387868;  
RA Blaser M.J., Gotschlich E.C.;  
RT "Surface array protein of Campylobacter fetus. Cloning and gene  
RT structure";  
RL J. Biol. Chem. 265:14529-14535(1990).  
RN [2]  
RN ERRATUM.  
RP MEDLINE=91035477; PubMed=2229082;  
RX Blaser M.J., Gotschlich E.C.;  
RA Blaser M.J., Gotschlich E.C.;  
RL J. Biol. Chem. 265:19372-19372(1990).  
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS  
CC CRITICAL FOR VIRULENCE.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -----  
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CC -----  
DR EMBL; J05577; AAA23032.1; -  
KW Cell wall; S-layer.  
KW SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;  
SQ

Query Match 6.4%; Score 196.5; DB 1; Length 933;  
Best Local Similarity 22.7%; Pred. No. 0.0078;  
Matches 141; Conservative 74; Mismatches 249; Indels 157; Gaps 29;

QY 78 GCNENEST-----GNICWSIYYDHNHILHGATVTLKAGDNLKIKON---TNKNTN-ENTND 129  
DB 222 GNCNTKSTLAFEDKTRWSVL--GRDTLNAIFTAITRAALLDQAEILIKRRTNVENIN- 278  
QY 130 SSTYSLKKDLT---DLTSVETELKSGANGKNVITSD--TKGLNFAKETAGT----- 178  
DB 279 -----IISDLETSGDFVNGYKGVNGLDIVSFATDASKSVNV--ETTGTITTAFTAA 330  
QY 179 -----NGDVTVHLNIGISTLTDLTLLNTGATTNVNDVNTDDKKRAAS 221  
DB 331 GTCKVDVWAGKISALRADSRTSVNLATNDTITLSANAATSVNLKORQAKD-----AT 384  
QY 222 VKDVLNAGNVIKVKPGT---TASDNDVPH-----TYDTEVEFLSA-D 260  
DB 385 ITSAMOQKYNNRNRNRIATITSATAVENLTVKHATVNALNGMDKLATVTLDNAALTAAD 444  
QY 261 TKT-TTVN-VEKSDNG-----KRTEVKIGAKTSVKEK-----DGKL 295  
DB 445 IKSASTLNILNSVNGPKHLYSKRRYCKFKRAAAKVKLNTAATDQTVTLKANATDNL 504  
QY 296 VTGKRGKNGSSYDEGE---LVTAKEVIDAVNKGAKWRMKTITAN-----GQTGOADK 345  
DB 505 EPDSATAKTTSTVATSGSGKTLVKGAEVETLVN-----IDTTAFNALQSVSFGKGGGK 559  
QY 346 FEVTSGTNVTFASGKGTATVSK--DDOIGNITVKVDVNVGDALNVQNLQNSGNWLDLSKA 403  
DB 560 F-SVKTGTGDDKLEFVGTTLTEGVSVIDAPGNDTIAMKSAALTSANFTMIKNIENVAISDA 618  
QY 404 VAG---SSGKVISGNVSPSKGMDFTVNNAGNNIETRNKKNIDATSMTPFSSVSLG 460  
DB 619 VATADLSSSAFKNSVIITTKAAADTTLTINKQVI-----NFTAADAGSVKLITVKNL 671  
QY 461 AGADAPTLSVDDKALNVGSKDANKPVRITNVAPGVKEGD-----VTNVAQL--- 507

DB 672 ---DVTALMIVVKIVLVDAAAKD-----TNIALGTAADKALVIDTGTIETLNTISLVKA 721  
QY 508 ---KGVAQNLNNRIDNVDGNARAGIAQATATAGLVQAYLPKSKMMAIGGTYGEAGYAI 564  
DB 722 TSPETTANTVNAKLTDVTSIIIDGMQITLGHACTAGTDYSKVSMDASA-----LKAGLTF 777  
QY 565 GYSSISDGGNWIIGKTASGNS 585  
DB 778 DASAITLGNATIKGGSGADS 798  
RESULT 10  
HLVA\_SERMA  
ID HLVA\_SERMA STANDARD; PRT; 1608 AA.  
AC P15320;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Hemolysin precursor.  
GN SHLA.  
OS Serratia marcescens.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Serratia.  
OX NCBI\_TaxID=615;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
RC STRAIN=SN8;  
RX MEDLINE=88257037; PubMed=3290200;  
RA Poole K., Schiebel E., Braun V.;  
RT "Molecular Characterization of the hemolysin determinant of Serratia  
RT marcescens";  
RL J. Bacteriol. 170:3177-3188(1988).  
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD  
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY  
CC DEFINED.  
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA  
CC REQUIRES SHLB FUNCTION.  
CC -!- SUBCELLULAR LOCATION: Outer membrane.  
CC -!- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).  
CC -----  
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CC -----  
DR EMBL; M22618; AAA50323.1; -  
DR PIR; A28182; A28182.  
KW Hemolysis; Toxin; Outer membrane; Signal.  
FT SIGNAL 1 30  
FT CHAIN 31 1608 HEMOLYSIN.  
SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;  
Query Match 6.2%; Score 189.5; DB 1; Length 1608;  
Best Local Similarity 22.3%; Pred. No. 0.033;  
Matches 138; Conservative 68; Mismatches 217; Indels 195; Gaps 29;

QY 78 GCNENESTGN---IGWSIYYDHNHNL-----HGATVT-----LKAG-----DN 112  
DB 544 GGDGNKNNRRREISHASELTSGGTURLNQOQVITIGSKARGQKGEVATHGGLRID 603  
QY 113 L-----KIQNTKNTN-----ENTNDSFTYSLKKDLTDLTSVEVEKL-----SFG 154  
DB 604 ALSTTVDKIDARTGTAFTNITSSSHKADNSYQSSTASLAKSD--TNLTIVSHKADVIGSQV 662  
QY 155 ANGNKVNITSDTKGLNFAKETAGTNGD---TTVHLNIGISTLTDLTLLNTGATTNVNDNV 211  
DB 663 ASGGELSVESKTCGNINVKAAERQONIDEQKALTALTVNGYAKEAGDKQYRAGLRTEHTRDSE 722

```
QY 212 TDDKKRAAS-----VKDLNAGWNKGVKPGTTASDNDVFTVDTVEFLSAD 260
   : : : : :
Db 723 KTTTENSASSLSGGSVKLAKEKDVTFSGSKLVADKGDASVSGN-----KVSFLAAD 774
   : : : : :
QY 261 TKTTTVNVESKDNKRTVEKTKAKTSVKEKDGKLVTKGKGKENGSSDDEGEGLVTAKEV 320
   : : : : :
Db 775 DKTAS-NTE-----QTKIGG-----GFYITG----- 794

QY 321 IDAVNKAGWRMKTTTANGOTQADKEETVTSNTVTFASGKGTATVSKDDQGNITVKYD 380
   : : : : :
Db 795 --GIDKLGSGVEAGYENKKT--QAQSSKAITSGSDV-----KGNLT----- 831

QY 381 VNVGDALNVNQLNSGWNLDKAVAGSGKGVISGNVSPSKGMDETVINAGNNIEITRN 440
   : : : : :
Db 832 INARDKLTQOQAQHSVGGAYOENAGVDHLAAADTASTTTTKTDGVNI----- 880

QY 441 GKNIDTATSMTPQPSFSSVLAGADAPLTVSDDKG-----ALNVGSKDANKPVRIRN-- 491
   : : : : :
Db 881 GANVDYSAVTRPVERAVGKAAKLDA-TGVINDIGGIGAPNVGLDIGAQQSGSEKRSSSQ 939

QY 492 -VAPGVKGDV-----TNVAOLKGVAQNLN-----NRIDNVGDNARAG 528
   : : : : :
Db 940 AVWSVQAGSIDNAKGEVRQGTQYQASKG-AVNLTADSHRSEAAANRQDEQSRDTR-- 996

QY 529 IAQATATAGLVQAYLPKGSMAIG-----GGTYRGEAGYAGISYSISDGNW----- 575
   : : : : :
Db 997 -----GSAG-VRVYTTGSDLTVDKAGGGTQRSNSASQAVTSIDAANGINNVKKDA 1050

QY 576 IIKGTASNSRGHPGASA 593
   : : : : :
Db 1051 IYQGTALNGRGRKTAUNA 1068

RESULT 11
HLXA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMa.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
RT hemolysin genes (hpmA and hpmB) reveals sequence similarity with the
RT Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
CC CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
CC DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMa
CC REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMa
CC MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC -----
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CC -----
DR EMBL; M30186; AAA25657.1; -.
DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.1%; Score 187.5; DB 1; Length 1577;
Best Local Similarity 20.2%; Pred. No. 0.04; 225; Indels 161; Gaps 27;
Matches 119; Conservative 84; Mismatches 25;

QY 73 MIDKEGGENESTGNI-----GWSIVYDNH--NTLHGATVT----- 106
   : : : : :
Db 435 LVEKESSENGKNKHHSTRLESWS---NSHQETETLKASELTAGKDLGLDAQGSITAAQ 491

QY 107 --LKAGDNLKI--KONTNKNNTNENTSSFT-----YSLKKDITDITSV 146
   : : : : :
Db 492 AKLHANENVLVNAKDNLNLNVOKTNDKTVTDNHHVMGIGGGQKNKNNNQOVSHATQL 551

QY 147 ETEKLSFGANGKNYNIIT-SDTKGLNFAKETAGTNGDTTVHLNGIGSLTDTLLNTGATTN 205
   : : : : :
Db 552 TADGQLLEAADNNVNIITGSQYKG--NQGAFTYKTQGDVVVID--NALSETISKIDERTGTAFN 609

QY 206 VTNDNVTDKKKRAASVKDVLN-----AGWNKGVKPGTTASDNDVFTVDTVEFLS 258
   : : : : :
Db 610 ITKSSHNETNKTSTGSELISDAQLTVVSGNDVNVIGSLIKSADKLG-IHSLGDIINVKS 668

QY 259 ADTKTTTVNVESKDNKRTVEYKIGAKTSVKEKDGKLVTKGKGKENGSSDDEGEGLVTAK 318
   : : : : :
Db 669 AQ-----QVTKIDDEKTSLAITGH-----AK 689

QY 319 EVIDAVNKAGWRMKTTTANGOTQADKEETVTSCTNVTFASSGKGTATVS--KDDQGNIT 376
   : : : : :
Db 690 EVEDKQYSAGFHITHTTNKNTSTETEANGSTISGANVDLQANKDVTFAAGDLKTTAGNAS 749

QY 377 VKYDVNVGDALNVNQLNSGWNLDKAVAGSGKGVISGNVSPSKGMDETVINAGNNIE 436
   : : : : :
Db 750 ITGD-NVAFVSTENKQTD--NTDTTISGGFS---YTGVDKVGSKADFOYD-KOHTQTE 802

QY 437 ITRN-GKNIDIATSMTPQFSVSLGAGA-----DAPTLVDDK-----GALN 477
   : : : : :
Db 803 VTKNRGSQTEVAGDLTITANKDLLHEGASHVEGRYOESGENIQHVLAVNDSETSKTDSL 862

QY 478 VG-----SKDANKPVR-----ITNVPVKVEGDVTVNAQLKGVAQLNNRIDNVDG 523
   : : : : :
Db 863 VGIDGVNLDYSGVTKPVKKAIEDGVNTTKPG-NTDILTCKVTARDATAIANLAN-LSNLE- 919

QY 524 NARAGIAQAATATAGLVQAYLPKGSMAIGGTYRGEAGYAGISYSISDG 572
   : : : : :
Db 920 TPNVGVVEVGIK-----GGGSGQSQSDSQAVSTISINAG 951

RESULT 12
ICEN_XANCT STANDARD; PRT; 1567 AA.
ID ICEN_XANCT
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-X56S;
RX MEDLINE=91080859; PubMed=2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
```

RT Xanthomonas campestris pv. translucens.";  
 RL Mol. Gen. Genet. 223:163-166(1990).  
 CC -!- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE  
 CC CRYSTALLIZATION IN SUPERCOOLED WATER.  
 CC -!- SUBCELLULAR LOCATION: Outer membrane (By similarity).  
 CC -!- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS  
 CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A  
 CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.  
 CC -!- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE  
 CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.  
 CC -!- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN  
 CC FAMILY.  
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 CC  
 CC EMBL: X52970; CAA37140.1; -  
 DR PIR: S11672; S11672.  
 DR HSSP: P06620; I1NA.  
 DR InterPro: IPR000258; Ice\_nucleatn.  
 DR Pfam: PF00818; Ice\_nucleation; 81.  
 DR PRINTS: PR00327; ICNUCLEATN.  
 DR PROSITE: PS00314; ICE\_NUCLEATION; 57.  
 KW Ice nucleation; Repeat; Outer membrane.  
 SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;  
 Query Match 6.1%; Score 185.5; DB 1; Length 1567;  
 Best Local Similarity 19.8%; Pred. No. 0.05;  
 Matches 124; Conservative 94; Mismatches 279; Indels 129; Gaps 23;  
 QY 20 SELTRNHRKASATVKTAVLATLFLATVQANATDEDEEELEPVRSALVLOF---MIDK 76  
 Db 712 SDVTAGYGTGTAGADSTLIAG-YGSTQTSQSD-----SSLTAGYGSTQTAR 757  
 QY 77 EGNGENESTGNTGWSYIYDNHNTLHGATVTLKAGDMKIKQNTNKNNTNNDSSSYSL 136  
 Db 758 KGSVDVAGYGTGCTA-----GADSTLIAGY-----STQTSQSDSSLTAGY 798  
 -QY 137 KRDLT-----DLTSVTEKLSEFA-----NGKNVNIITSDTKLNFKE---- 174  
 Db 799 GSTQTARKGSDITAGYGTGTAGADSTLIAGYGSTQTSQSDSSLTAGYGSTQTAREGSDV 858  
 QY 175 -----TAGTNGDPTVHLNGIGSTLT---DTLLNTGATNTVNDVTDKRAASVKDYL 226  
 Db 859 TAGYGTGTAGADSTLIAGYGTGTAGSDSSLTAGYGTQTARKGSD-----V 906  
 QY 227 NAGWNTKGVPKPTASNDVDFVHYDTVFLSADTKTTVNVESKDKGRKTEVIGAKTS 286  
 Db 907 TAGYGTGT-----TAGADSTLIAGYGSTQTSQSDSSLTAGYGTQTARKGSDMTAGYGT 961  
 QY 287 VIKEDKGLVTKGKGENSGSTDEGELVTAKEVIDAVNKAGHRMKTITANGOTGQADKF 346  
 Db 962 GTAGADSTLIAGYGTQTSQSGS-----DSSLTAGYGTQTAREGSDVDTAGY 1007  
 QY 347 ETVTSGTNTVTFAGKGTGTATVSKDDOGNITVYDVNVGDAINVLQNSGNWLNDSKAVAG 406  
 Db 1008 STGTAGADSTLIAGYGTQTAGSD--SSLTAGY-----GSTQTARQSDVDTAGYGTGTAG 1061  
 QY 407 SSGKVISGNVSPSKGMDVETVNIAGNNTIEITRNGKNIDIAATMTQFQSVSLGAGADAP 466  
 Db 1062 ADSTLIAGYGTQTAGSDSSLTAGYGT--QTARQSGDI-----TAGYGTGT--AGADSS 1113  
 QY 467 TLSVDDKGLNVLGSKDANKPVRITNVAPGVKEGDVTNVLAQLKGVANLNINRINDVGNAR 526  
 Db 1114 LIA--GYGSTQTAGYDSNLITAGYGTQTAGSDSSLTAGYGTSTAGHSDSSLTAGYGTQT 1171  
 QY 527 AGIAQAIATA-GLVQAYLPKSKMMAIGGGCTYRGEAGY----AIGYSSISDGG--NWIIG 579

Db 1172 AGVNSILTTGYGSTQTARQESSSLTAGYGT--STAGYDSTLTAGYGSTQTAKYKSTLTAG 1229  
 QY 580 TASGNSRGR-----FGASASVGYQ 598  
 Db 1230 YGSNSTAGHSSLIAGYGSTQIAGYE 1255  
 RESULT 13  
 OMPB\_RICRI  
 ID OMPB\_RICRI STANDARD; PRT; 1654 AA.  
 AC Q53047;  
 DT 30-MAY-2000 (Rel. 39, Created)  
 DT 30-MAY-2000 (Rel. 39, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Scs5) (römpB)  
 DE (römp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
 DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB.  
 OS Rickettsia rickettsii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsieae; Rickettsia.  
 OX NCBI\_TaxID=783;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=92167802; PubMed=1724278;  
 RA Gilmore R.D. Jr., Cleplak W. Jr., Policastro P.F., Hackstadt T.;  
 RT "The 120 kilodalton outer membrane protein (römp B) of Rickettsia  
 RT rickettsii is encoded by an unusually long open reading frame:  
 RT evidence for protein processing from a large precursor.";  
 RL Mol. Microbiol. 5:2361-2370(1991).  
 RN [2]  
 RP SEQUENCE OF 279-1654 FROM N.A.  
 RC STRAIN=R;  
 RX MEDLINE=90136087; PubMed=2515418;  
 RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
 RT "Cloning, expression and sequence analysis of the gene encoding the  
 RT 120 kD surface-exposed protein of Rickettsia rickettsii.";  
 RL Mol. Microbiol. 3:1579-1586(1989).  
 CC -!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION  
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY.  
 CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
 CC  
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 CC  
 CC EMBL: X16353; CAA34403.1; -  
 DR InterPro: IPR003858; römpA\_römpB.  
 DR Pfam: PF02708; römpA\_römpB; 1.  
 KW Antigen; S-layer; Cell wall.  
 FT CHAIN 1 1333 120 KDa SURFACE-EXPOSED PROTEIN.  
 FT CHAIN 1334 1654 32 KDa BETA PEPTIDE.  
 FT DOMAIN 1181 1188 POLY-THR.  
 SQ SEQUENCE 1654 AA; 168184 MW; D/AB70FB7087F618 CRC64;  
 Query Match 6.1%; Score 185.5; DB 1; Length 1654;  
 Best Local Similarity 22.9%; Pred. No. 0.053;  
 Matches 178; Conservative 83; Mismatches 264; Indels 251; Gaps 44;  
 QY 7 IWNLSALNWAYVSELTR-----NHTKRASATVKTAVLATLFLATVQANAT 52  
 Db 92 LLLNTANNLAVTVSEDTTLGFTITNVVHAHSPNLTNAG---KTLITGGVTVNAQAAT 148



QY 53 DEDEEELEPVRSALVLOF-----MIDKEGGENESTGNGIGWS-----IYDHNHTLHG 102  
Db 149 KNAQN-----VVQFNNGRAID--NNDLKGVRIDFGAPASTLVFNLANPTQK 195  
QY 103 ATVTLLKAGDNLKIKONTKN---TNEWNDSSTFYSLKKDL-----TDLTSVET 148  
Db 196 APLIL--GDNNAVIVNGTILNVTNGFIQVSNKSFATVKAINIADGQGIIFNTDANNANT 253  
QY 149 EKLSEFGANGKVNIT-SDTKG--LNEFAKETAGTNGDITVHLNG-----IGSTL 193  
Db 254 --LNLQAGGTITNGTGTGRULLSKHAAATNFNITGSLGGKLGKGVIEFNTVAVDQGL 311  
QY 194 TDTLLNTGATTNVTNDN-----VTDKKKRA-----ASVKDLNAGWNIKGV--- 235  
Db 312 T--ANAGANAVIGTNNAGRAAGFVVSVDNGKVAIDGOVYAKDMVIOANATGQVNF 368  
QY 236 -----KPGTTA-----SONVDF----- 247  
Db 369 RHIVDVGADGTTAFKTAASKVTITQDSNFGNTDFGNLAAQIKVPNAITLTGNTGDASNP 428  
QY 248 -----VHTYD--TVEFLSADTKTTVN---VESKONG-----KRTVEKIGAKTSVI 288  
Db 429 GNTAGVITFDANGTLESASADANNAVNTNITAIEASGAGVVQJSGTHAAELRLGNAGSIF 488  
QY 289 KEKDGKLVTKG-----GKGENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQT 340  
Db 489 KLADGTIVCKVNOTALVGGALAAAGTITLDSATITGD--IGNAGGAALQRTILAN--- 543  
QY 341 GOADKFEVTV--SGTNVTFASG-----KGTATVSKDDOGNITVKYDV-----NVGD 385  
Db 544 ---DAKRTLGLGIANIIGAGGGTTDLQANGOTIKLT--STQNNIVVDFDLAIAITDOTGWD 599  
QY 386 ALNVNOLQNSGN-----LDSKAVA-----GSSGKVIS--CNVSPSKGMDVETVNIAG- 432  
Db 600 ASSLTNAQTTLINGIKTIGANNKTLGOFNIGSKTIVLSNGVA-----INELVIGNDGA 654  
QY 433 -----NRIETR-----NGKNI--DIATSMTPQFSSVSLGAGADAPTLSYDDKRGALNVG 479  
Db 655 VQFAHDYTLITRTTNAAGQCKIIFNPVNVNGTTLAAGTNLGS-----ATNPLAEINFG 707  
QY 480 SKDANKPVRTNAPVKEGVDVTVNAOLKQVNAQNLNRIDNVGD--NARAGIAQAIATAGL 538  
Db 708 SKGVNVDVTVLNVGEGVNL-YATNITTDTA---NVGSFVFNAGGTIVVSG-----TVGG 756  
QY 539 VQ-----AYLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTAGNSRG 587  
Db 757 QQGNKFTVALENGTTVKFLGNATFNNGTITIAAN-STLQIGGNTYADCVASADGTG 811

RESULT 14  
YMBJ\_CAEEL STANDARD; PRT; 918 AA.  
AC P34487;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 01-FEB-1995 (Rel. 31, Last sequence update)  
DE 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Hypothetical 96.6 kDa protein F59B2.12 in chromosome III.  
GN F59B2.12.  
OC Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidae;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BRISTOL N2;  
RX MEDLINE=94150718; PubMed=7906398;  
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,  
RA Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,  
RA Craxton M., Dear S., Du Z., Durbin R., Favell A., Fraser A.,  
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,  
RA Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,  
RA Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,

RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,  
RA Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden R.,  
RA Sulston J., Thierry-Mieg J., Thomas K., Vaubin M., Vaughan K.,  
RA Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,  
RA Wohlman P.;  
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.  
RT elegans.";  
RL Nature 368:32-38(1994).  
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CC -----  
CC EMBL: Z11505; CAA77581.1; -  
DR PIR: S31132;  
DR WormPep: F59B2.12; CE01024.  
KW Hypothetical protein.  
SQ SEQUENCE 918 AA; 96560 MW; E464FD86B14945DE CRC64;

Query Match 5.9%; Score 180.5; DB 1; Length 918;  
Best Local Similarity 22.6%; Pred. No. 0.047;  
Matches 122; Conservative 85; Mismatches 227; Indels 107; Gaps 25;

QY 108 KAGDNLKIKO-----NTNKNNTNNTNDSSTFYSLKKDLTDLTSVETKLSFGANGKVN 161  
Db 118 EANTKIKSADGVSIVETGKSHKSSDDAS--SYGLER--SSKTYADKNGTMLSNTNKN 174  
QY 162 ITSDTKCLNFAKETAG--TNGDITVHLNGIGSTLTD-----TLNLTGATTNVTNDVNDK 215  
Db 175 NQSRSAALDEGENEFVNOONADGTFRLNNTGKHNDEHLNHLNLDENAOISIGADGTSN 234  
QY 216 KRAASVQDVLNAGWNIKGVKPGTASDNDYVHTYDTVEFLSADTKTTTVNVESKONG 275  
Db 235 TNRKSGVGDASHA-----ASD-----NPFSLDAQG---NKKSQNSYK 271  
QY 276 RTEVKIGAKTSV-----IKEKDGKLVTKGKGENGSSTDEGEGLVTAKEVIDA--V 327  
Db 272 KAASAGSNADPFENLESLEKNADGTSMSNTGNFNNTSYDK-----ATAEEVMSKKYN 327  
QY 328 GW-RMKTTTANGOTGOADKPEVTVTGNTVTFASGCKGTATATVSKDDQ-----GNIT 376  
Db 328 GTSMEASHAGSNKINSASGQSSDLSVMGPNKIGKSHSTSNKTDNVALDEANQASGIS 387  
QY 377 VKYDVNVYGDALNVNQLQNSGNLDSK--AVAGSSGKV--ISGNVSPSKGMDVETVNIAG 433  
Db 388 EQIGKNGORSINESSIE--SGRKAESRNTAATDLSVDANGTVSSSHSKSASGTSLDENH 446  
QY 434 N-----IEITRNGKNIDIATIS---WTPQFSSVSLGA---GADAPTLSYDDKGLNV 478  
Db 447 NKTHALQASVDEHGNMKNHSDIGSYRNKKTGEGENSEMSASIKNADGTSQVNVKNTNR 506  
QY 479 GSDANKPVRTITNAPVKEGVDVTVNAQLKQVNAQNLNRIDNVGDGNARAGIAQAIATAGL 538  
Db 507 NTEAEKSALEKN---HEKNSDGT-----FDESKGNSRVNRTDGGSNLAVG----- 551  
QY 539 VOAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGG-----NWIKGTASGNSRHFAGAS 594  
Db 552 --SYSVGK-----GGVSSNETIASSNAFTSDAESNQFDHLHQKTANGTITHAQSKQ 603  
QY 595 V 595  
Db 604 V 604

RESULT 15  
YPJA\_ECOLI  
ID YPJA\_ECOLI  
AC P52143; P76610; P77017; P77019; PRT; 1569 AA.



QY	287	V I K E D G K L - V T G K G K G S N S D B S E G L V A K E - - - - - V I D A V N - - - - -	325
D b	525	V L E N T G E L T V V A K S A K N - : : T I D T G K L I V O K E A K T D S T R L N N G G V L E V Q D G E A K H V E	583
QY	326	- R A G W R M K T T T A N G O T G Q A D K F E T V T S G T N V - - - T P A S C K G T T A T V S K D D O G N I T V - - - -	377
D b	584	Q O S G G A I A S T T S G - - - - - : :       : :       : :       : :       : :       : :       : :	634
QY	378	- - - - - R Y D V - - - N V G D A L N V N Q L N - - S G M N L D S K A V A G S S - - - - G K V I S G N V S	417
D b	635	R A V D T I I N A N G M D V Y K D V G T V L N S A G T Q T I V A S A T S D K A N I K G K Q T V Y G L A T E A N I E	694
QY	418	P S K - - - - G K M D E T V N T N A G N N I E T R N G K - N I D I A T S M - - - - - T P O F S S V S U C A - - - -	461
D b	695	S G E Q I V D G S S T E K T I N G T Q - T V Q Y N G R A I N T D I V S G L Q Q I M A N G T A B E S T I N G S Q V V	753
QY	462	--GADAPTLSVDDBKALNKGVSKDANKPVRTTNVAPGVKEGDVTNV AOLKGVAQNLRND	519
D b	754	N E G G L A E N S V L N D G G T L D V R E K - - - - - G S A T G I Q O S S G Q A L V A T T R A T	796
QY	520	N V D G N A R A G I A Q A I A T A G L V Q A Y L P G K S M X A I G G G T Y R G E A G Y A I G Y S S I D G G N M I I - -	577
D b	797	R V T G T R A D G V A P S I E Q G A - - - - - A N N I L L A N G G V L T V E S D T S D K T Q V N M G G R E I V K T	849
QY	578	K G T A S G N S	585
D b	850	K A T A T G T T	857

Search completed: July 3, 2002, 08:30:20  
Job time: 1191 sec

Query Match	5.9%;	Score 180;	DB 1;	Length 1569;
Best Local Similarity	21.4%;	Pred. NO. 0.093;		
Matches 130; Conservative	83;	Mismatches 245;	Indels 150;	Gaps 30;

  

QY	81	ENESTGIGWSIYYDNHNTLHGATVT-LKAGDNLKTONTNKNTEMENTNDSSFTYSLUKD	139
	:	: : :	:
	:	: : :	:
	:	: : :	:
	:	: : :	:
Db	297	DNTSTDV-IEVYSGGVLDYRGGTAINVTQHDCAILKTNCTNGTIVSCTN-SEGAFSIHH	354
	:	: : :	:
	:	: : :	:
	:	: : :	:
	:	: : :	:
QY	140	LTDLTSVETKELSFGANGKNVNIT---SDTKGLNFAKET-----AGTNGDDTVHLNG----	188
	:	: : :	:
	:	: : :	:
	:	: : :	:
Db	355	VADNVILLE-----NGGHLDINAYCSANKTIIDKRGTMVSLTNAKADATRINDGGVMD	406
	:	: : :	:
	:	: : :	:
	:	: : :	:
	:	: : :	:
QY	189	IGSTLTDTLLNTGATTNVNTNDNV-----TDDKKRAASVKVDYLACGNWIKGVKPGT	239
	:	: : :	:
	:	: : :	:
	:	: : :	:
Db	407	VAGNATNTIIN-GGTQNINNYGATGTNINSCTONIKSGGKADTTIISSGRQWEKDG	465
	:	: : :	:
	:	: : :	:
	:	: : :	:
	:	: : :	:
QY	240	TASDNVD-----FVVHT-----YDTVEFLSADTKTTTVNVESKONGKRREYKIGAKTS	286
	:	: : :	:
	:	: : :	:
	:	: : :	:
Db	466	AIGNSISAGSGLLYVGIAHGYNOETGSALVANTCAGT-DIEGYNKLSHFTITGGBANY	524
	:	: : :	:
	:	: : :	:
	:	: : :	:
	:	: : :	:



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:28:45 ; Search time 168.02 Seconds  
(without alignments)  
616.736 Million cell updates/sec

Title: US-09-771-382-6  
Perfect score: 3060  
Sequence: 1 MNRYRIINWALSNAWAVS.....TASNSRGHFCASASGVQW 599

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19:\*

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mhc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriap:\*
- 17: sp\_archaea:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3060	100.0	599	2	Q9JPR8	Q9jpr8 neisseria m
2	2832.5	92.6	598	2	Q9JPR9	Q9jpr9 neisseria m
3	2830.5	92.5	598	2	Q9JPT0	Q9jpt0 neisseria m
4	2824.5	92.3	598	2	Q9JPS0	Q9jps0 neisseria m
5	2821.5	92.2	598	2	Q9JQY5	Q9jqy5 neisseria m
6	2802.5	91.6	594	2	Q9JPH7	Q9jph7 neisseria m
7	2792	91.2	595	2	Q9JPH0	Q9jph0 neisseria m
8	2781.5	90.9	600	2	Q9JPS6	Q9jps6 neisseria m
9	2776.5	90.7	594	2	Q9JPI3	Q9jpi3 neisseria m
10	2772.5	90.6	594	2	Q9JPS2	Q9jps2 neisseria m
11	2768.5	90.5	590	2	Q9JPS3	Q9jps3 neisseria m
12	2762.5	90.3	594	2	Q9JQY4	Q9jqy4 neisseria m
13	2737.5	89.5	592	2	Q9JPS9	Q9jps9 neisseria m
14	2710	88.6	589	2	Q9JPI0	Q9jpi0 neisseria m
15	2709	88.5	599	2	Q9JPS8	Q9jps8 neisseria m
16	2699.5	88.2	592	2	Q9JQY2	Q9jqy2 neisseria m

17	2694	88.0	589	2	Q93QY1	Q93qy1 neisseria m
18	2685	87.7	591	16	Q9JRI8	Q9jri8 neisseria m
19	2681	87.6	591	2	Q9JPS7	Q9jps7 neisseria m
20	2676.5	87.5	598	2	Q9JPR7	Q9jpr7 neisseria m
21	2676	87.5	591	2	Q9JQY3	Q9jqy3 neisseria m
22	2663.5	87.0	526	2	Q9JPS4	Q9jps4 neisseria m
23	2663.5	87.0	592	2	Q9AOF0	Q9adf0 neisseria m
24	2660.5	86.9	600	2	Q9JPS5	Q9jps5 neisseria m
25	2651.5	86.7	530	2	Q9JPS1	Q9jps1 neisseria m
26	2587.5	84.6	592	16	Q9JQW4	Q9jqw4 neisseria m
27	1271	41.5	2353	2	P71401	P71401 haemophilus
28	1070.5	35.0	1098	2	Q48152	Q48152 haemophilus
29	455.5	14.9	1299	16	Q9F3X6	Q9f3x6 pasteurella
30	410.5	13.4	1190	16	Q9PC04	Q9pc04 xylella fas
31	407	13.3	1107	2	Q9F2D8	Q9f2d8 salmonella
32	406.5	13.3	2059	16	Q9PD50	Q9pd50 xylella fas
33	361.5	11.8	2712	16	Q9F3X5	Q9f3x5 pasteurella
34	264.5	8.6	1004	16	Q9PD63	Q9pd63 xylella fas
35	256	8.4	1291	16	Q92KQ7	Q92kq7 rhizobium m
36	252.5	8.3	1953	16	Q98HJ2	Q98hj2 rhizobium l
37	240	7.8	1039	2	Q9L6T7	Q9l6t7 escherichia
38	237	7.7	1039	2	Q9L6T8	Q9l6t8 escherichia
39	236	7.7	2276	2	Q93TY6	Q93ty6 staphylococ
40	234.5	7.7	873	2	Q9L960	Q9l960 moraxella c
41	234.5	7.7	1040	2	Q9AL50	Q9al50 shigella fl
42	233.5	7.6	3930	16	Q98E20	Q98e20 rhizobium l
43	233	7.6	989	2	Q9XD84	Q9xd84 escherichia
44	231	7.5	4919	2	Q9ZHL0	Q9zhl0 haemophilus
45	227	7.4	1265	2	Q9FDA0	Q9fda0 xanthomonas

ALIGNMENTS

RESULT 1

Q9JPR8	PRELIMINARY;	PRT;	599 AA.
ID	Q9JPR8		
AC	Q9JPR8;		
DC	01-OCT-2000 (TREMREL. 15, Created)		
DT	01-OCT-2000 (TREMREL. 15, Last sequence update)		
DT	01-DEC-2001 (TREMREL. 19, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).		
GN	GNA992 OR NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RC	SEQUENCE FROM N.A.		
RP	STRAIN=NGH38;		
RX	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.		
RT	"Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing."		
RL	Science 287:1816-1820(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=H38;		
RA	Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis."		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL; AF226383; AAF42532.1; -		
DR	EMBL; AF157608; AAK68869.1; -		
SQ	SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;		

Query Match 100.0%; Score 3060; DB 2; Length 599;

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Best Local Similarity 100.0%; Pred. No. 6.3e-121;
Matches 599; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVOANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVOANATDEDEEEL 60
QY 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 120
Db 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 120
QY 121 KNTNENTNDSFYSYLSKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
Db 121 KNTNENTNDSFYSYLSKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
QY 181 DTTVHLNGIGSTLTDLLNTGATNTVNDVTDKKRAASVKDVLNAGNVIKGVKPGTT 240
Db 181 DTTVHLNGIGSTLTDLLNTGATNTVNDVTDKKRAASVKDVLNAGNVIKGVKPGTT 240
QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVIKEKDKLVTGK 300
Db 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVIKEKDKLVTGK 300
QY 301 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFFETVTSNTVTFASG 360
Db 301 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFFETVTSNTVTFASG 360
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
QY 421 GKMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Db 421 GKMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
QY 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKVAQNLRNIDVNDGNARAGIAQAATATAGLVQ 540
Db 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKVAQNLRNIDVNDGNARAGIAQAATATAGLVQ 540
QY 541 AYLPGKSMAIAGGTYRGEAGYAGIYSSISDGGNWIITKTASGNSRHFASASVGYOW 599
Db 541 AYLPGKSMAIAGGTYRGEAGYAGIYSSISDGGNWIITKTASGNSRHFASASVGYOW 599

RESULT 2
Q9JPR9 PRELIMINARY; PRT; 598 AA.
ID Q9JPR9
AC Q9JPR9;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGH36;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlati V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226382; AAF42531.1; -.
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;
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Query Match 92.6%; Score 2832.5; DB 2; Length 598;
Best Local Similarity 93.0%; Pred. No. 2.1e-111;
Matches 557; Conservative 13; Mismatches 28; Indels 1; Gaps 1;

QY 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVOANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVOANATD-DDDLYL 59
QY 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 120
Db 61 EPVRSALVLOFMIDKEGNESTGNIGWSIYDHNHTLHGATVTLKAGDNLKIKQNTN 119
QY 121 KNTNENTNDSFYSYLSKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 180
Db 121 KNTNENTNDSFYSYLSKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAGTNG 179
QY 181 DTTVHLNGIGSTLTDLLNTGATNTVNDVTDKKRAASVKDVLNAGNVIKGVKPGTT 240
Db 181 DTTVHLNGIGSTLTDLLNTGATNTVNDVTDKKRAASVKDVLNAGNVIKGVKPGTT 239
QY 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVIKEKDKLVTGK 300
Db 241 ASDNVDFVHTYDVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVIKEKDKLVTGK 299
QY 301 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFFETVTSNTVTFASG 360
Db 301 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFFETVTSNTVTFASG 359
QY 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
Db 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 419
QY 421 GKMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 480
Db 421 GKMDETVNIAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDKALNVGS 479
QY 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKVAQNLRNIDVNDGNARAGIAQAATATAGLVQ 540
Db 481 KDANKPVRIITNAPGVKEGDTVNTVAQLKVAQNLRNIDVNDGNALAGIAQAATATAGLVQ 539
QY 541 AYLPGKSMAIAGGTYRGEAGYAGIYSSISDGGNWIITKTASGNSRHFASASVGYOW 599
Db 541 AYLPGKSMAIAGGTYRGEAGYAGIYSSISDGGNWIITKTASGNSRHFASASVGYOW 598

RESULT 3
Q9JPT0 PRELIMINARY; PRT; 598 AA.
ID Q9JPT0
AC Q9JPT0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizze M., Scarlati V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226359; AAF42508.1; -.
```



RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RL membrane protein of *Neisseria meningitidis*."  
Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157603; AA68864.1; -.  
SQ SEQUENCE 598 AA; 62687 MW; 18CEFFE6410A15DF CRC64;

Query Match 92.2%; Score 2821.5; DB 2; Length 598;  
Best Local Similarity 92.7%; Pred. No. 6e-111;  
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;  
QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
DB 1 MNKIYRIIWSALNAWVSELTRNHTKRASATVATVATLATLLFATVQANATD-DDDLYL 59  
QY 61 EPVVSALVLFQMTDKGNGENESTGNIGWSIYYDNTLHGATVTLKAGDNLKIKQNTN 120  
DB 60 EPVQRTAVLSFRSKDEKTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN 119  
QY 121 KNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180  
DB 120 ENTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179  
QY 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDKKRAASVKDVLNAGWNIKGVPKPTT 240  
DB 180 DPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKRAASVKDVLNAGWNIKGVPKPTT 239  
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKREVKIGAKTSVIKEKDGKLVTKGK 300  
DB 240 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKREVKIGAKTSVIKEKDGKLVTKGK 299  
QY 301 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTQADKFEFTVSGTNNVTASG 360  
DB 300 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTQADKFEFTVSGTNNVTASG 359  
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420  
DB 360 NGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 419  
QY 421 GKMDETVNNAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDKALNVGS 480  
DB 420 GKMDETVNNAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDKALNVGS 479  
QY 481 KDANKPVRITNVAPGVKEGDTNVNQLKGVQAOQNNRNDNVDGNARAGIAQAIATAGLVQ 540  
DB 480 KDANKPVRITNVAPGVKEGDTNVNQLKGVQAOQNNRNDNVDGNARAGIAQAIATAGLVQ 539  
QY 541 AYLPGKSMMAIGGTYRGEAGYAGYISISDGGNWIKTGTASGNSRHFHGASASVGYQW 599  
DB 540 AYLPGKSMMAIGGTYRGEAGYAGYISISDGTGNWIKGTASGNSRHFHGTSASVGYQW 598

RESULT 6

Q9JPH7 PRELIMINARY; PRT; 594 AA.  
AC Q9JPH7;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2198, AND 297-0;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing."  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2198;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226368; AAF42517.1; -.  
DR EMBL: AF226358; AAF42507.1; -.  
DR EMBL: AF157604; AAK68865.1; -.  
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 91.6%; Score 2802.5; DB 2; Length 594;  
Best Local Similarity 92.5%; Pred. No. 3.7e-110;  
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
DB 1 MNKIYRIIWSALNAWVSELTRNHTKRASATVATVATLATLLFATVQANATD-DDDLYL 59  
QY 61 EPVVSALVLFQMTDKGNGENESTGNIGWSIYYDNTLHGATVTLKAGDNLKIKQNTN 120  
DB 60 EPVQRTAVLSFRSKDEKTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKO--- 116  
QY 121 KNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180  
DB 117 -NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175  
QY 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDNVTDKKRAASVKDVLNAGWNIKGVPKPTT 240  
DB 176 DPTVHLNGIGSTLTDLLNTGATTNVTNDNVTDDEKRAASVKDVLNAGWNIKGVPKPTT 235  
QY 241 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKREVKIGAKTSVIKEKDGKLVTKGK 300  
DB 236 ASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKREVKIGAKTSVIKEKDGKLVTKGK 295  
QY 301 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTQADKFEFTVSGTNNVTASG 360  
DB 296 KGENSSTDEGEGLVTAKEVIDAVNKAGWRMKTNTTANGOTQADKFEFTVSGTNNVTASG 355  
QY 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420  
DB 356 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 415  
QY 421 GKMDETVNNAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDKALNVGS 480  
DB 416 GKMDETVNNAGNIEITRNKKNIDTATSMAPQFSSVSLGAGADAPTLSDVDKALNVGS 475  
QY 481 KDANKPVRITNVAPGVKEGDTNVNQLKGVQAOQNNRNDNVDGNARAGIAQAIATAGLVQ 540  
DB 476 KDTNKPVRITNVAPGVKEGDTNVNQLKGVQAOQNNRNDNVDGNARAGIAQAIATAGLVQ 535  
QY 541 AYLPGKSMMAIGGTYRGEAGYAGYISISDGGNWIKTGTASGNSRHFHGASASVGYQW 599  
DB 536 AYLPGKSMMAIGGTYRGEAGYAGYISISDGGNWIKTGTASGNSRHFHGASASVGYQW 594

RESULT 7

Q9JPHO PRELIMINARY; PRT; 595 AA.  
AC Q9JPHO;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.

OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=528, AND 1000;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.;  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226356; AAF42505.1; -;  
DR EMBL; AF226356; AAF42505.1; -;  
SQ SEQUENCE 595 AA; 62120 MW; 8212C96380142BFC CRC64;

Query Match 91.2%; Score 2792; DB 2; Length 595;  
Best Local Similarity 92.5%; Pred. No. 1e-109;  
Matches 556; Conservative 15; Mismatches 22; Indels 8; Gaps 3;

QY 1 MNKIYRIIWSALNANWVAVSELNRHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
DB 1 MNKIYRIIWSALNANWVAVSELNRHTKRASATVKTAVLATLLFATVQANATDEDEEL 60  
QY 61 EPVRSALVQFMIDKEGNESTGNIGWSIYDDNHTLHGATVTLKAGDNLKIKQNTN 120  
DB 61 EPVRSALVQFMIDKEGNESTGNIGWSIYDDNHTLHGATVTLKAGDNLKIKQ--- 117  
QY 121 KNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDFKGLNFAKETAGTNG 180  
DB 118 -NTDENTNASSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDFKGLNFAKKTAGTNG 176  
QY 181 DTTVHLNGIGSTLDTLLNTGATNTVNDVTDKRAASVKDVLNAGNWKGVPGTT 240  
DB 177 DTTVHLNGIGSTLDTLLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNWKGVKTGST 234  
QY 241 A--SDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVKEKDGKLVG 298  
DB 235 TGSSENVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVKEKDGKLVG 294  
QY 299 KKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTF 358  
DB 295 KKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTNVTF 354  
QY 359 SGKGTATVSKDQGNITVKYDYNVGDALNVQNSGNLDSKAVAGSSGKVISGNVSP 418  
DB 355 SGKGTATVSKDQGNITVKYDYNVGDALNVQNSGNLDSKAVAGSSGKVISGNVSP 414  
QY 419 SKGKMDETVNIAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDKGNLV 478  
DB 415 SKGKMDETVNIAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDKGNLV 474  
QY 479 GSKDANKPVRITNAPGVKEGVDVTVNAQLKGVQNLNRRIDNVDGNARAGIAQAIATAGL 538  
DB 475 GSKDANKPVRITNAPGVKEGVDVTVNAQLKGVQNLNRRIDNVDGNARAGIAQAIATAGL 534  
QY 539 VQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIINKGTASGNSRGHFGASASVGYQ 598  
DB 535 VQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIINKGTASGNSRGHFGASASVGYQ 594  
QY 599 W 599  
DB 595 W 595

RESULT 8  
Q9JPS6

ID Q9JPS6 PRELIMINARY; PRT; 600 AA.  
AC Q9JPS6;  
DT 01-OCT-2000 (TReMBLrel. 15, Created)  
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TReMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.;  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226371; AAF42520.1; -;  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 90.9%; Score 2781.5; DB 2; Length 600;  
Best Local Similarity 91.6%; Pred. No. 2.8e-109;  
Matches 554; Conservative 12; Mismatches 28; Indels 11; Gaps 3;

QY 1 MNKIYRIIWSALNANWVAVSELNRHTKRASATVKTAVLATLLFATVQANA-----TDE 54  
DB 1 MNKIYRIIWSALNANWVAVSELNRHTKRASATVKTAVLATLLFATVQASADNVQASADN 60  
QY 55 DEEEELPPVRSALVQFMIDKEGNESTGNIGWSIYDDNHTLHGATVTLKAGDNLK 114  
DB 61 EEEYLEPPVRSALVQFMIDKEGNESTGNIGWSIYDDNHTLHGATVTLKAGDNLK 120  
QY 115 IKONTNKTNTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDFKGLNFAKE 174  
DB 121 IK-NTDENTNASSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDFKGLNFAKE 176  
QY 175 TAGTNGDTTVHLNGIGSTLDTLLNTGATNTVNDVTDKRAASVKDVLNAGNWK 234  
DB 177 TAGTNGDTTVHLNGIGSTLDTLLNTGATNTVNDVTDKRAASVKDVLNAGNWK 236  
QY 235 VKPGTTASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVKEKDGK 294  
DB 237 VKPGTTASDNVDFVHTYDTVEFLSADTKTTTVNVESKDNKRTVEKIGAKTSVKEKDGK 296  
QY 295 LVTKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTN 354  
DB 297 LVTKGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGQTQADKFETVTSGTN 356  
QY 355 VTASGKGTATVSKDQGNITVKYDYNVGDALNVQNSGNLDSKAVAGSSGKVISG 414  
DB 357 VTASGKGTATVSKDQGNITVKYDYNVGDALNVQNSGNLDSKAVAGSSGKVISG 416  
QY 415 NVSPSKGKMDETVNIAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVDKG 474  
DB 417 NVSPSKGKMDETVNIAGNIEITRNKKNIDTATSMTPQFSSVSLGAGADAPTLSDVG-D 475  
QY 475 ALNVGSKDANKPVRITNAPGVKEGVDVTVNAQLKGVQNLNRRIDNVDGNARAGIAQIA 534  
DB 476 ALNVGSKDANKPVRITNAPGVKEGVDVTVNAQLKGVQNLNRRIDNVDGNARAGIAQIA 535  
QY 535 TAGLVQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIINKGTASGNSRGHFGAS 594  
DB 536 TAGLVQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIINKGTASGNSRGHFGAS 595  
QY 595 VGYOW 599

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|||||
Db 596 VGYQW 600

RESULT 9
Q9JPI3 PRELIMINARY; PRT; 594 AA.
ID Q9JPI3
AC Q9JPI3
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NG3/89, AND BZ232;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RA "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226376; AAF42525.1; -.
DR EMBL: AF226369; AAF42518.1; -.
SQ SEQUENCE 594 AA; 62086 MW; 1B25B03B90D04B46 CRC64;

Query Match 90.78; Score 2776.5; DB 2; Length 594;
Best Local Similarity 92.08; Pred. No. 4.5e-109;
Matches 551; Conservative 12; Mismatches 31; Indels 5; Gaps 2;

Qy 1 MNKYRIIWNALNAWAVSELTRNHTKRASATVKTAVLATLLFATVOANATDEDEEL 60
Db 1 MNKYRIIWNALNAWAVSELTRNHTKRASATVKTAVLATLLFATVOANATDEDEEL 59
Qy 61 EPVRSALVLQFMIDKEGNESTGNIGWSIYYDNHNLHGATVTLKAGDNLKIKONTN 120
Db 61 EPVRSALVLQFMIDKEGNESTGNIGWSIYYDNHNLHGATVTLKAGDNLKIKONTN 120
Qy 60 EPVQRTAPVLSFHADSEGTGEKVEDTSNMGVYFDKKGVLTAGTITLKAGDNLKIKQ--- 116
Db 60 EPVQRTAPVLSFHADSEGTGEKVEDTSNMGVYFDKKGVLTAGTITLKAGDNLKIKQ--- 116
Qy 121 KNTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
Db 117 -NTDENTNASSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175
Qy 181 DTTVHLNIGSTLTDLLNTGATTNVNDVTDKKRAASVKDVLNAGWNKIKVPGCTT 240
Db 176 DTTVHLNIGSTLTDLLNTGATTNVNDVTDKKRAASVKDVLNAGWNKIKVPGCTT 235
Qy 241 ASDNVDFVHTYDVEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSVKEKDGKLVTKGK 300
Db 236 ASDNVDFVHTYDVEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSVKEKDGKLVTKGD 295
Qy 301 KGENGSTDEGEGLVTAKEVIDAYNKGWRMKTNTANGQTQADKFFETVTSCTVNTFASG 360
Db 296 KGENGSTDEGEGLVTAKEVIDAYNKGWRMKTNTANGQTQADKFFETVTSCTVNTFASG 355
Qy 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLQNSGNWLDKAVAGSGKVISGNVSPSK 420
Db 356 NGTTATVSKDDQGNITVKYDYNVGDALNVNQLQNSGNWLDKAVAGSGKVISGNVSPSK 415
Qy 421 GKMDETVNNAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDKALNVGS 480
Db 416 GKMDETVNNAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDKALNVGS 475
Qy 481 KDANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLNHNIDVNGNARAGIAQAIATAGLVQ 540
Db 476 KDANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLNHNIDVNGNARAGIAQAIATAGLVQ 535
541 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFASVGYQW 599
536 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRHFASVGYQW 594

RESULT 10
Q9JPS2 PRELIMINARY; PRT; 594 AA.
ID Q9JPS2
AC Q9JPS2
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NGE31;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;
RA "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL: AF226379; AAF42528.1; -.
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F5D256 CRC64;
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QY 481 KDANKPVRITNVPAGVKEGDTNVAQLKGVQALNNRINDVGNRAGIAQAIAATAGLVQ 540  
Db 476 KDANKPVRITNVPAGVKEGDTNVAQLKGVQALNNHIDVGNRAGIAQAIAATAGLV 535  
QY 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 599  
Db 536 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 594

RESULT 11  
QJPS3  
ID Q9JPS3 PRELIMINARY; PRT; 590 AA.  
AC Q9JPS3;  
DT 01-OCT-2000 (TremBLrel. 15, Created)  
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzo M., Scarlato V., Masiagnani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.  
RT \*Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226378; AAF42527.1; -.  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 90.5%; Score 2768.5; DB 2; Length 590;  
Best Local Similarity 91.5%; Pred. No. 9.7e-109;  
Matches 549; Conservative 14; Mismatches 26; Indels 11; Gaps 2;

QY 1 MKKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60  
Db 1 MKKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60

QY 61 EPVRSALVLOFMIDKEGNGENEST-GNIGWSIYDNNHTLHGATVTLKAGDNLKIKONT 119  
Db 61 DPVQRTVAVLIVNSDKEGTKEKEVEENSDWAVYFNEKGVLTAGTITLKAGDNLKIKQ-- 118

QY 120 NKNENTNDSSTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTN 179  
Db 119 -----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTN 170

QY 180 GDTVHLNGIGSTLDTLLNTGATTNVTNDVTDKKRAASVKOVNLNAGWIKGVKPGT 239  
Db 171 GDTVHLNGIGSTLDTLLNTGATTNVTNDVTDKKRAASVKOVNLNAGWIKGVKPGT 230

QY 240 TASDNVDFVHTYDTVEFLSADTKTTVNVEKDNKRTVEKIGAKTSVKEKDGKLVTKG 299  
Db 231 TASDNVDFVHTYDTVEFLSADTKTTVNVEKDNKRTVEKIGAKTSVKEKDGKLVTKG 290

QY 300 KGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFETVTSNTVTFAS 359  
Db 291 KGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFETVTSNTVTFAS 350

QY 360 KGKGTATVSKDDQGNITVVKYDNNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPS 419  
Db 351 KGKGTATVSKDDQGNITVVKYDNNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPS 410

QY 420 KGKMDETVINAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVG 479  
Db 411 KGKMDETVINAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVG 470

Db 411 KGKMDETVINAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVG 470  
QY 480 SDANKPVRITNVPAGVKEGDTNVAQLKGVQALNNRINDVGNRAGIAQAIAATAGLV 539  
Db 471 SDANKPVRITNVPAGVKEGDTNVAQLKGVQALNNRINDVGNRAGIAQAIAATAGLV 530  
QY 540 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 599  
Db 531 QAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 590

RESULT 12  
Q93QV4  
ID Q93QV4 PRELIMINARY; PRT; 594 AA.  
AC Q93QV4;  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EG327;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT \*Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.\*;  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF157605; AAK68866.1; -.  
SQ SEQUENCE 594 AA; 62297 MW; 9DDD48B04B3A8EA2 CRC64;

Query Match 90.3%; Score 2762.5; DB 2; Length 594;  
Best Local Similarity 91.7%; Pred. No. 1.7e-108;  
Matches 549; Conservative 13; Mismatches 32; Indels 5; Gaps 2;

QY 1 MKKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60  
Db 1 MKKIYRIIWNALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 59

QY 61 EPVRSALVLOFMIDKEGNGENESTGNIGWSIYDNNHTLHGATVTLKAGDNLKIKONT 120  
Db 60 EPVQRTAVVLSFRSDEGTEGKEVEDSNWGYFDFKKGVLTAGTITLKAGDNLKIKQ--- 116

QY 121 KNTNENTNDSSTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTN 180  
Db 117 -NTNENTNASSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTN 175

QY 181 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKKRAASVKOVNLNAGWIKGVKPGT 240  
Db 176 DTTVHLNGIGSTLDTLLNTGATTNVTNDVTDKKRAASVKOVNLNAGWIKGVKPGT 235

QY 241 ASDNVDFVHTYDTVEFLSADTKTTVNVEKDNKRTVEKIGAKTSVKEKDGKLVTKG 300  
Db 236 ASDNVDFVHTYDTVEFLSADTKTTVNVEKDNKRTVEKIGAKTSVKEKDGKLVTKG 295

QY 301 KGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFETVTSNTVTFAS 360  
Db 296 KGKNGSSSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTGOADKFETVTSNTVTFAS 355

QY 361 KGKGTATVSKDDQGNITVVKYDNNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPK 420  
Db 356 KGKGTATVSKDDQGNITVVKYDNNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPK 415

QY 421 KGKMDETVINAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVG 480  
Db 416 KGKMDETVINAGNIEITRNKGNIDIAATSMTPQFSSVSLGAGADAPTLSDVDDKALNVG 475

QY 481 KDANKPVRITNVPAGVKEGDTNVAQLKGVQALNNRINDVGNRAGIAQAIAATAGLVQ 540  
Db 476 KDANKPVRITNVPAGVKEGDTNVAQLKGVQALNNHIDVGNRAGIAQAIAATAGLVQ 535

QY	541	AYLPCKSMAAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRHFHGASASVGTQW	599
Db	536	AYLPCKSMAAIGGGTYRGEAGYAIGYSSISDGGNWIITKGTASGNSRHFHGASASVGTQW	594
RESULT 13			
QY	Q9JPS9	PRELIMINARY; PRT; 592 AA.	
AC	Q9JPS9		
DT	01-OCT-2000 (TrEMBLrel. 15, Created)		
DT	01-OCT-2000 (TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2001 (TrEMBLrel. 16, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992.		
GN	GNA992.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria		
OX	NCBI_TaxID=487;		
RP	[1]		
RN	SEQUENCE FROM N.A.		
RC	STRAIN=860800;		
RC	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing.";		
RL	Science 287:1816-1820(2000).		
DR	EMBL; AF226361; AAF42510.1; -.		
SQ	SEQUENCE 592 AA; 61917 MW; 4A3471514FD3C879 CRC64;		
Query Match 89.5%; Score 2737.5; DB 2; Length 592;			
Best Local Similarity 92.2%; Pred. No. 1.9e-107;			
Matches 553; Conservative 9; Mismatches 29; Indels 9; Gaps			
QY	1	MNKYRIIWSALNAWAVASELTENHTKRASATVKTAVLATLLFATVOANATDEDEEL 60	
Db	1	MNKYRIIWSALNAWAVASELTENHTKRASATVKTAVLATLLFATVOANATDEDEEL 60	
QY	61	EPVYRSALVQFMIDKEGGENESTGNIWGSYYDHNHTLHG-ATVTLKAGDNLKIKQNT 119	
Db	61	ESVQRS-VVGSIQASMEGSGELET--ISLSMTNDSKEFVDPYIVTLKAGDNLKIKQ-- 114	
QY	120	NKNTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTN 179	
Db	115	--NTNENTNASSFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTN 177	
QY	180	GDTTVHLNGIGSTLTDPLLNTGATTNTNDNVTDKKRAASKYKDVLNAGNNIKGVFPGT 238	
Db	173	GDTTVHLNGIGSTLTDMLLNTGATTNTNDNVTDDEKKRAASKYKDVLNAGNNIKGVFPGT 233	
QY	240	TASNVDVFRTYDVEFLSADTKTTTVNVSCKONGKKEVYKIGAKTSVYKEKGDKLVYTK 299	
Db	233	TASNVDVFRTYDVEFLSADTKTTTVNVSCKONGKKEVYKIGAKTSVYKEKGDKLVYTK 299	
QY	300	KGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGQADKFETVTSGTNVTFAS 359	
Db	293	KGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGQADKFETVTSGTNVTFAS 355	
QY	360	KGKNTATVSKDDQGNITVYKDVVNGDALNVQLNSGNWLDLSRAVAGSSKVISGNVSPS 419	
Db	353	KGKNTATVSKDDQGNITVYKDVVNGDALNVQLNSGNWLDLSRAVAGSSKVISGNVSPS 413	
QY	420	KGKMDETVNTNAGNNIEITRNGKNIDTATSWTPOFSSVSLGAGADAPTLSDVDKGLNVG 479	
Db	413	KGKMDETVNTNAGNNIEITRNGKNIDTATSWTPOFSSVSLGAGADAPTLSDVDKGLNVG 477	
QY	480	SKDANKPVRITNTNAPGVKEGSDVTNVAQLKGVAQNNLRIDNVGNARAGTAQATATAGLV 539	

Db 473 SKDANKPVRITNVPAGVKEGDVTNVAQLGVAQNLRNDVNGNARAGIAQAIATAGLV 532

Qy 540 QAYLPGRKSMMAIGGGTYRGAGYAIGYSSISDGGNNIIKGTASGNSRGHFGASASYGQW 599

Db 533 QAYLPGRKSMMAIGGGTYRGAGYAIGYSSISDGGNNIIKGTASGNSRGHFGASASYGQW 592

RESULT 14

Q9JPIO PRELIMINARY; PRT; 589 AA.

AC O9PI0:

DT 01-OCT-2000 (TremBrel. 15, Created)

DT 01-OCT-2000 (TremBrel. 15, last sequence update)

DT 01-MAR-2001 (TremBrel. 16, last annotation update)

GN OUTER MEMBRANE PROTEIN GNA992.

OS Neisseria meningitidis

OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria

OX NCBI\_TaxID=487;

RP [1]

RN SEQUENCE FROM N.A.

RC STRAIN=NGP165, 90/18311, AND 93/4286;

EX MEDLINE=20175756; PubMed=10710308;

RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,

RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,

RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,

RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,

RA Moxon E.R., Grandi G., Rappuoli R.;

RT "Identification of Vaccine Candidates Against Serogroup B

RT Meningococcus by Whole-Genome Sequencing.";

RL Science 287:1816-1820(2000).

DR EMBL: AF226384; AAF42533.1; -

DR EMBL: AF226362; AAF42511.1; -

DR EMBL: AF226363; AAF42512.1; -

SQ SEQUENCE 589 AA; 61520 MW; 2B2A95D4868566A6 CRC64;

Query Match 88.6%; Score 2710; DB 2; Length 589;

Best Local Similarity 90.2%; Pred. No. 2.7e-106;

Matches 542; Conservative 13; Mismatches 32; Indels 14; Gaps

Qy 1 MNKIYRIWNSALNAWVAVSELNRNHTKRASATVATVATLTLFATVQANATDEDEEL 60

Db 1 MNKIYRIWNSALNAWVAVSELNRNHTKRASATVATVATLTLFATVQANATDEDEEL 60

Qy 61 EPVYRSALVLFQFMIDKEGNGENESTGNIGWSIYYDHNHTLHGATVTLKAGDNLIKONTN 120

Db 61 ESVYRSALVLFQFMIDKEGNGEISTGDIWSIYYDDHNTLHGATVTLKAGDNLIKQ--- 117

Qy 121 KNTNENTNDSFFYSLAKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNC 180

Db 118 -----SGKDFYSLAKELKDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 170

Qy 181 DTTVHLNGIGSTLTDTLTNGTATTNTNDVNTDKKRAASVKDVLNAGNWKVAPGPT 240

Db 171 DPTVHLNGIGSTLTDTLTAGSASHVDAGNST--HYTRAASIKDVLNAGNWKVKTGST 228

Qy 241 A--SDNYDFVHTYDTVEFLSADTKTTTVNVYESKDNKRTEVKIGAKTSVIXEKDGKLVTG 298

Db 229 TQGENVDVRYTYDTVEFLSADTKTTTVNVYESKDNKRTEVKIGAKTSVIXEKDGKLVTG 288

Qy 299 KGKGENSGSTDEGBGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTWVTF 358

Db 289 KGKGENSGSTDEGBGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTWVTF 348

Qy 359 SGKGTATVSKDDOGNTTVKYDVGNDALVNLQNSGNWLDKSAVAGSSGKVISGNVSP 418

Db 349 SGNGTATVSKDDOGNTTVKYDVGNDALVNLQNSGNWLDKSAVAGSSGKVISGNVSP 408

Qy 419 SKGMDETVINAGNNIEITRNKGNIIDIAITSMTPQFSSVSLGAGADPTLSVDKGLNLY 478

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|||||
Db 409 SKGKMDETVNIAGNIEITRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDEGALNV 468
QY 479 GSKDANKPVRITNVAPGVKEGDTNVQAQLKGVQAQNLNNRIDNVNVDGNARAGIAQAATAGL 538
Db 469 GSKDANKPVRITNVAPGVKEGDTNVQAQLKGVQAQNLNNRIDNVNVDGNARAGIAQAATAGL 528
QY 539 VOAYLPKSMMAIGGCTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFGASASVGQ 598
Db 529 AOAYLPKSMMAIGGCTYRGEAGYATGYSSISDGTGNWIKGTASGNSRGHFGTSASVGQ 588
QY 599 W 599
Db 589 W 589

RESULT 15
Q9JPS8
ID Q9JPS8 PRELIMINARY; PRT: 599 AA.
AC Q9JPS8;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-MAR-2001 (TremBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A22;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecechi B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
RT Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226364; AAF42513.1; -.
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;
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Query Match 88.5%; Score 2709; DB 2; Length 599;
Best Local Similarity 89.7%; Pred. No. 3.le-106;
Matches 539; Conservative 17; Mismatches 41; Indels 4; Gaps 2;

QY 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
Db 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVKTAVLATLLSATVQANTTDEDEEYL 60
QY 61 EPVRSALVQFMIDKEGNGENSTGNIGWYIDNHNFTLHGATVTLKAGDNLKIKONTN 120
Db 61 EPVKRTAVVLSFRSDEKGEVTEDSHWGYFDEKGVKAGTITLKAGDNLKIKONTD 120
QY 121 KNTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
Db 121 ENTDENTNASSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 180
QY 181 DTTVHLNGIGSLTDLTLNLTGATNTVNDVDDKKRAASVKDVLNAGWNKIGVKPGTT 240
Db 181 DTTVHLNGIGSLTDLTLNLTGATNTVNDVDDKKRAASVKDVLNAGWNKIGVKPGTT 240
QY 241 A--SDNVDVHTYDVEFLSADTKTTNVNVEKDNCKRTEVKIGAKTSVKEKDKLVTG 298
Db 239 TQGSNVDVHTYDVEFLSADTKTTNVNVEKDNCKRTEVKIGAKTSVKEKDKLVTG 298
QY 299 KGKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITTANGOTQADKFFETVTSNTVTPA 358
Db 299 KGKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITTANGOTQADKFFETVTSNTVTPA 358
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QY 359 SKGTTATVSKDDOGNITVKYDYNVGDALNVOLQNSGNLDSKAVAGSSGKVISGNVSP 418
Db 359 SKGTTATVSKDDOGNITVKYDYNVGDALNVOLQNSGNLDSKAVAGSSGKVISGNVSP 418
QY 419 SKGKMDETVNIAGNIEITRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDDKALNV 478
Db 419 SKGKMDETVNIAGNIEITRNGKNIDIAATMTPOFSSVSLGAGADAPTLSDVDDKALNV 478
QY 479 GSKDANKPVRITNVAPGVKEGDTNVQAQLKGVQAQNLNNRIDNVNVDGNARAGIAQAATAGL 538
Db 479 GSKDANKPVRITNVAPGVKEGDTNVQAQLKGVQAQNLNNRIDNVNVDGNARAGIAQAATAGL 538
QY 539 VOAYLPKSMMAIGGCTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFGASASVGQ 598
Db 539 VOAYLPKSMMAIGGCTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFGASASVGQ 598
QY 599 W 599
Db 599 W 599
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Search completed: July 3, 2002, 08:28:47  
Job time: 1168 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:31:04 ; Search time 104.77 seconds  
(without alignments)  
533.980 Million cell updates/sec

Title: US-09-771-382-7

Perfect score: 3044

Sequence: 1 MNKYRIWNSALNAWVVS.....TASGSRGFCASAGVQW 598

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11107396 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

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2: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA1981.DAT.\*  
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22: /SIDSI/gcgdata/hold-geneq/geneq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3044	100.0	598	20	AA23742
2	3044	100.0	598	22	AAU06177
3	3021	99.2	598	22	AAU23738
4	3021	99.2	598	22	AAU06178
5	2971	97.6	594	20	AA23739
6	2971	97.6	594	22	AAU06179
7	2855	93.8	594	20	AA23740
8	2855	93.8	594	21	AAU57044
9	2855	93.8	594	22	AAU06174
10	2824.5	92.8	599	20	AA23743
11	2824.5	92.8	599	22	AAU06176

12	2735.5	89.9	591	21	AAV57045	BASB029 amino acid
13	2725.5	89.5	591	20	AAV27202	Amino acid sequenc
14	2725.5	89.5	591	20	AAV23746	A surface protein
15	2725.5	89.5	591	22	AAU06171	N. meningitidis PM
16	2718	89.3	592	20	AAV23737	A surface protein
17	2706.5	88.9	591	20	AAV23741	A surface protein
18	2706.5	88.9	591	22	AAU06175	N. meningitidis EG
19	2667	87.6	592	20	AAV23744	A surface protein
20	2667	87.6	592	22	AAU06172	N. meningitidis H4
21	2610.5	85.8	589	20	AAV23745	A surface protein
22	2610.5	85.8	589	22	AAU06173	N. meningitidis P2
23	2524	82.9	592	22	AAU06180	N. meningitidis Z2
24	2488	81.7	592	20	AAV27203	Amino acid sequenc
25	2460.5	80.8	513	22	AAU06183	N. meningitidis H4
26	2427	79.7	512	22	AAU06182	N. meningitidis PM
27	2344	77.0	502	22	AAU06186	N. meningitidis PM
28	2234	73.4	604	22	AAU06181	N. meningitidis PM
29	2010.5	66.0	433	22	AAU06185	N. meningitidis PM
30	1864.5	61.3	407	22	AAU06184	N. meningitidis PM
31	1318.5	43.3	2353	17	AAU99393	Haemophilus influe
32	1292.5	42.5	2411	21	AAU23860	Haemophilus influe
33	1078	35.4	1094	21	AAU23858	Haemophilus influe
34	1057	34.7	1098	17	AAU99392	Haemophilus influe
35	1041	34.2	245	20	AAV27201	Amino acid sequenc
36	1010.5	33.2	679	17	AAU99394	Haemophilus influe
37	1010.5	33.2	679	21	AAU23855	Haemophilus influe
38	767	25.2	1002	21	AAU23854	Haemophilus influe
39	758	24.9	1004	21	AAU23857	Haemophilus influe
40	712	23.4	1104	21	AAU23856	Haemophilus influe
41	712	23.4	1104	21	AAU23859	Haemophilus influe
42	597	19.3	116	21	AAU37832	Neisseria conserv
43	416.5	13.7	2314	22	AAU69136	M. catarrhalis les
44	393.5	12.9	2123	22	AAU00701	Moraxella catarrha
45	391.5	12.9	1992	17	AAU04505	Moraxella 200 kDa

#### ALIGNMENTS

RESULT 1

AA23742

ID AAY23742 standard; Protein; 598 AA.

XX AC AAY23742;

XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX DE Surface protein; surface glycoprotein; infection; vaccine;

XX KW Immunoreactive peptide.

XX OS Neisseria meningitidis.

XX PN WO9931132-AL.

XX PD 24-JUN-1999.

XX PF 14-DEC-1998; 98WO-AU01031.

XX PR 12-DEC-1997; 97GB-0026398.

XX PA (ISIS-) ISIS INNOVATION LTD.

XX PA (UYOU ) UNIV QUEENSLAND.

XX PI Jennings MP, Moxon ER, Peak IRA;

XX DR WPI; 1999-418754/35.

XX DR N-PSDB; AAX85794.

XX PT Neisseria meningitidis surface proteins useful for treating N.

XX PT meningitidis infections

```

PS Claim 1; Page 108-110; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 598 AA;

Query Match 100.0%; Score 3044; DB 20; Length 598;
Best Local Similarity 100.0%; Pred. No. 1.2e-175;
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MNKYRIIWNALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 mnkyriiwnsalnawvvsseitnrhtrksatvatvatlflfatvqanattddddyile 60

Qy 61 PVQRTAVVLSFRSKEGTGEKEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120
Db 61 pvqrtavvlsfrskegtgekedsnwavyfdekrvllkagaitllkagdnllkikqntne 120

Qy 121 NTNENTNDSSFTYSLKRDLTDLTSVEFEKLSFGANGKNVNITSDTKGLNFAKETAGIND 180
Db 121 ntntentndssftyslkrdltdltsveteklsfgangknvnitsdtkglnfaketagntgd 180

Qy 181 PTVHLNGIGSTLDTLNTGATTTNVDNVDDEKKRAASVKVDVNLGNWNTKVKPQGTTA 240
Db 181 ptvhlngigstltdlntgattvndvndvtddekkraasvkvdlvnlgnwnkvgkpqgtta 240

Qy 241 SDNVDFVRYTYTVFELSADTKTTTVNVESKDNGKTEVKIGAKTSVIEKDKGLVTKGK 300
Db 241 sdnvdfvrytytvfelsadtktttvnnveskdngkktevkiagaktsviekgdkglvtgk 300

Qy 301 DENGSSTDEGEGLYTAKEVIDAVNKAGWRMTTANGTGQADKFEVTSGTKVTFASGN 360
Db 301 dengsstdegeglvtakevidavnkagwrmtttangtgqadkfetvtsgtkvtfasgn 360

Qy 361 GTTATVSKDDGNTVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVSIGNVSPSKG 420
Db 361 gttatvskddgntvkydvnvgdalnvqnlqnsqwnldskavagssgkvsgnvspskg 420

Qy 421 KMDETVINAGNNTIETRNKNIDTATSMTPQFSVSLGAGADAPTLSDVDEGALNVGSK 480
Db 421 kmdetvinagnnietrnknidiatstmpqfssvslgagadaptilsvddegalnvvg 480

Qy 481 DANKPVRTNVPAGVKEGVDVTVNQLKGVAQNANLNRRIDNVGNRAGTAQAIATAGLAQA 540
Db 481 dankpvrtnvpagvkegdvtnvqnlkgvaqnlnrridnvdnvnraglaqaiaataglaqa 540

Qy 541 YLPKSMMAIGGGYRGAGYAGYSSISDTGNVWIKGTASGNSRGHFGASASVGYOW 598
Db 541 ylpksmmaigggryrgagyagysyssidtgnvwikgtasgnsrghfgasasvgyow 598

RESULT 2
AAU06177
ID AAU06177 standard; Protein; 598 AA.
AC AAU06177;
XX
XX 24-OCT-2001 (first entry)
XX
XX N. meningitidis H15 surface antigen Naha polypeptide sequence.
XX
XX Surface antigen Naha; meningococcal disease; meningitis vaccine.
XX
XX Neisseria meningitidis strain H15.

```

```

XX PH Region Location/Qualifiers
XX 1..50
XX /label= C1
XX /note= "Conserved region 1"
XX 51..104
XX /label= V1
XX /note= "Variable region 1"
XX 105..116
XX /label= C2
XX /note= "Conserved region 2"
XX 117..130
XX /label= V2
XX /note= "Variable region 2"
XX 131..194
XX /label= C3
XX /note= "Conserved region 3"
XX 195..216
XX /label= V3
XX /note= "Variable region 3"
XX 217..235
XX /label= C4
XX /note= "Conserved region 4"
XX 236..242
XX /label= V4
XX /note= "Variable region 4"
XX 243..598
XX /label= C5
XX /note= "Conserved region 5"
XX
XX W020015182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU000069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
XX
XX N-PSDB; AAS09167.
XX
XX
XX New Naha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 9lpp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Naha
XX (AAU06182-AAU06186). The modified or mutant Naha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Naha
XX from N. meningitidis strain H15 is 1 of 10 Naha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
XX Sequence 598 AA;

```

Query Match 100.0%; Score 3044; DB 22; Length 598;  
Best Local Similarity 100.0%; Pred. No. 1.2e-175;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAWVWSELTRNHTKRASATVATVATLATLLFATVQANATDDDDLYLE 60  
Db 1 mnkiyriiwsalnawvwseltrnhtkrasatvatvatlatllfatvqanatdddlyle 60

QY 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120  
Db 61 pvertavvlsfrsdkegtgekedtsnwavyfdekrvllkagaitlkagdnlikqntne 120

QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTGLNFAKETAGTNGD 180  
Db 121 ntntentndsfstyslkkdltdltsveteklsfgangknvntsdgtlgnfaketagngd 180

QY 181 PTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240  
Db 181 ptvhlingigstltdltllntgattntvntdndvtddekkraasvkdvlagnwnikgvkpgtta 240

QY 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKGK 300  
Db 241 sdnvdfvrtvdtveflsadtktttvnvveskdngkktvkgaktsvikekdkglvtgkgk 300

QY 301 DENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFEFVTSGTKVTFASGN 360  
Db 301 dengssstdegeglvtakevidavnkgawrmktttangotgoadkfevvtsgtkvtfasgn 360

QY 361 GTTATVSKDDQGNITVKYIDVNVGDALNVNQLONGSNWNLDSKAVAGSSGKVISGNVSPSKG 420  
Db 361 gttatvskddqgnitvkiyidvnnvgdalnnvnlqngsnwlnldskavagsgkvisgnvspkg 420

QY 421 KMDETVNIAGNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSK 480  
Db 421 kmdetvniagnieitrngknidiaatstmpqfssvslgagadaptilsvddgalnvsgk 480

QY 481 DANKPVRITNVAPGVKEGDDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLAQA 540  
Db 481 dankpvrtnvapgvkegddvtnvaqlkgvaqnlnrindnvgnaragiaqaiataglaqa 540

QY 541 YLPKSNMAIGGGTYRGEAGYAIYSSISDTGNWIKGTASGNSRHFASASVGYQW 598  
Db 541 ylpksgmmaigggtyrgeagyaiysssdsdtgnwviktasgnsrghfgasasvgyqw 598

## RESULT 3

AAU06178  
ID AAU06178 standard; Protein; 598 AA.

AC AAU06178;

XX 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

XX Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.

XX Neisseria meningitidis.

XX WO9311132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

XX (UYQU ) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

XX N-PSDB; AAX85790.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

XX

PS Claim 1; Page 91-93; 132pp; English.

XX The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

XX Sequence 598 AA;

Query Match 99.2%; Score 3021; DB 20; Length 598;  
Best Local Similarity 99.3%; Pred. No. 2.8e-174;  
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAWVWSELTRNHTKRASATVATVATLATLLFATVQANATDDDDLYLE 60

Db 1 mnkiyriiwsalnawvwseltrnhtkrasatvatvatlatllfatvqanatdddlyle 60

QY 61 PVORTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120

Db 61 pvertavvlsfrsdkegtgekedtsnwavyfdekrvllkagaitlkagdnlikqntne 120

QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTGLNFAKETAGTNGD 180

Db 121 ntntentndsfstyslkkdltdltsveteklsfgangknvntsdgtlgnfaketagngd 180

QY 181 PTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240

Db 181 ptvhlingigstltdltllntgattntvntdndvtddekkraasvkdvlagnwnikgvkpgtta 240

QY 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIKEKDKGLVTGKGK 300

Db 241 sdnvdfvrtvdtveflsadtktttvnvveskdngkktvkgaktsvikekdkglvtgkgk 300

QY 301 DENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFEFVTSGTKVTFASGN 360

Db 301 dengssstdegeglvtakevidavnkgawrmktttangotgoadkfevvtsgtkvtfasgn 360

QY 361 GTTATVSKDDQGNITVKYIDVNVGDALNVNQLONGSNWNLDSKAVAGSSGKVISGNVSPSKG 420

Db 361 gttatvskddqgnitvkiyidvnnvgdalnnvnlqngsnwlnldskavagsgkvisgnvspkg 420

QY 421 KMDETVNIAGNIEITRNKKNIDIAATSMTPQFSSVSLGAGADAPTLSVDDGALNVGSK 480

Db 421 kmdetvniagnieitrngknidiaatstmpqfssvslgagadaptilsvddgalnvsgk 480

QY 481 DANKPVRITNVAPGVKEGDDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLAQA 540

Db 481 dankpvrtnvapgvkegddvtnvaqlkgvaqnlnrindnvgnaragiaqaiataglaqa 540

QY 541 YLPKSNMAIGGGTYRGEAGYAIYSSISDTGNWIKGTASGNSRHFASASVGYQW 598

Db 541 ylpksgmmaigggtyrgeagyaiysssdsdtgnwviktasgnsrghfgasasvgyqw 598

## RESULT 4

AAU06178

ID AAU06178 standard; Protein; 598 AA.

XX AAU06178;

XX 24-OCT-2001 (first entry)

XX N. meningitidis BZ10 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

```
XX OS Neisseria meningitidis strain B210.
XX Key Location/Qualifiers
XX PH Region 1..50
FT FT /label= C1
FT FT /note= "Conserved region 1"
FT FT 51..104
FT FT /label= V1
FT FT /note= "Variable region 1"
FT FT 105..116
FT FT /label= C2
FT FT /note= "Conserved region 2"
FT FT 117..130
FT FT /label= V2
FT FT /note= "Variable region 2"
FT FT 131..194
FT FT /label= C3
FT FT /note= "Conserved region 3"
FT FT 195..216
FT FT /label= V3
FT FT /note= "Variable region 3"
FT FT 217..235
FT FT /label= C4
FT FT /note= "Conserved region 4"
FT FT 236..242
FT FT /label= V4
FT FT /note= "Variable region 4"
FT FT 243..598
FT FT /label= C5
FT FT /note= "Conserved region 5"
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU000069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09168.
XX
XX New Noha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Noha
XX (AAU06182-AAU06186). The modified or mutant Noha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Noha
XX from N. meningitidis strain B210 is 1 of 10 Noha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
XX Sequence 598 AA;
XX
XX Query Match 99.28; Score 3021; DB 22; Length 598;
XX Best Local Similarity 99.3%; Pred. No. 2.8e-174;
XX
```

```
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 MNKIYRIIWNNSALNAWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDLYLE 60
Db 1 mnkisriiwnsalnawvvsseletrnhtkrasatvatacliflfcvqanacdddlyle 60
Qy 61 PVQRTAVVLSFRSDKEGTGEKEDTSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120
Db 61 pvqrtavvlsfrsdkegtgekedtsnnavyfdkrylkagaitlkagdnlikqntne 120
Qy 121 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180
Db 121 ntntentndssftyslkdltdltsveteklsfgangknvntsdtkglnfaketagtngd 180
Qy 181 PTVHLNGIGSTLTDLLNTGATTNTVNDTDEKKRAASKVDVLNAGWNKGVKPGTTA 240
Db 181 ptvhlingigstltdllntgattntvndtdekkraasvkvdlngwnlkgvpgtta 240
Qy 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKDNGKTEYKIGAKTSVIREKDGKLVTKGK 300
Db 241 sdnvdfvrydtveflsadtktttvnnveskdngkrtvkgaktsvirekdgklvtgk 300
Qy 301 DENGSSDTDEGGLVTAKEVIDAVNKAQWPMKTTTANGOTGQADKFTVTSKTVTFASGN 360
Db 301 dengssdtdegeglvtakevidavnkagwrmktttnggtgqadkfetvtsgtkvtfasgn 360
Qy 361 GTTATVSKDDOGNITVKYDVNVGDALNVQLNSGWNLDKAVAGSSGKVSIGNVSPSKG 420
Db 361 gttatvskddognitvkvdyvnnvgdnlvnqnlqnsqwnldskavagssgkvsgnvspskg 420
Qy 421 KMDETVINAGNNIEITRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480
Db 421 kmdevtninagnnieitrngknidiatsmtptqfssvslgagadaptlsvddegalnvsgk 480
Qy 481 DANKPVRITNVAPGVKEGDTNVAOLKGAQNLNRRIDNVGNARAGIAQAIATAGLAQA 540
Db 481 dankpvritynvapgvkegdvtnvaqlkgvaqnlrridnvdgnaragialataglaqa 540
Qy 541 YLPKSMMAIGGTYRGEAGYAGYSSISDPTGNVWIKGTASGNSRHFCSASVGYQW 598
Db 541 ylpksmmaiggytyrgeagyagysisdtgnvwwikgtasgnsrghrftsasvgyqw 598
RESULT 5
AA23739
ID AAY23739 standard; Protein; 594 AA.
XX
XX AC AAY23739;
XX
XX DT 08-SEP-1999 (first entry)
XX
XX DE A surface protein of Neisseria meningitidis.
XX
XX KW Surface protein; surface glycoprotein; infection; vaccine;
XX immunoreactive peptide.
XX
XX OS Neisseria meningitidis.
XX
XX PN WO9931132-A1.
XX
XX PD 24-JUN-1999.
XX
XX PF 14-DEC-1998; 98WO-AU01031.
XX
XX PR 12-DEC-1997; 97GB-0026398.
XX
XX PA (ISIS-) ISIS INNOVATION LTD.
XX (UYQU ) UNIV QUEENSLAND.
XX
XX PI Jennings MP, Moxon ER, Peak IRA;
XX
XX WPI; 1999-418754/35.
XX N-PSDB; AAX85791.
XX
```



```
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
PS
XX Claim 1; Page 95-97; 132pp; English.
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
SQ Sequence 594 AA;

Query Match          97.6%; Score 2971; DB 20; Length 594;
Best Local Similarity 98.0%; Pred. No. 2.9e-171;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 1 MKKIVRIINNSALNAVWVSEITRNHTRKRASATVATVATLTLFATVQANATDDDDLYLE 60
   |||||||
Db 1 mkiyriiwnsalnavwvseitrnhtkrasatvatvatlallfatvqanattdddllyle 60
   |||||||

QY 61 PVQRTAVVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
   |||||||
Db 61 pvgrtavvlsfrsdkegtegedtsnwavyfdekrvllkagaitlkagdnllkikq---- 116
   |||||||

QY 121 NTNENTNDSFYSYSLKKDLTSLTSETKLSFGANGKNVNIITSDTKGLNFAKETAGTNGD 180
   |||||||
Db 117 ntentndsfyslkkdltdltseteklsfgangknvniitsdtkglnfaketagtn 176
   |||||||

QY 181 PTVHLNGIGSTLTDLLNTGATNTVNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240
   |||||||
Db 177 ptvhngigstltdllntgattvndvntddekraasvkdvlntagwnikgvkpgtta 236
   |||||||

QY 241 SDNVDFVRYDVVEFLSADTKTTNVNVEKNDGKTEVKIGAKTSVKEKDGKLYTGK 300
   |||||||
Db 237 sdnvdfvrydvveflsadtkttnvnveskndgkktevkigaktvikekdgklytgk 296
   |||||||

QY 301 DENGSTDEGEGLVTAKEVIDAVNKGWRMKTNTANGOTQADKFTVTSGTKVTFASGN 360
   |||||||
Db 297 dengstdegeglvtakevidavnkgwrmtntangotqgqadkftvtsgrtnvtfask 356
   |||||||

QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
   |||||||
Db 357 gttatvskddqgnitvkydvnvvgdnlvnlqnsqwnldskavagsgkvvisgnvpskg 416
   |||||||

QY 421 KWDFTVNIAGNNIETRNKKNIDATSMTPQSFSSVSLGAGADAPTLSDDEGALNVGSK 480
   |||||||
Db 417 kndetvniagnnieitrngknidatsmapqsfssvslgagadaptlsvddegalnvg 476
   |||||||

QY 481 DANKPVRITNPAGVKEGVDVTVNVAQLKGAQNLNRRIDNVNNGNARAGIAQALATAGLAQA 540
   |||||||
Db 477 dtnkpvritnvpagvkegdvtnvaqlkgvaqlnrridnvngnarnagiataglatagla 536
   |||||||

QY 541 YLPGKSMMAIGGTVRGEAGYAIYSSISDGTGNWVTKGTASGNSRGRHFGASVGVQW 598
   |||||||
Db 537 ylpgksmmaiggtvrygeagyaigyssisdggnwvliikgtasgnsrghfgasavgyq 594
   |||||||

RESULT 6
AAU06179
ID AAU06179 standard; Protein; 594 AA.
XX
AC AAU06179;
XX
DT 24-OCT-2001 (first entry)
XX
DE N. meningitidis Bz198 surface antigen Nhha polypeptide sequence.
```

```
XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.
KW Neisseria meningitidis strain Bz198.
OS
XX
FH Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..104 /label= V1
FT /note= "Variable region 1"
FT Region 105..116 /label= C2
FT /note= "Conserved region 2"
FT Region 117..126 /label= V2
FT /note= "Variable region 2"
FT Region 127..190 /label= C3
FT /note= "Conserved region 3"
FT Region 191..212 /label= V3
FT /note= "Variable region 3"
FT Region 213..231 /label= C4
FT /note= "Conserved region 4"
FT Region 232..238 /label= V4
FT /note= "Variable region 4"
FT Region 239..594 /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
PD 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09169.
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhha
XX from N. meningitidis strain Bz198 is 1 of 10 Nhha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
SQ Sequence 594 AA;
```

Query Match 97.6%; Score 2971; DB 22; Length 594;  
Best Local Similarity 98.0%; Pred. No. 2.9e-171;  
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVVVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
DB 1 mnkiyriiwsalnawvvvseltrnhtkrasatvatvatltilfatvganatdddddyle 60

QY 61 PVQRTAVVLSFRSDKEGTGEGEDSNWAVYFDEKRVLKAGAITLTKAGNLIKQNTNE 120  
DB 61 pvqrtavvlsfrsdegtgegedsnwavyfdekrvllkagaitlkgagdnlikq---- 116

QY 121 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
DB 117 ntentndssftysllkdltdltsveteklsfgangknvitsdtkglnfaketagtn 176

QY 181 PTVHLNGIGSTLTDLTLNTGATTNVTNDVTDDEKKRAASVKOVNLNAGWNIKGVPQTGA 240  
DB 177 ptvhlngigstltdlntgattntvndvtddekkraasvkdvlnagwnikgvpqgta 236

QY 241 SDNVDFVRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVLIKEKDKGLVTGKG 300  
DB 237 sdnvdfvrtvdtveflsadtktttvnveskdngkktvkiaktsvlikekdkglvtgkg 296

QY 301 DENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTITTTANGQTGQADKFETVTSCTKVFASGN 360  
DB 297 dengssddegeglvtakevidavnkaqwrmttttangqtgqadkfetvtsctnvtfasgk 356

QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
DB 357 gttatvskddqgnitvkydvnvgdalnvnglqnsqwnldskavagssgkvisgnvspsgk 416

QY 421 KMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSVDDGALNVGSK 480  
DB 417 kmdetvinagnnieitrngknidiaismtpofssvslgagadaptsvddgalnvgsk 476

QY 481 DANKPVRITNVAPGVKEGDTVNVQALKGVAQNLRNNDVNDGNARAGIAQAIATAGLAQA 540  
DB 477 dtnkpvrntnvapgvkegdtvntvaqlkgvaqnlrnrndvndgnaragiaqaiataglvqa 536

QY 541 YLPKGSMAIAGGTYRGEAGYAGYSSISDTGNVVIKGTASGNSRGHFGASASVGYQW 598  
DB 537 ylpqksmaiaaggdyrgeagyaygyssisdggnwilkgtasgnsrghfgasasvgyqw 594

RESULT 7  
AAV23740  
ID AAV23740 standard; Protein; 594 AA.  
XX  
AC AAV23740;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX

DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85792.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
XX Claim 1; Page 100-101; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 594 AA;

Query Match 93.8%; Score 2855; DB 20; Length 594;  
Best Local Similarity 94.8%; Pred. No. 2.9e-164;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVVVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
DB 1 mnkiyriiwsalnawvvvseltrnhtkrasatvatvatltilfatvgastdddddyle 60

QY 61 PVQRTAVVLSFRSDKEGTGEGEDSNWAVYFDEKRVLKAGAITLTKAGNLIKQNTNE 120  
DB 61 pvqrtavvlsfrsdegtgegedsnwavyfdekrvllkagaitlkgagdnlikqntne 120

QY 121 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
DB 121 ntne-----sftysllkdltdltsveteklsfgangknvitsdtkglnfakktacn 176

QY 181 PTVHLNGIGSTLTDLTLNTGATTNVTNDVTDDEKKRAASVKOVNLNAGWNIKGVPQTGA 240  
DB 177 tlvhlngigstltdlntgattntvndvtddekkraasvkdvlnagwnikgvpqgta 236

QY 241 SDNVDFVRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVLIKEKDKGLVTGKG 300  
DB 237 sdnvdfvrtvdtveflsadtktttvnveskdngkktvkiaktsvlikekdkglvtgkdk 296

QY 301 DENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTITTTANGQTGQADKFETVTSCTKVFASGN 360  
DB 297 dengssddegeglvtakevidavnkaqwrmttttangqtgqadkfetvtsctnvtfasgk 356

QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
DB 357 gttatvskddqgnitvkydvnvgdalnvnglqnsqwnldskavagssgkvisgnvspsgk 416

QY 421 KMDETVINAGNNIEITRNKNIDIAISMTPOFSSVSLGAGADAPTLSVDDGALNVGSK 480  
DB 417 kmdetvinagnnieitrngknidiaismtpofssvslgagadaptsvddgalnvgsk 476

QY 481 DANKPVRITNVAPGVKEGDTVNVQALKGVAQNLRNNDVNDGNARAGIAQAIATAGLAQA 540  
DB 477 dtnkpvrntnvapgvkegdtvntvaqlkgvaqnlrnrndvndgnaragiaqaiataglvqa 536

QY 541 YLPKGSMAIAGGTYRGEAGYAGYSSISDTGNVVIKGTASGNSRGHFGASASVGYQW 598  
DB 537 ylpqksmaiaaggdyrgeagyaygyssisdggnwilkgtasgnsrghfgasasvgyqw 594

RESULT 8  
AAV57044  
ID AAV57044 standard; Protein; 594 AA.  
XX  
AC AAV57044;  
XX  
DT 21-FEB-2000 (first entry)

xx BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
xx  
xx  
xx BASB029; Nisseria meningitidis; surface fibril protein; HSF; diagnosis;  
xx Infection; treatment; prevent; antibacterial drug.  
xx  
xx Nisseria meningitidis.  
xx  
xx  
xx Key Location/Qualifiers  
xx Misc-difference 104 /note= "Encoded by AATC"  
xx  
xx WO958683-A2.  
xx  
xx PD 18-NOV-1999.  
xx  
xx PF 07-MAY-1999; 99WO-EP03255.  
xx  
xx PR 13-MAY-1998; 98GB-0010276.  
xx (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
xx PA Ruelle J;  
xx  
xx  
xx WPI; 2000-053103/04.  
xx N-PSDB; AA239864.  
xx  
xx New polypeptide from neisseria meningitidis useful for diagnosis,  
xx treatment or prevention of bacterial infections in mammal -  
xx  
xx Claim 4; Fig 2; 74pp; English.  
xx  
xx This is the Nisseria meningitidis BASB029 amino acid sequence from  
xx serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
xx Haemophilus influenzae surface fibril (HSF) protein. The invention  
xx relates to BASB029 polynucleotide sequences (AA239864-239865) and  
xx polypeptide sequences (AA239864-239865) and their immunogenic fragments.  
xx BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
xx meningitidis infection in a mammal. Compositions containing a Neisseria  
xx polynucleotides and polypeptides are useful for generating an immune  
xx response in an animal. A therapeutic composition comprising an antibody  
xx directed against BASB029 is useful in treating humans with Neisseria  
xx meningitidis disease. The polynucleotide is useful in the diagnosis of  
xx the stage of infection, type of infection, susceptibility to an  
xx infection which results from increased or decreased expression of the  
xx polynucleotide, and for therapeutic or prophylactic purposes.  
xx particularly genetic immunisation. Antibodies against BASB029  
xx polynucleotides and polypeptides are also useful for treating infections  
xx particularly bacterial infections. The protein is useful in the  
xx screening and development of antibacterial drugs. Fused recombinant  
xx protein is useful for the stimulation of the immune system of an organism  
xx receiving the protein.  
xx  
xx SQ Sequence 594 AA;  
  
Query Match 93.8%; Score 2855; DB 21; Length 594;  
Best Local Similarity 94.6%; Pred. No. 2.9e-164;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;  
  
QY 1 MNKIYRIIWSALNAWVVSSELNRHTKRASATVAVATVATLTLFATVQANATDDDLYLE 60  
Db 1 mnkiyriiwsalnawvvsselelrhtkrasatvatvatvatllfatvqastdddlyle 60  
  
QY 61 PVQRTAVLSFRSDKEGTGEBKEDSNNAVYFDEKRVKAGAITLKAGDNLKIKQNTNE 120  
Db 61 pvqrtavlsfrsdkegtgekedtsnwgvyfdkkgvltagtitlkagdnlikqntne 120  
  
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNPAKETAGTNGD 180  
Db 121 ntne----ssftyssllkddltldtsvteklfsfnsankvnitsdtkglnfakktatngd 176  
  
QY 181 PTVHLNGIGSTLTDTLLNTCATTNVTNDNVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 240

Db 177 ttvhlngigstltdtllntgattnvtndnvtddkkraasvkvlnagwnkvgkpgtta 236  
QY 241 SDNVDFVRYDYVEFLSADTKTTTVNVESKDNGKTEVKIGAKTSYIKEKDGKLVTKGKG 300  
Db 237 sdnvdfvrydytveflsadtktttvneskdngkrtvkvigaktsvikekdgklvtgkdk 296  
QY 301 DENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTTANGOTQADKFEVTSVGTGKVTFASGN 360  
Db 297 gendstdekgeglvtakevidavnkagwrmttttangotqadkfevtsvgtntvtfasgk 356  
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNMLDSKAVAGSSGKVISGNVSPSKG 420  
Db 357 gttatvskddqgnitvmydvnvgdalnvnlqnsqwnldskavagesgkvisgnvpskg 416  
QY 421 KMDETVNNAGNIEITRNCKNIDTATSPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
Db 417 kmdetvnnagnieitrncknidatstmpqfssvslgagadaptlsvddegalnvgsk 476  
QY 481 DANKPVRITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNDGNARAGIAQAIATAGLAQA 540  
Db 477 dankpvrithvapgvegdvtnvaqlkgvaqnlhndndgnaragiaqaiataglvqa 536  
QY 541 YLPKCSMAIIGGTYRGEAGYAIQYSSISDTGNWIKGTASGNSRHFASASVGYQW 598  
Db 537 ylpkcsmaiaiggtyrgeagyaiqyssisdggnwikgtasgnsrghfgasasvgyqw 594  
  
RESULT 9  
AAU06174  
ID AAU06174 standard; Protein; 594 AA.  
XX  
AC AAU06174;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.  
XX  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain EG327.  
XX  
FH Key Location/Qualifiers  
FT Region 1..50 /label= C1  
FT /note= "Conserved region 1"  
FT Region 51..104 /label= V1  
FT /note= "Variable region 1"  
FT Region 105..116 /label= C2  
FT /note= "Conserved region 2"  
FT Region 117..126 /label= V2  
FT /note= "Variable region 2"  
FT Region 127..190 /label= C3  
FT /note= "Conserved region 3"  
FT Region 191..212 /label= V3  
FT /note= "Variable region 3"  
FT Region 213..231 /label= C4  
FT /note= "Conserved region 4"  
FT Region 232..238 /label= V4  
FT /note= "Variable region 4"  
FT Region 239..594 /label= C5  
FT /note= "Conserved region 5"  
XX  
PN WO200155182-A1.  
XX

PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-AU00069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Peak IRA, Jennings MP;  
XX  
XX WPI; 2001-488774/53.  
DR N-PSDB; AAS09164.  
XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 9lpp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
SQ Sequence 594 AA;

Query Match 93.8%; Score 2855; DB 22; Length 594;  
Best Local Similarity 94.6%; Pred. No. 2.9e-164;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

Qy 1 MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDLYLE 60  
Db 1 mnkyriiwnsalnawvavseltrnhtkrasatvatavlatlilfatvqastdddlyle 60

Qy 61 PVORTAVVLSFRSDKEGTEGSDSNWVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
Db 61 pvqrtavvlsfrsdsdkegtevedsnwgyfdkkgvltagtitlkagdnlikqntne 120

Qy 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180  
Db 121 ntntentndssftyslkkdltltsveteklsfgangkvnitstdkglnfaketagtngd 180

Qy 181 PTVHLNGIGSTLTDTLNLGATVNTVNDVTDDEKKRAASVKDVLNAGWNKGVKPGPTA 240  
Db 177 ttvhlngigstltdtlnlgatvntvndvtddekkraasvkdvlagnagwnkvgkpgpta 236

Qy 241 SDNVDFVETVDTVEFLSADTTVTNNVESKDKGKTEVKIGAKTSVKEKGKLVTKGK 300  
Db 237 sdnvdfvetydtveflsadtvttnveskdngkrtevkigaktsvkekgkltvkgkd 296

Qy 301 DENGSSDDEGELVTAKEDVAVNKAQWRMKTITANGOTQADKPFETVTSKTVTFASGN 360  
Db 297 gendssdkgelvtakeidavnkagwrmtttangotqadkfetvtsgtntvtfasgk 356

Qy 361 GTTATVSKDDGNTVTKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVTSGNVSPSKG 420  
Db 357 gttatvskddgntvmydvnvgdalnvqnqlnsgwnldskavagsgkvtsgnvspsgk 416

Qy 421 KMDETVNIACNNEITRNGKNIDIASMTPOFSSVSIGACADAPTLISVDDEGALNVCSK 480  
Db 417 kmdecvlnagnneitrngknidiasmtppfssvsigadadaptlisvdddegalnvcsk 476

Qy 481 DANKPVRITNVPAGVKEGDTNVAQLKGVAQNLRNIDVNGNRAGIAQAIATAGLAQA 540  
Db 477 dankpvrtnvapgvkegdvtnvaqlkgvaqnlhndvngnragiaqaiataglvqa 536

Qy 541 YLPKSMMAIGGGTYRGAGYAIGYSSISDTGNNVWIKTAGSNGSRGHFGASGVQYW 598  
Db 537 ylpgksmmaigggtyrgeagyaigyssisdggnwiikgtasngsrghfgasvgyqw 594

RESULT 10  
AAV23743  
ID AAY23743 standard; Protein; 599 AA.  
XX  
XX AAY23743;  
XX AC  
XX 08-SEP-1999 (first entry)  
XX DT  
XX DE  
XX A surface protein of Neisseria meningitidis.  
XX KW  
XX Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX OS  
XX Neisseria meningitidis.  
XX PN  
XX WO9931132-A1.  
XX PD  
XX 24-JUN-1999.  
XX PF  
XX 14-DEC-1998; 98WO-AU01031.  
XX PR  
XX 12-DEC-1997; 97GB-0026398.  
XX PA  
XX (ISIS-) ISIS INNOVATION LTD.  
XX PA  
XX (UYQU ) UNIV QUEENSLAND.  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
XX  
XX WPI; 1999-418754/35.  
XX DR  
XX N-PSDB; AAX85795.  
XX  
XX Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections  
XX  
XX Claim 1; Page 114-115; 132pp; English.  
XX  
XX The present sequence represents a surface protein of Neisseria  
XX meningitidis which is approximately 62 kDa. The N. meningitidis  
XX surface glycoproteins, nucleic acids, the primers and optionally  
XX a thermostable polymerase, or antibodies are useful in a kit for  
XX the detection or diagnosis of N. meningitidis infection in humans.  
XX CC  
XX The N. meningitidis surface glycoproteins can also be used to  
XX prevent or treat N. meningitidis infection in humans, especially  
XX in the form of vaccines. The proteins and antibodies can also  
XX be used to identify immunoreactive peptides.  
XX  
XX Sequence 599 AA;

Query Match 92.8%; Score 2824.5; DB 20; Length 599;  
Best Local Similarity 92.7%; Pred. No. 2e-162;  
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

Qy 1 MNKYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLYL 59  
Db 1 mnkyriiwnsalnawvavseltrnhtkrasatvatavlatlilfatvqanattede 60

Qy 60 EPVORTAVVLSFRSDKEGTEGSDSNWVYFDEKRVLKAGAITLKAGDNLKIKQNTN 119  
Db 61 epvortavvlsfrsdsdkegtevedsnwgyfdkkgvltagtitlkagdnlikqntn 120

Qy 120 ENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNG 179  
Db 121 knntentndssftyslkkdltltsveteklsfgangkvnitstdkglnfaketagtn 180

Qy	180	DPTVHLNGIGSTLTDFLLNTGATTNTVNDNVDTDEKKRAASVKDVLNAGWNKIGVKPGTT	230
Db	181	dtvhlngigstltdtllntgattntdntdtkkkraasvkdvlnagwnikgvpkpgtt	240
Qy	240	ASDNVDFRIVDYVEFLSADTKTTTVNVESKDKGKTEVKIGAKTSVIEKEKDGKLVTKGK	299
Db	241	asdnvdfvhtydtveflsadtktttvnveskdngkrtvdkigaktsvikedgklvtgk	300
Qy	300	KDENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKPETVTSGTFTVTFASG	359
Db	301	kgengsdsdegeglvtakevidavnnkagwrmtktangtqgadtetvtsgtntvtfasg	360
Qy	360	NGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGNWLDLSKAVAGSSGKVIISGNVSPSK	419
Db	361	kgttatvskddqgnitvkymvnygdalnvnyqlnsgwnldskavagssgkvisgnvpsk	420
Qy	420	GKMDETVINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTLISVDDGALNVGS	479
Db	421	gkmdetvniinagnietrngknidatmtptqfssvslgagadaptlisvddkgaInvgs	480
Qy	480	KDANKPVRITNPAPGVKEGSDVTINVAQLKGVAQNLNLRIDNVGDNARAGTAQAIATAGLAQ	539
Db	481	kdanpvrithnvaagvkegdvtnvaqlkgvaqnlrindvndgnaragiataglvq	540
Qy	540	AYLPCKSMAIGGTYRGRENGYAIGYSSISDTONWIKGTASNSRGHFCASASGVGYQW	598
Db	541	aylpcksmiaiggtyrgeagyaigysisidgnwilkgtasnsrghfgasvgyqw	599
RESULT 11			
AAU06176			
ID	AAU06176 standard; Protein: 599 AA.		
XX	AAU06176;		
XX	24-OCT-2001 (first entry)		
DE	N. meningitidis H38 surface antigen NhhA polypeptide sequence.		
KW	Surface antigen NhhA; meningococcal disease; meningitis vaccine.		
OS	Neisseria meningitidis strain H38.		
FH	Key	Location/Qualifiers	
FT	Region	1..50	
FT		/label= C1	
FT		/note= "Conserved region 1"	
FT	Region	51..105	
FT		/label= V1	
FT		/note= "Variable region 1"	
FT	Region	106..117	
FT		/label= C2	
FT		/note= "Conserved region 2"	
FT	Region	118..131	
FT		/label= V2	
FT		/note= "Variable region 2"	
FT	Region	132..195	
FT		/label= C3	
FT		/note= "Conserved region 3"	
FT	Region	196..217	
FT		/label= V3	
FT		/note= "Variable region 3"	
FT	Region	218..236	
FT		/label= C4	
FT		/note= "Conserved region 4"	
FT	Region	237..243	
FT		/label= V4	
FT		/note= "Variable region 4"	
FT	Region	244..599	
FT		/label= C5	
FT		/note= "Conserved region 5"	
XX			

PN	WO200155182-A1.	
XX		
PD	02-AUG-2001.	
XX		
PF	25-JAN-2001; 2001WO-AU00069.	
XX		
PR	25-JAN-2000; 2000US-0177917.	
XX		
PA	(UYQU ) UNIV QUEENSLAND.	
XX		
PI	Peak IRA, Jennings MP;	
XX		
DR	WPI; 2001-488774/53.	
DR	N-PSDB; AAS09166.	
XX		
PT	New Nhha surface antigen polypeptides and polynucleotides from	
PT	Neisseria meningitidis, useful in producing vaccines for treating or	
PT	preventing broad spectrum of Neisseria meningitidis -	
XX		
PS	Claim 9; Fig 1; 91pp; English.	
XX		
CC	The present invention relates to the isolation of novel Neisseria	
CC	meningitidis mutant polypeptides of the surface antigen Nhha	
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are	
CC	characterised by deletions of non-conserved amino acids, particularly	
CC	the deletion of variable regions. The deletion mutants are useful in	
CC	diagnostics, therapeutic and prophylactic vaccines against a broader	
CC	spectrum of N. meningitidis, and in designing and/or screening of	
CC	medicaments. The mutant proteins when used as a vaccine can effectively	
CC	immunise against a broader spectrum of N. meningitidis strains than	
CC	would be expected from a corresponding wild-type surface antigen.	
CC	The present sequence representing the wild type surface antigen Nhha	
CC	from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences	
CC	(AAU06171-AAU06180) from 10 different N. meningitidis strains given in	
CC	the present invention.	
XX		
SO	Sequence 599 AA;	

Query Match	92.8%	Score	2824.5	DB	22	Length	599
Best Local Similarity	92.7%	Pred. No.	2e-162				
Matches	555	Conservative	14	Mismatches	29	Indels	1
Qy	1	MNKYIRIIWNSALNAWVVS	ELTRNTHKRASATVATAVLATILFATVQANATD-DDDLYL	59			
Db	1	mnkYIRIIwNsAlNaWvVs	elTrnThKraSAtVaTAVLaTILfATvQANaTdDeDeeEl	60			
Qy	60	EPVQRTAVVLFSRDSKEGTEKEDTSNVAWYFDEKRVLLKAGAILTKAGDNLKIQTNT	119				
Db	61	epvQrSaLvlfqfMidkeGneGeStgnIgwSlyDhnhTlghAtvTlKagDnIkKqTnT	120				
Qy	120	ENTNENTNDSFTYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTAC	179				
Db	121	kntnEntnDnSfTysllKdLlDlTsVeTeKlSfGangKnViTsDtkGlnfAkEtAgTgn	180				
Qy	180	DPTVHLNGIGSTLTDLTLTGATNTVNTDNTDDEKRAASVKDVLNAGWNILGKVPGCTT	239				
Db	181	dPtVhLNgIGStLdTLtLTgATnTvNTdNtDdEkRaaSvKdVlNAGWnIlGkVpGcTt	240				
Qy	240	ASDNVDFYRTYDTVEFLSADTKTTTVNVYESKDNGKTEKVIKAKTSVLEKDGKLVTKGK	299				
Db	241	asDnVdfYrtYdtVeflSadtKttTvNvYeSkDngKrtEvIkAgKtsvIkEdgKlvtGkG	300				
Qy	300	KDENGSSDTDEGGLYTAKEVIDAVNKAQWRMKTTTANGQTQADQKFEVTVSGTKVTFASG	359				
Db	301	kGengSsdTeGglYtAkEviDavnKaqWrMkTtTANGqtQAdQkFevTtVsgTkVtFasG	360				
Qy	360	NGTTFATVSKDDQGNITTVKYDYNVGDALNVNOLONSGWNLDSKAVAGSSGKVIYSIGNVSPSK	419				
Db	361	NgTtFAtvSkDdQgnItTvKyDyNvgDaLnvNqLqngSgWnlDsKavAgSsgKviYsgNvSpSk	420				
Qy	420	GKMDETVMINAGNNIEITIRNGKNIDIAITSMTPQFSSSVSLGAGADAPTLVSDDGELNNGVS	479				

Db 421 gkmdetvnaagnnieitrngkndiatmtppqfssvslgagadaptilsvddkgalnvgs 480  
Qy 480 KDANKPVRITNVAPGVKGGDVTNVAQLKGVAQNLNRRIDNDGNARAGIAQAIATAGLAQ 539  
Db 481 kdankpvrinvapgvkgegdvtnvaqlkgvagnlnrindvndgnaragiataglvq 540  
Qy 540 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDPTGNMVIKGTASGNSRHFSGASVGYQW 598  
Db 541 aylpgksmmaigggtyrgeagyaigyssisdggnwlikgtasgnrghfsgasvgyqw 599

## RESULT 12

AA57045  
ID AAY57045 standard; Protein; 591 AA.

AC AAY57045;

XX 21-FEB-2000 (first entry)

DT BASB029 amino acid sequence from N. meningitidis strain H44/76.

DE BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.

XX OS Neisseria meningitidis.

XX Key Location/Qualifiers

FT Misc-difference 90 /note= "Encoded by AAT"

FT Misc-difference 92 /note= "Encoded by GAT"

FT Misc-difference 98 /note= "Encoded by AAC"

FT Misc-difference 108 /note= "Encoded by AATC"

FT Misc-difference 123 /note= "Encoded by ACA"

FT Misc-difference 269 /note= "Encoded by AAA"

FT Misc-difference 389 /note= "Encoded by CGT"

XX WO9958683-A2.

XX 18-NOV-1999.

XX 07-MAY-1999; 99WO-EP03255.

XX 13-MAY-1998; 98GB-0010276.

XX (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX Ruelle J;

XX WPI; 2000-053103/04.

XX N-PSDB; AAZ39865.

PT New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -

XX Claim 4; Fig 2; 74pp; English.

XX This is the Neisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain H44/76. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-239865) and  
CC polypeptide sequences (AAY57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of

CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.

XX Sequence 591 AA;

Query Match 89.9%; Score 2735.5; DB 21; Length 591;

Best Local Similarity 91.4%; Pred. No. 4.5e-157;

Matches 550; Conservative 9; Mismatches 28; Indels 15; Gaps 4;

Qy 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVATVATLALLFATVQANATD---DDDL 57

Db 1 mnkiyriiwsalnawvavseltrnhtkrasatvktavltilfatvqasannee 60

Qy 58 YLEPQRTAVVLSPRSDEKTEGTEGECT-EDSNWAVYFDEKRVLRKAGATLKGADNLKIKQ 116

Db 61 yldpqvrtvavlivnsdkegveednwavfyfdekvltareitlkgadnlkikq 120

Qy 117 NTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNFAKETAG 176

Db 121 -----ngsnftyslkkdltdltsvgteklsfsangknvnitsdtkglnfaketag 170

Qy 177 TNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNKIGVKP 236

Db 171 tngdptvhlingigstltdllntgattntvndvtddekkraasvkdvl Nagwnikgvpk 230

Qy 237 GTTASDNVDFVRYTDTVEFLSADTKTITVNVESKDNGKTEVKIGAKTSVKEKDKLVT 296

Db 231 gttasdnvdfvrytdtveflsadtktttvnnveskdngkrtevkigaktsvikekdglvt 290

Qy 297 CKGKDENGSSDDEGEGLVTAKEVIDAVNKGWRMKTNTTANGQTGOADKFETVTSKVTVF 356

Db 291 gkdgengsstdegeglvtakevidavnnkgwrmtnttangtqgdkfetsgtntvf 350

Qy 357 ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGNWLDKAVAGSGSKVTSGNVS 416

Db 351 asggttatvskddggnitvmydvngdalnvnglqnsngwldskavagsgskvtsngvns 410

Qy 417 PSKGMDETVAINAGNNIEITRNGKNIDIAISMTPOFSSVSLGACADAPTILSVDDGALN 476

Db 411 pskgmdetvnaingnnieitrngknidiatmtppqfssvslgagadaptilsvdgd-aln 469

Qy 477 VGSKDANKPVRITNVAPGVKGGDVTNVAQLKGVAQNLNRRIDNDGNARAGIAQAIATAG 536

Db 470 vgskdankpvrinvapgvkgegdvtnvaqlkgvagnlnrindvndgnaragiatag 529

Qy 537 LAQAYLPKSMMAIGGGTYRGEAGYAGYSSISDPTGNMVIKGTASGNSRHFSGASVGY 596

Db 530 lvqaylpksmmaigggtyrgeagyaigyssisdggnwlikgtasgnrghfsgasvgy 589

Qy 597 QW 598

Db 590 qw 591

## RESULT 13

AA57202  
ID AAY27202 standard; Protein; 591 AA.

XX AAY27202;

XX 24-SEP-1999 (first entry)

XX Amino acid sequence of N. meningitidis protein ORF40-1.

XX Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;

KW bacterial infection; treatment.

OS Neisseria meningitidis.

PN WO9936544-A2.

XX 22-JUL-1999.

XX 14-JAN-1999; 99WO-IB00103.

XX 09-OCT-1998; 98GB-0022143.

PR 14-JAN-1998; 98GB-0000760.

PR 01-SEP-1998; 98GB-0019015.

XX (CHIR-) CHIRON SPA.

XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;

XX WPI; 1999-444400/37.

DR N-PSDB; AAX99124.

XX New protein and its nucleotide sequence, useful in vaccines or

PT diagnostic compositions for treating and/or preventing Neisseria

PT meningitidis infections

XX Claim 1; Page 62; 123pp; English.

PS The invention provides proteins (AAY27201-245) from Neisseria

CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)

CC encoding the proteins. Compositions comprising the protein, nucleic acid

CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a

CC vaccine composition or a diagnostic composition. The composition is also

CC useful for treating or preventing an infection due to Neisseria

CC bacteria, especially Neisseria meningitidis.

XX SQ Sequence 591 AA;

Query Match 89.5%; Score 2725.5; DB 20; Length 591;  
Best Local Similarity 91.0%; Pred. No. 1.8e-156;  
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

QY 1 MNKIYRIIWNLSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57

Db 1 mnkiyriiwnsalnawvvsselftrnhtrkrasatvktavlallfatvqasanneegee 60

QY 58 YLEPVORTAVVLSFRSDKEGTGKEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116

Db 61 yldpvqrtvavlivnsdkegtgekeveensdwavfnekgvitareititlkagdnikikq 120

QY 117 NTNENTNENTNDSFYSLSKKDLTDLTSVETEKLSFGANGKNYNTSDTKGLNFAKETAG 176

Db 121 -----ngcnfyslskdltdltsvgtelksisangknvntsdtkglnfaketag 170

QY 177 TNGDPTVHLNGIGSTLDTLLNTGATNTVNDVNDDEKRAASVDKDLNAGNNIKGVKP 236

Db 171 tngdptvhlngigstltdlntgattvndvnddtkraasvdkvlnagwnikgvkp 230

QY 237 GTTASNVDVRYDVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVIREKDKGLYT 296

Db 231 gttasndvdfvrydveflsadtktttvnveskdngkktvkgaktsvirekdkglvt 290

QY 297 GKKGDENGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFTVTSKTVTF 356

Db 291 gkgdengsstdegeglvtakevldavnkagwrmtktntangqtdgdkftvtsktnvtf 350

QY 357 ASGNGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGNWLDLSKAVAGSSGKVISGNVS 416

Db 351 asggtatvskddqgnitvmydvngdnlvnlqnsqwnldskavagssgkvisgnvs 410

QY 417 PSKGKMDETVNIWAGNNIETRNKINIDATSMTPQFSSVSLGAGADAPTLSDVEGALN 476

Db 411 pskgkmdetvniwagnniettrngknidatsmtpqfssvslgagadaptsldvgd-aln 469

QY 477 VGSKDANKPVRITNVAPGVKEGDTNVNVAOLKGVAQNLNRRIDNVGNNARAGIAQALATAG 536

Db 470 vsgkdnkpvritnvapgvkegdvtnvaqlkgvaqnlrridnvgnaragiagialatag 529

QY 537 LAQAYLPKGSMMMAIGGTYRGEAGYAIQYSSISDGTGNWVIKGTASGNSRHFASASVGY 596

Db 530 lvqaylpqksmmaiggytyrgeagyaigyssisdggnwniikgtasngsrhfgasasvgy 589

QY 597 QW 598

Db 590 qw 591

RESULT 14

AAY23746

ID AAY23746 standard; Protein; 591 AA.

XX AAY23746;

DT 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

DE Surface protein; surface glycoprotein; infection; vaccine;

KW immunoreactive peptide.

OS Neisseria meningitidis.

PN WO99311132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

XX (YUQU ) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

DR WPI; 1999-418754/35.

DR N-PSDB; AAX85798.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

PS Claim 1; Page 127-128; 132pp; English.

XX The present sequence represents a surface protein of Neisseria

CC meningitidis which is approximately 62 kDa. The N. meningitidis

CC surface glycoproteins, nucleic acids, the primers and optionally

CC a thermostable polymerase, or antibodies are useful in a kit for

CC the detection or diagnosis of N. meningitidis infection in humans.

CC The N. meningitidis surface glycoproteins can also be used to

CC prevent or treat N. meningitidis infection in humans, especially

CC in the form of vaccines. The proteins and antibodies can also

XX be used to identify immunoreactive peptides.

Query Match 89.5%; Score 2725.5; DB 20; Length 591;  
Best Local Similarity 91.0%; Pred. No. 1.8e-156;  
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

QY 1 MNKIYRIIWNLSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57

Db 1 mnkiyriiwnsalnawvvsselftrnhtrkrasatvktavlallfatvqasanneegee 60

QY 58 YLEPVORTAVVLSFRSDKEGTGKEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116

Db 61 yldpvqrtvavlivnsdkegtgekeveensdwavfnekgvitareititlkagdnikikq 120

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Db 61 yldpqrvtavvlvnsdkegtgekeveensdwavyfnekvgiltareitlkagdnklkq 120
QY 117 NTNENTNENTNDSFYSYSLKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKETAG 176
Db 121 -----ngcnfyslkkdltdltsvgtelksfsangknvntsdtkglnfaketag 170
QY 177 TNGDPTVHLNGIGSTLTLTNTGATTVNTNDVDEKKRAASVKDVLNAGWNIGVKVP 236
Db 171 tngdtvhlngigstltdtllngattnvndvntddekkrasvkdvlvlnagwnikgvp 230
QY 237 GTTASDNVDFRYDYVDFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVIERKDGKLV 296
Db 231 gttasdnvdfrydyvdfelsadtktttvnvveskdnkgktevkgikgtsviekdgk 290
QY 297 GKGDENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGOTGOADKFEVTSVSGTKV 356
Db 291 gkdgengsstdegeglvtakevidavnkagwrmttftangotgoadkfevtsvsgt 350
QY 357 ASGNGTTATVSKDDQGNITVKYDYNVGDALNVQLNSGWNLDKSAVAGSGKVISGNVS 416
Db 351 asgngttatvskddqgnitvmydvnygdalnvnyqlnsgwnldskavagsgkvisgn 410
QY 417 PSKGKMDETVINAGNIEITRNGKNIDTATSMTPQSFSSVSLGAGADAPILSVDDGALN 476
Db 411 pskgkmdetvinagnieitrngknidatmtptqsfssvslgagadaptilsvdgd- 469
QY 477 VGSKDANKPVRITNVAPVKEGDTNVNAQLKGVAQNLNNRDNVDGNARAGIAQAIATAG 536
Db 470 vgskkdkpvrtnvapvkegdvtnvaqlkgvaqnlnnrldvndgnaragiqaiatag 529
QY 537 LAQAYLPKSMMAIGGTGTYRGEAGYAIYSSISDTGNWVIGKTASGNSRGHFGASASVGY 596
Db 530 lvqaylpkgsmmaiggtgyrgeagyaigyssisdggnwvliktasgnsrghfgasavgy 589
QY 597 QW 598
Db 590 qw 591

RESULT 15
AAU06171
ID AAU06171 standard; Protein; 591 AA.
AC
XX AAU06171;
XX
XX 24-OCT-2001 (first entry)
XX
XX N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
DE Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX
XX Neisseria meningitidis strain PMC21.
XX
FH Key Location/Qualifiers
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FT Region 1..50
FT /label= Signal_peptide
FT /note= "Conserved region 1"
FT Region 51..108
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..108
FT /label= V1
FT /note= "Variable region 1"
FT Protein 52..591
FT /label= Mature_Nhha
FT /note= "Predicted mature protein, specifically claimed in claim 12"
FT Region 109..120
FT /label= C2
FT /note= "Conserved region 2"
FT Region 121..124
FT /label= V2
FT /note= "Variable region 2"
FT Region 125..188
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FT 189..210
FT /label= V3
FT /note= "Variable region 3"
FT 211..229
FT /label= C4
FT /note= "Conserved region 4"
FT 230..236
FT /label= V4
FT /note= "Variable region 4"
FT 237..591
FT /label= C5
FT /note= "Conserved region 5"
XX
XX WO200155182-A1.
PN
XX
XX 02-AUG-2001.
PD
XX
XX 25-JAN-2001; 2001WO-AU00069.
PF
XX
XX 25-JAN-2000; 2000US-0177917.
PR
XX
XX (UYQU ) UNIV QUEENSLAND.
PA
XX
XX Peak IRA, Jennings MP;
PI
XX
XX WPI: 2001-488774/53.
DR
XX
XX N-PSDB; AAS09161.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
PT Neisseria meningitidis, useful in producing vaccines for treating or
PT preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhha
XX from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
XX Sequence 591 AA;
```

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Query Match 89.5%; Score 2725.5; DB 22; Length 591;
Best Local Similarity 91.0%; Pred. No. 1.8e-156;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;
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QY 1 MNKIYRIWNSALNAWVVSSELTRNHTKRASATVATVATLFLFATVQANATD---DDDL 57
Db 1 mnkiyriwnsalnawvvsseltrnhtrkrasatvktavlatlflfatvqasannee 60
QY 58 YLEPVQRTAVVLSFRSDKEGTGEKGTED-SNWAVYFDEKRVLKAGATTLKAGDNLKIKQ 116
Db 61 yldpvqrtavvlvnsdkegtgekeveensdwavyfnekvgiltareitlkagdnklkq 120
QY 117 NTNENTNENTNDSFYSYSLKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKETAG 176
Db 121 -----ngtnftyslkkdltdltsvgtelksfsangknvntsdtkglnfaketag 170
QY 177 TNGDPTVHLNGIGSTLTLTNTGATTVNTNDVDEKKRAASVKDVLNAGWNIGVKVP 236
Db 171 tngdtvhlngigstltdtllngattnvndvntddekkrasvkdvlvlnagwnikgvp 230
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QY 237 GTTASDNVDFVRTYDTVEFLSADTKTTTVNBSKDNKGKTEVKIGAKTSVIKEKDGKLV 296  
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QY 297 GKGDENGSTDEGGLVTAKEVIDAVNKAQNMKTATTANGQTQADKFETVTSGTKVTF 356  
Db 291 gkdkgengstdeglvtakevidavnkagwrmktttanggtgqadkfetvtsgtnvtf 350  
QY 357 ASGNGTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNLDSKAVAGSSGKVISGNVS 416  
Db 351 asgkgctatvskddqgnitvmydvnvvgdalnvnqlqnsqwnldskavagssgkvisgnvs 410  
QY 417 PSKGMDETVNINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSVDDGALN 476  
Db 411 pskgmde tvn in agnn iettrng knidiat smtpqfssvslgagadap t lsvdgd- aln 469  
QY 477 VGSKDANKPVRTNAPGVKEGDTNVAQLKGVAQNLNNRIDNVGNARAGIAQAIATAG 536  
Db 470 vgskkdnkpvr itnvapgvkegdvtnvaqlkgvaqnl n nridnvgnarag iaqaiatag 529  
QY 537 LAQAYLPGKSMMAIGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRCHFGASASVGY 596  
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QY 597 QW 598  
Db 590 qw 591

Search completed: July 3, 2002, 08:36:22  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:31:34 ; Search time 39.66 Seconds  
(without alignments)  
368.293 Million cell updates/sec

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Perfect score: 3044  
Sequence: 1 MNKYRIIWSALNAWVVS.....TASGNSRGHFGASASVGVQW 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Issued\_Patents\_AA:\*

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- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/iaa/PTUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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2	3044	100.0	598	4	US-09-669-974-13
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5	2971	97.6	594	4	US-09-377-155-7
6	2971	97.6	594	4	US-09-669-974-7
7	2855	93.8	594	4	US-09-377-155-9
8	2855	93.8	594	4	US-09-669-974-9
9	2824.5	92.8	599	4	US-09-377-155-15
10	2824.5	92.8	599	4	US-09-669-974-15
11	2725.5	89.5	591	4	US-09-377-155-21
12	2725.5	89.5	591	4	US-09-669-974-21
13	2718	89.3	592	4	US-09-377-155-2
14	2718	89.3	592	4	US-09-669-974-2
15	2706.5	88.9	591	4	US-09-377-155-11
16	2706.5	88.9	591	4	US-09-669-974-11
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21	1318.5	43.3	2353	4	US-09-377-155-33
22	1318.5	43.3	2353	4	US-08-913-942-4
23	1318.5	43.3	2353	4	US-09-669-974-33
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45	712	23.4	1104	4	US-09-268-347-28	Sequence 28, Appli

## ALIGNMENTS

## RESULT 1

US-09-377-155-13  
; Sequence 13, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-13

Query Match 100.0%; Score 3044; DB 4; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.9e-238;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	121	NTNENTNDSFTYSLKKDLTDLTTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD	180
Qy	181	PTVHLNGIGSTLTLLNTGATTNVTNDNVTDDEKRAASVKDVLNAGWNIGKVGPGTTA	240
Db	181	PTVHLNGIGSTLTLLNTGATTNVTNDNVTDDEKRAASVKDVLNAGWNIGKVGPGTTA	240
Qy	241	SDNVDFVRTYDTVFELSDADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGKG	300
Db	241	SDNVDFVRTYDTVFELSDADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGKG	300
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Db 301 DENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSKVTTFASGN 360  
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Db 361 GTTATVSKDDOGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKG 420  
QY 421 KMDETVNIAGNNIETIRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
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Db 481 DANKPVRITNAPGVKEGDVTNVAOLKGAQNLRNDRIDNVGNARAGIAQAATATAGLAQA 540  
QY 541 YLPKSMMAIGGTYRGEAGYAGYSSISDTGNWIKGTASGNSRGHFGASASVGYQW 598  
Db 541 YLPKSMMAIGGTYRGEAGYAGYSSISDTGNWIKGTASGNSRGHFGASASVGYQW 598

## RESULT 2

US-09-669-974-13  
; Sequence 13, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-13

Query Match 100.0%; Score 3044; DB 4; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.9e-238;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWSALNAWVYVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWVYVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTGEKGTEDSNWYVDFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTGEKGTEDSNWYVDFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
QY 181 PTVHLNGIGSTLTDPLLTGATTNTVNDTDEKRAASVKDVLNAGNINIKVPGTGA 240  
Db 181 PTVHLNGIGSTLTDPLLTGATTNTVNDTDEKRAASVKDVLNAGNINIKVPGTGA 240  
QY 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKTEVKIGAKTSVIREKDKLVTGRGK 300  
Db 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKTEVKIGAKTSVIREKDKLVTGRGK 300  
QY 301 DENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSKVTTFASGN 360  
QY 301 DENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSKVTTFASGN 360

Db 301 DENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSKVTTFASGN 360  
QY 361 GTTATVSKDDOGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKG 420  
Db 361 GTTATVSKDDOGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKG 420  
QY 421 KMDETVNIAGNNIETIRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
Db 421 KMDETVNIAGNNIETIRNGKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 481 DANKPVRITNAPGVKEGDVTNVAOLKGAQNLRNDRIDNVGNARAGIAQAATATAGLAQA 540  
Db 481 DANKPVRITNAPGVKEGDVTNVAOLKGAQNLRNDRIDNVGNARAGIAQAATATAGLAQA 540  
QY 541 YLPKSMMAIGGTYRGEAGYAGYSSISDTGNWIKGTASGNSRGHFGASASVGYQW 598  
Db 541 YLPKSMMAIGGTYRGEAGYAGYSSISDTGNWIKGTASGNSRGHFGASASVGYQW 598

## RESULT 3

US-09-377-155-5  
; Sequence 5, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-5

Query Match 99.2%; Score 3021; DB 4; Length 598;  
Best Local Similarity 99.3%; Pred. No. 3.6e-236;  
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWSALNAWVYVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWVYVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTGEKGTEDSNWYVDFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTGEKGTEDSNWYVDFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
QY 181 PTVHLNGIGSTLTDPLLTGATTNTVNDTDEKRAASVKDVLNAGNINIKVPGTGA 240  
Db 181 PTVHLNGIGSTLTDPLLTGATTNTVNDTDEKRAASVKDVLNAGNINIKVPGTGA 240  
QY 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKTEVKIGAKTSVIREKDKLVTGRGK 300  
Db 241 SDNVDFVRYDTVEFLSADTKTTTVNVESKONGKKTEVKIGAKTSVIREKDKLVTGRGK 300  
QY 301 DENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSKVTTFASGN 360  
Db 301 DENGSTDEGGLVTAKEVIDAVNKAGWRMKTTTANGOTGQADKFETVTSKVTTFASGN 360  
QY 361 GTTATVSKDDOGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSSGKVISGNVSPSKG 420

Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
QY 421 KMDETVINAGNNIETRNCKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
Db 421 KMDETVINAGNNIETRNCKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 481 DANKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA 540  
Db 481 DANKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA 540  
QY 541 YLPKSNMAIGGTYRGEAGYAIYSSISDGTGNWVIKGTASGNSRGRHFGASASVGYQW 598  
Db 541 YLPKSNMAIGGTYRGEAGYAIYSSISDGTGNWVIKGTASGNSRGRHFGTSASVGYQW 598

## RESULT 4

US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 6331173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; TYPE: PRT  
; LENGTH: 598  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 99.2%; Score 3021; DB 4; Length 598;

Best Local Similarity 99.3%; Pred. No. 3.6e-236; Mismatches 1; Indels 0; Gaps 0;

Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNNAVYVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
Db 1 MNKISRIIWNLSALNNAVYVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKSGTGEKGTEDSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
Db 61 PVORTAVVLSFRSDKSGTGEKGTEDSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
QY 181 PTVHLNGIGSTLTDLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKIKVKGPGTTA 240  
Db 181 PTVHLNGIGSTLTDLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKIKVKGPGTTA 240  
QY 241 SDNVDFRVTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGK 300  
Db 241 SDNVDFRVTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGK 300  
QY 301 DENGSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVTSGETVTFASGN 360  
Db 301 DENGSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVTSGETVTFASGN 360  
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420

Db 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
QY 421 KMDETVINAGNNIETRNCKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
Db 421 KMDETVINAGNNIETRNCKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 481 DANKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA 540  
Db 481 DANKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNRIDNVDGNARAGIAQAIATAGLAQA 540  
QY 541 YLPKSNMAIGGTYRGEAGYAIYSSISDGTGNWVIKGTASGNSRGRHFGASASVGYQW 598  
Db 541 YLPKSNMAIGGTYRGEAGYAIYSSISDGTGNWVIKGTASGNSRGRHFGTSASVGYQW 598

## RESULT 5

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 97.6%; Score 2971; DB 4; Length 594;

Best Local Similarity 98.0%; Pred. No. 3.9e-232;

Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 1 MNKIYRIIWNLSALNNAVYVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWNLSALNNAVYVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKSGTGEKGTEDSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
Db 61 PVORTAVVLSFRSDKSGTGEKGTEDSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
QY 181 PTVHLNGIGSTLTDLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKIKVKGPGTTA 240  
Db 177 PTVHLNGIGSTLTDLLNTGATTNVTNDVDEKRAASVKDVLNAGWNKIKVKGPGTTA 236  
QY 241 SDNVDFRVTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGK 300  
Db 237 SDNVDFRVTYDVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDGKLVTKGK 296  
QY 301 DENGSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVTSGETVTFASGN 360  
Db 297 DENGSSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTQADKFFETVTSGETVTFASGN 356  
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
Db 357 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
QY 421 KMDETVINAGNNIETRNCKNIDIATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480

Db 417 KMDFTVINAGNNIEITRNKNIDIAISMAPOQFSSVSLGAGADAPTLLSVDDDEGALNVGSK 476  
QY 481 DANKPVRITNVAPGVKGGDVTVNAQLKGVAQNLANRINDVGNARAGTAQAIAIATAGLAQA 540  
Db 477 DTNKPVRITNVAPGVKGGDVTVNAQLKGVAQNLANRINDVGNARAGTAQAIAIATAGLVQA 536  
QY 541 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGASASVGYOW 598  
Db 537 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGASASVGYOW 594

## RESULT 6

US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 6331173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 97.68; Score 2971; DB 4; Length 594;  
Best Local Similarity 98.08; Pred. No. 3.9e-232;  
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;  
QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDEKTEGEGTSDSNWAVYFDEKRVLKAGAITLKGADNLIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDEKTEGEGTSDSNWAVYFDEKRVLKAGAITLKGADNLIKQNTNE 116  
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176  
QY 181 PTVHLNGIGSLTDLTLNTGATTNVTNDVDDDEKRAASVKDVLNAGWNKGVKPGTTA 240  
Db 177 PTVHLNGIGSLTDLTLNTGATTNVTNDVDDDEKRAASVKDVLNAGWNKGVKPGTTA 236  
QY 241 SDNVDFVRTYDTVFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 300  
Db 237 SDNVDFVRTYDTVFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 296  
QY 301 DENGSSTDEGGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKFEFVTSCTKVTFSAGN 360  
Db 297 DENGSSTDEGGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKFEFVTSCTKVTFSAGK 356  
QY 361 GTTATVSKDDOGNITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
Db 357 GTTATVSKDDOGNITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
QY 421 KMDFTVINAGNNIEITRNKNIDIAISMAPOQFSSVSLGAGADAPTLLSVDDDEGALNVGSK 480  
Db 417 KMDFTVINAGNNIEITRNKNIDIAISMAPOQFSSVSLGAGADAPTLLSVDDDEGALNVGSK 476

Db 417 KMDFTVINAGNNIEITRNKNIDIAISMAPOQFSSVSLGAGADAPTLLSVDDDEGALNVGSK 476  
QY 481 DANKPVRITNVAPGVKGGDVTVNAQLKGVAQNLANRINDVGNARAGTAQAIAIATAGLAQA 540  
Db 477 DTNKPVRITNVAPGVKGGDVTVNAQLKGVAQNLANRINDVGNARAGTAQAIAIATAGLVQA 536  
QY 541 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGASASVGYOW 598  
Db 537 YLPKSMMAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGASASVGYOW 594

## RESULT 7

US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 93.88; Score 2855; DB 4; Length 594;  
Best Local Similarity 94.68; Pred. No. 9.3e-223;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;  
QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLFLFATVQASSTDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDEKTEGEGTSDSNWAVYFDEKRVLKAGAITLKGADNLIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDEKTEGEGTSDSNWAVYFDEKRVLKAGAITLKGADNLIKQNTNE 120  
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 121 NTNA---SSFTYSLKKDLTDLTSVGTSEKLSFSANSKNVITSDTKGLNFAKTAETNGD 176  
QY 181 PTVHLNGIGSLTDLTLNTGATTNVTNDVDDDEKRAASVKDVLNAGWNKGVKPGTTA 240  
Db 177 PTVHLNGIGSLTDLTLNTGATTNVTNDVDDDEKRAASVKDVLNAGWNKGVKPGTTA 236  
QY 241 SDNVDFVRTYDTVFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 300  
Db 237 SDNVDFVRTYDTVFLSADTKTTTVNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 296  
QY 301 DENGSSTDEGGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKFEFVTSCTKVTFSAGN 360  
Db 297 DENGSSTDEGGLVTAKEVIDAVNKGARMKTTTTANGOTGOADKFEFVTSCTNVTFSAGK 356  
QY 361 GTTATVSKDDOGNITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
Db 357 GTTATVSKDDOGNITVYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
QY 421 KMDFTVINAGNNIEITRNKNIDIAISMAPOQFSSVSLGAGADAPTLLSVDDDEGALNVGSK 480  
Db 417 KMDFTVINAGNNIEITRNKNIDIAISMAPOQFSSVSLGAGADAPTLLSVDDDEGALNVGSK 476  
QY 481 DANKPVRITNVAPGVKGGDVTVNAQLKGVAQNLANRINDVGNARAGTAQAIAIATAGLAQA 540

Db 477 DANKPVRITNAPGVKRGDVTNVAQLKGVAQNLNNHIDNVGNARAGIAQAATATAGLVA 536  
QY 541 YLPGKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRHFASASVGYQW 598  
Db 537 YLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKTASGNSRHFASASVGYQW 594

RESULT 8  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6331173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 93.8%; Score 2855; DB 4; Length 594;  
Best Local Similarity 94.6%; Pred. No. 9.3e-223;  
Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;  
QY 1 MNKIYRIIWSALNANWVYSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNANWVYSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60  
QY 61 PVQRTAVLSFRSKDGEKTEGSDSNVAVFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
Db 61 PVQRTAVLSFRSKDGEKTEGSDSNVAVFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
QY 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAETNGD 180  
Db 121 NTNA-----SSFTYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAETNGD 176  
QY 181 PTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNVIKGVKPGTTA 240  
Db 177 TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNVIKGVKPGTTA 236  
QY 241 SDNVDFVRTYDVFELSDTKTTTVNVEKSKNGKTEVKIGAKTSVIKEKDGKLVTKGCK 300  
Db 237 SDNVDFVRTYDVFELSDTKTTTVNVEKSKNGKTEVKIGAKTSVIKEKDGKLVTKGDK 296  
QY 301 DENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSKTVTFASGN 360  
Db 297 GENDSTDKGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSKTVTFASCK 356  
QY 361 GTTATVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKSAVAGSGKVISGNVSPSKG 420  
Db 357 GTTATVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKSAVAGSGKVISGNVSPSKG 416  
QY 421 KMDETVINAGNNIETIRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
Db 417 KMDETVINAGNNIETIRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
QY 481 DANKPVRITNAPGVKRGDVTNVAQLKGVAQNLNNHIDNVGNARAGIAQAATATAGLVA 540

Db 477 DANKPVRITNAPGVKRGDVTNVAQLKGVAQNLNNHIDNVGNARAGIAQAATATAGLVA 536  
QY 541 YLPGKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRHFASASVGYQW 598  
Db 537 YLPGKSMMAIGGTYRGEAGYAGYSSISDGGNWIITKTASGNSRHFASASVGYQW 594

RESULT 9  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 92.8%; Score 2824.5; DB 4; Length 599;  
Best Local Similarity 92.7%; Pred. No. 2.8e-220;  
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;  
QY 1 MNKIYRIIWSALNANWVYSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLYL 59  
Db 1 MNKIYRIIWSALNANWVYSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL 60  
QY 60 EPVQRTAVLSFRSKDGEKTEGSDSNVAVFDEKRVLKAGAITLKAGDNLKIKONTN 119  
Db 61 EPVRSALVQLPMIDKEGNESTGNIWSIYDHNHTLHGATVTLKAGDNLKIKONTN 120  
QY 120 EYNTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAETNG 179  
Db 121 KNTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAETNG 180  
QY 180 DPTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNVIKGVKPGTT 239  
Db 181 DPTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGNVIKGVKPGTT 240  
QY 240 ASDNVDFVRTYDVFELSDTKTTTVNVEKSKNGKTEVKIGAKTSVIKEKDGKLVTKGK 299  
Db 241 ASDNVDFVRTYDVFELSDTKTTTVNVEKSKNGKTEVKIGAKTSVIKEKDGKLVTKGK 300  
QY 300 KDBNGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSKTVTFASG 359  
Db 301 KDBNGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSKTVTFASG 360  
QY 360 NGTATVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKSAVAGSGKVISGNVSPSK 419  
Db 361 KGTATVSKDDQGNITVYDVNVGDALNVNQLNSGNWLDKSAVAGSGKVISGNVSPSK 420  
QY 420 GKMDETVINAGNNIETIRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 479  
Db 421 GKMDETVINAGNNIETIRNGKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGS 480  
QY 480 KDANKPVRITNAPGVKRGDVTNVAQLKGVAQNLNNHIDNVGNARAGIAQAATATAGLVA 539  
Db 481 KDANKPVRITNAPGVKRGDVTNVAQLKGVAQNLNNHIDNVGNARAGIAQAATATAGLVA 540  
QY 540 AYLPGKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRHFASASVGYQW 598

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Db 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKTASGNSRGRHFGCASASVGQW 599
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RESULT 10
US-09-669-974-15
; Sequence 15, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
; LENGTH: 599
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-15

Query Match 92.8%; Score 2824.5; DB 4; Length 599;
Best Local Similarity 92.7%; Pred. No. 2.8e-220;
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

QY 1 MNKIYRIIWSALNAWVVSSELNRHTKRASATVATAVLATLFLFATVQANATD-DDDLYL 59
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Db 1 MNKIYRIIWSALNAWVVSSELNRHTKRASATVATAVLATLFLFATVQANATDEDEEL 60
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QY 60 EPVORTAVLSFRSDKEGTEGKEDSDNAVYFDEKRVLKAGAITLKAGDNLIKIKONTN 119
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Db 61 EPVRSALVLFQMDKEGGENESTGNIGWSIYYDHNHTLHGATVTLKAGDNLIKIKONTN 120
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QY 120 ENTNENTNDSFYSYLSKKDLTDLTSVETKLSFGANGKNYITSDTKGLNFAKETAGTNG 179
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Db 121 KNTNENTNDSFYSYLSKKDLTDLTSVETKLSFGANGKNYITSDTKGLNFAKETAGTNG 180
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QY 180 DPTVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKPGTT 239
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Db 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKPGTT 240
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QY 240 ASDNVDFVRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLVTKG 299
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Db 241 ASDNVDFVRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLVTKG 300
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QY 300 KDENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTQVTFASG 359
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Db 301 KGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTQVTFASG 360
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QY 360 NGTTATVSKDDQGNITVKYDVNVDGALNVQLNSGWNLDKAVAGSSGKVISGNVSPSK 419
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Db 361 KGTTATVSKDDQGNITVKYDVNVDGALNVQLNSGWNLDKAVAGSSGKVISGNVSPSK 420
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QY 420 GKMDETVINAGNIEITRNKKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALNVGS 479
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Db 421 GKMDETVINAGNIEITRNKKNIDATSMTPQSSVSLGAGADAPTLSDVDDKALNVGS 480
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QY 480 KDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLLNNRIDNVNDRAGIAQAATAGLAQ 539
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Db 481 KDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLLNNRIDNVNDRAGIAQAATAGLVQ 540
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QY 540 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGTGNWVIKGTASGNSRGRHFGCASASVGQW 598
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Db 541 AYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKTASGNSRGRHFGCASASVGQW 599
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RESULT 11
US-09-377-155-21
; Sequence 21, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 21
; LENGTH: 591
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-21

Query Match 89.5%; Score 2725.5; DB 4; Length 591;
Best Local Similarity 91.0%; Pred. No. 2.8e-212;
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

QY 1 MNKIYRIIWSALNAWVVSSELNRHTKRASATVATAVLATLFLFATVQANATD---DDDL 57
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Db 1 MNKIYRIIWSALNAWVVSSELNRHTKRASATVATAVLATLFLFATVQANNEEQEEDL 60
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QY 58 YLEPVQRTAVLSFRSDKEGTEGKEDG--SNNAVYFDEKRVLKAGAITLKAGDNLIKIK 116
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Db 61 YLDPVQRTAVLVNSDKEGTEGKEKEVENSNAVYFNEKGVLTAREITLKAGDNLIKIK 120
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QY 117 NTNENTNENTNDSFYSYLSKKDLTDLTSVETKLSFGANGKNYITSDTKGLNFAKETAG 176
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Db 121 -----NGNFTYSLKKDLTDLTSVETKLSFGANGKNYITSDTKGLNFAKETAG 170
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QY 177 TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKP 236
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Db 171 TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIGVKP 230
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QY 237 GTTASDNVDVVRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLV 296
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Db 231 GTTASDNVDVVRTYDTVEFLSADTKTTTVNVEKDNKGKTEVKIGAKTSVKEKDGKLV 290
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QY 297 GKDKDENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTQVTF 356
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Db 291 GKDKDENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFETVTSGTQVTF 350
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QY 357 ASNGTTTATVSKDDQGNITVKYDVNVDGALNVQLNSGWNLDKAVAGSSGKVISGNVS 416
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Db 351 ASNGTTTATVSKDDQGNITVKYDVNVDGALNVQLNSGWNLDKAVAGSSGKVISGNVS 410
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QY 417 PSKGKMDETVINAGNIEITRNKKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALN 476
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Db 411 PSKGKMDETVINAGNIEITRNKKNIDATSMTPQSSVSLGAGADAPTLSDVGDG-ALN 469
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QY 477 VGSKDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLLNNRIDNVNDRAGIAQAATAG 536
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Db 470 VGSKDANKPVRIITNAPGVKEGDTVNVQALKGVAQNLLNNRIDNVNDRAGIAQAATAG 529
|||||
QY 537 LAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGTGNWVIKGTASGNSRGRHFGCASASVG 596
|||||
Db 530 LVAQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGTGNWVIKGTASGNSRGRHFGCASASVG 589
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QY 597 QW 598
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Qy	1	MNKYRIIWSALNANWVVVSELFRNHTK	KRASATVATVAVLATL	LFATVQANATDD	----	DD	56
Db	1	MNKYRIIWSALNANWVVVSELFRNHTK	KRASATVATVAVLATL	LFATVQASANNRP	KRKD	60	
Qy	57	LYLEPVORTAVLSPRSDKEGT	EGTED-SNWAYVFEKRVLKAGATL	KAGONLKIT	115		
Db	61	LYLDPVORTAVLIVNSDKEGT	GEKVBENSOMAYFNEKGVLTAREITL	KAGONLKIT	120		
Qy	116	QNTNENTNENTDSSFTYSLKKDLT	DLTSTVETEKLSFGANGKNVNTSDTK	GLNEFAKETA	175		
Db	121	Q-----NGTNYFYSLLKDLT	DLTSTVETEKLSFGANGKNVNTSDTK	GLNEFAKETA	170		
Qy	176	GTNGDPVTHLNGTSTLTDPL	LNTGATNTVNDNVTDDEK	KRAASVKDVLNAGWNI	KGVK	235	
Db	171	GTNGDTPVHLNGTSTLTDPL	LNTGATNTVNDNVTDDEK	KRAASVKDVLNAGWNI	KGVK	230	
Qy	236	PGTITASNVDVFRVTDYD	TVFELSADTKTTVNVESKDN	GKKTEVKKICAKTSV	KEKDGKLV	295	
Db	231	PGTITASNVDVFRVTDYD	TVFELSADTKTTVNVESKDN	GKKTEVKKICAKTSV	KEKDGKLV	290	
Qy	296	TGKDKBENGSTDEBGLVTA	KEVIDAVNKA	GHRMKTITTTANGOT	GOADFEVITSGTKVT	355	
Db	291	TGRDKBENGSTDEBGLVTA	KEVIDAVNKA	GHRMKTITTTANGOT	GOADFEVITSGTNVT	350	
Qy	356	FASNGHTATVSKDDQGNIT	VKYDVNVGDALNVQ	LONSGWNLDSKAVAGSSG	KVILSGNV	415	
Db	351	FASGKGTATVSKDDQGNIT	VKYDVNVGDALNVQ	LONSGWNLDSKAVAGSSG	KVILSGNV	410	
Qy	416	SPSKGKMDETVNI	NAGNNIEITRNGKNIDI	ATSNTPQFSSVSLGACADAPT	LSVDDEGAL	475	
Db	411	SPSKGKMDETVNI	NAGNNIEITRNGKNIDI	ATSNTPQFSSVSLGACADAPT	LSVDGD-AL	469	
Qy	476	NVGSKDANKPVRITNV	APGVKEGDVTNVAQLK	GVAONLNRINDVGNARAGIA	QAIAATA	535	
Db	470	NVGSKDANKPVRITNV	APGVKEGDVTNVAQLK	GVAONLNRINDVGNARAGIA	QAIAATA	529	
Qy	536	GLAQAYLPKGSMAIGA	GGTYRGEAGYAIGYSS	ISDSTGNVWIKGTASGNSGRHFGAS	ASVG	595	

Db 530 GLVQAYLPCKSMMAIGGTYRGEAGYATGYSSISDGGNWIIRKGTASGNSRGHFGASASVG 589  
Qy 596 YQW 598  
Db 590 YQW 592

RESULT 14  
US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; PRIOR FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 89.3%; Score 2718; DB 4; Length 592;  
Best Local Similarity 90.7%; Pred. No. 1.le-211;  
Matches 547; Conservative 11; Mismatches 29; Indels 16; Gaps 4;  
Qy 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDD---DD 56  
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASANNRPKRD 60  
Qy 57 LYLEPVQRTAVVLSRSPDKEGTGEKED- SNWAVYFEKRVLKAGAITLKAGDNLKIK 115  
Db 61 LYLPVQRTAVVLSRSPDKEGTGEKED- SNWAVYFEKRVLKAGAITLKAGDNLKIK 120  
Qy 116 QNTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA 175  
Db 121 Q-----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA 170  
Qy 176 GTNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVNDDEKKRAASVKDVLNAGWNKIGVK 235  
Db 171 GTNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVNDDEKKRAASVKDVLNAGWNKIGVK 230  
Qy 236 PGTASDNVDFVRTYDTVEFLSADTKTTVNVESKDNKKTEVKIGAKTSVKEKDGKLV 295  
Db 231 PGTASDNVDFVRTYDTVEFLSADTKTTVNVESKDNKKTEVKIGAKTSVKEKDGKLV 290  
Qy 296 TGKGDENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTQADKFFETVTSKTVTF 355  
Db 291 TGKDGENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTQADKFFETVTSKTVTF 350  
Qy 356 PASNGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNV 415  
Db 351 PASGKGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNV 410  
Qy 416 SPSKGMDETVINAGNNIEITRNKNDIATSWTPQFSSVSLGAGADAPTLSDVDEGAL 475  
Db 411 SPSKGMDETVINAGNNIEITRNKNDIATSWTPQFSSVSLGAGADAPTLSDVDEG-AL 469  
Qy 476 NVGSKDANKPVRIITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATA 535

Db 470 NVGSKDANKPVRIITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATA 529  
Qy 536 GLAQAYLPCKSMMAIGGTYRGEAGYATGYSSISDTGNWIKGTASGNSRGHFGASASVG 595  
Db 530 GLVQAYLPCKSMMAIGGTYRGEAGYATGYSSISDGGNWIIRKGTASGNSRGHFGASASVG 589  
Qy 596 YQW 598  
Db 590 YQW 592

RESULT 15  
US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: Patentin Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 88.9%; Score 2706.5; DB 4; Length 591;  
Best Local Similarity 90.5%; Pred. No. 9.5e-211;  
Matches 545; Conservative 13; Mismatches 29; Indels 15; Gaps 4;  
Qy 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
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Qy 58 YLEPVQRTAVVLSRSPDKEGTGEKED- SNWAVYFEKRVLKAGAITLKAGDNLKIK 116  
Db 61 YLDPVLRVAVLVNSDKEGTGEKED- SNWAVYFEKRVLKAGAITLKAGDNLKIK 120  
Qy 117 NTNENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA 176  
Db 121 -----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETA 170  
Qy 177 TNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVNDDEKKRAASVKDVLNAGWNKIGVK 236  
Db 171 TNGDPTVHLNGIGSTLDTLLNTGATTNVTNDVNDDEKKRAASVKDVLNAGWNKIGVK 230  
Qy 237 GTTASDNVDFVRTYDTVEFLSADTKTTVNVESKDNKKTEVKIGAKTSVKEKDGKLV 296  
Db 231 GTTASDNVDFVRTYDTVEFLSADTKTTVNVESKDNKKTEVKIGAKTSVKEKDGKLV 290  
Qy 297 GKGDENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTQADKFFETVTSKTVTF 356  
Db 291 GKDGENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGOTQADKFFETVTSKTVTF 350  
Qy 357 ASGNGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNV 416  
Db 351 ASGKGTGTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKSAVAGSSGKVISGNV 410  
Qy 417 SPSKGMDETVINAGNNIEITRNKNDIATSWTPQFSSVSLGAGADAPTLSDVDEGAL 476  
Db 411 SPSKGMDETVINAGNNIEITRNKNDIATSWTPQFSSVSLGAGADAPTLSDVGD-ALN 469  
Qy 477 VGSKDANKPVRIITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATA 536

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Db 470 VGSKKDNKPVRTNVAPGVKEGDTNVAQLKGVQNLNNRIDNVDGNARAGIAQAIATAG 529
QY 537 LAQAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGASASVGY 596
Db 530 LVOAYLPCKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIKGTASGNSRGHFGASASVGY 589
QY 597 QW 598
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Db 590 QW 591
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Search completed: July 3, 2002, 08:37:08  
Job time: 334 sec

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2	2524	82.9	592	2	A81888		probable surface f
3	633	20.8	298	2	I64138		adhesin homolog HI
4	402	13.2	2059	2	D82671		surface protein XF
5	395	13.0	1107	2	AC0976		probable autotransp
6	382.5	12.6	1190	2	A83615		surface protein XF
7	368	12.1	1588	2	A86036		probable adhesin Z
8	368	12.1	1588	2	H91188		probable adhesin E
9	335	11.0	658	2	A90110		probable surface p
10	234	8.3	1004	2	C82672		surface-exposed ou
11	236	7.8	1091	2	G64964		hypothetical prote
12	222	7.3	949	2	D90803		Aida-I adhesin-lik
13	222	7.3	1005	2	H85611		probable adhesin Z
14	221.5	7.3	1910	2	AF0394		probable adhesin h
15	221	7.3	1018	2	H83135		probable adhesin P
16	220	7.2	1286	2	S28634		adhesin AIDA-I pre
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20	213	7.0	1536	2	A43855		high-molecular-we
21	211.5	6.9	1109	2	A56143		surface-array prot
22	210	6.9	1361	2	T03415		S-layer protein -
23	210	6.9	1608	2	A28182		hemolysin A - Ser
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25	207.5	6.8	961	2	AD0548		puative autotransp
26	207	6.8	5291	2	F90696		hypothetical prote
27	206	6.8	2551	2	B98047		hypothetical prote
28	203	6.7	1327	2	B90674		Aida-I adhesin-lik
29	203	6.7	1349	2	E85524		probable beta-bar

Query Match	89.5%;	Score	2725.5;	DB	2;	Length	591;
Best Local Similarity	91.0%;	Pred. No.	1.8e-130;				
Matches	548;	Conservative	12;	Mismatches	27;	Indels	15; Gaps
QY	1	MNKYRIIWSALNANWVVVSELTRNHTKRASATVATAVLATLLFATVQANATD---	DDDL	57			
Db	1	MNKYRIIWSALNANWVVVSELTRNHTKRASATVATAVLATLLFATVQASANNEQEDL	60				
QY	58	YLEPVQRTAVVLSPRSDEKTEGECTED--SNWAVYFDEKRVLKAGAITLKAGDNLAIQ	116				
Db	61	YLEPVQRTAVVLVNSDEKTEGKEKEVYEENSNAWYFNEKGVLTAREITLKAGDNLAIQ	120				
QY	117	NTNENTNENTDSFTVSLAKDLDLTLSVTEKLSFCANGKNVNI	176				
Db	121	-----NGNFTYSLAKDLDLTLSVTEKLSFCANGKNVNI	170				
QY	177	TNGDPTVHLNGIGSTLTDLTLLTGATTNVTDNDVTDDEKKRAASVKDVLNAGWNI	236				
Db	171	TNGDPTVHLNGIGSTLTDLTLLTGATTNVTDNDVTDDEKKRAASVKDVLNAGWNI	230				
QY	237	GTATSDNVDFRVYDVTVEFLSADTKTTTVNVEKDNCKKTEVKIGAKTSVIKEKDGLVT	296				
Db	231	GTATSDNVDFRVYDVTVEFLSADTKTTTVNVEKDNCKKTEVKIGAKTSVIKEKDGLVT	290				
QY	297	GKGDENGSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTS	356				
Db	291	GKDKGEMSGSSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTS	350				
QY	357	ASGNGTTFATYSKDDOGNITVKYDVNVGDALNVNOLONGSGWNLDSKAVAGSSGKVI	416				





Db 814 NVAAGSADTDVAVNGQLKVTDAQVSRNTQSTNLTNQVSNLDRVTRVNIENGIGDIVTGS 873  
Qy 451 PQF-----SSVSLGAGADAP-----TSLVDDDE-GALAVNGSKDANKPV 486  
Db 874 TKYFKTNTDGADANAAGDASVAIGSGSIAAENSVALGTNSVADEANTVSGSSTQQR-- 931  
Qy 487 RITVAVGVKGGVNTVNAQK-----  
Db 932 RITVAAAGVNTDVAVNAQLKASEAGSVRYETNADGSGVNYSVLNLGDSGGTTRIGNVSA 991  
Qy 508 -----GVAQ-----  
Db 992 AVNTDVAVNTAQLKRSVEEANTYTDQKMGEMNSKIKIGENKMSGGIASAMAGLPQAYA 1051  
Qy 543 PGKSMIAIGGTYRGEAGYAGISISDTGNWVTKGTASNGSRHFGASASVGYOW 598  
Db 1052 PGANWTSIAGCTFNGESAVALGVSWSGCVYKLOGTSNSQDYSAAICAGFQW 1107  
RESULT 6  
A82615  
surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: A82615  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1190 <SIM>  
A:Cross-references: GB:AE004017; GB:AE003849; MID:g9107083; PIDN:AAF84783.1; GSPDB:GN001  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, H  
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; From  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krueger, J.E.; Kuramae, E.E.; Laig  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.S.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
A:Genetics:  
A:Gene: XF1981

Query Match 12.6%; Score 382.5; DB 2; Length 1190;  
Best Local Similarity 24.6%; Pred. No. 8.7e-12;  
Matches 169; Conservative 89; Mismatches 226; Indels 203; Gaps 30;  
Qy 47 VQANATDDLLYLEPVRTAVVLSFRSDKECTGEGEDSNWAVYDFEKLKAGAILT 106  
Db 572 VAAGTADTDAVNSQLQ-----AVSTASKGNLLASGANS-----VPGESVDL 618  
Qy 107 KAGO-NLKIKNONTNENTNDSFTY--SLKKD--LTDLTSVETKLSFGAN----- 155  
Db 619 KNSDGNLLITKT-----DSNDVTFNLATALKVDSLTTGTNTMTDGVTVGSNVTLGST 672  
Qy 156 -----GNK--VNI--TSDTKGLNFA----- 171  
Db 673 GLVITDGPSTSSGISAGNQKITVAAAGTADTDAVNFSQLQAVSSTASKGNLLASGANS 732  
Qy 172 -----KETAGT-----NGDPTVHLNGIGS-----TLTDLTLNTGATT---NV 205  
Db 733 SNVAPGESVDLKTNDGNITVSKESGNDVLFNLSSSLKLDLKLTVGDTVMTTNGVTGSGV 792

Qy 206 TNDN-----VTDEKKRAASVKDVLNAG-WNIKGVKVPQTASD-----N 243  
Db 793 TLGSMGLVITDGPSTSSGI-----NAGSQKITVAAAGTADTDAVNLSQLNTAMAGSAGS 848  
Qy 244 VDFVRIYDTVEFLSADTKTTTVNVVESKDNKKTEVKGAKTSVKEKDKGLVYCKGKRDEN 303  
Db 849 VHYSTYD-----GCTQGGNYNGDGATGTRSTAVGCTTLASA-----EGATAVSGSAAAS 898  
Qy 304 G-SSTDGEGELVTAKEVIDAVNAGRWKMTTTANGOTGQADKPEFVTSGTGKVTFFASNGT 362  
Db 899 GKSTALGRNAVASADGSVALGD-GAKDGARGAESYTGKYSGLONNTVGTVSGVDASKGE 957  
Qy 363 TATVSKDDQGNITVKYDVNVGDALNVNLQ-----QNSGWNLDLSKAVAGSSKVKISGNVSPS 418  
Db 958 TRTVS-----NVADAKEAT--DAVNLRLQDRVAQDANRYVDNKNIESLSEGTFF----- 1003  
Qy 419 GKMDETVNTNAGNNIEITRNGKNIDTATSMTPQFSSVSLGACADA-----PTL 467  
Db 1004 -----VKVNSLNN-----SATPIAAGVDATAIGVGATSGADSIAMGNKASA 1045  
Qy 468 SVDDDEGAL-----NVGSKDANKPVRTNVPAGVKEGVDVTVNAQLKGVQAOLNN 515  
Db 1046 SADNAVAIGHNSVADRANTVSVGSAGSER--QVTNVAAGTADTDAVNVSQLNQLITAKQ 1103  
Qy 516 RIDNVGDNAR-----AGTAQAIATAGLAQAYLPGKSMMAIGGTYRGEAGYAGYSSISDT 571  
Db 1104 YTDGVVGSLLRRDTDGGVAAAIATANLPQAVIPGRGMTSVGVSSYRGQSAIAGVSSVSES 1163  
Qy 572 GNWVVKTAGSNGRHFASASVGYOW 598  
Db 1164 GRWVFKSGSANTRSQVIGAGVGYOW 1190  
RESULT 7  
A86036  
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: A86036  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A86036  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <STO>  
A:Cross-references: GB:AE005174; MID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UMGF:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5029

Query Match 12.1%; Score 368; DB 2; Length 1588;  
Best Local Similarity 24.9%; Pred. No. 6.8e-11;  
Matches 171; Conservative 79; Mismatches 221; Indels 216; Gaps 28;  
Qy 11 SALNAW-VVYSELTRNHTKRASATVATVATLTLFATVQANATDDDLYLEPVRT---A 66  
Db 1019 SOLNATNMIEQNTQIINQLAGNTDATYIOEN--GAGINVVRTNDDGLAFNDASAOQVGA 1076  
Qy 67 VLSFRSDKECTGEGEDSNWAV-----YFD-----EKRVLKAG-----AIT- 105  
Db 1077 TAIGYNSVAKG-----DSSVAIGOGSVDVDTGALGSSSVSSRVIAKGRDTSITE 1128  
Qy 106 -----LKAGDNLKIKONTNENTNENTNDSFTYSLKKDL----- 139  
Db 1129 NGVVIGYDTTDELLGALSIGDCKYKRIINVADGSEAHDAVTVRQLQNAIGAIVATPTK 1188  
Qy 140 -----TDLTSVETEKLSFGA-----NGNK-----VNITSDTKGLNFAKETAGTNGDPT 182



Db 1189 YFHANSTEEEDSLAVGTDLSLMAKAKTITVNGDKGIGIGYGAYVDANALNGI--AIGSNAQ-V 1245

Qy 183 VHLNGI-----GSTLTDTLLTGATTVNTNDVTDDEKKRAASVDVLNAGW--NLKGVPK 236

Db 1246 IHVNSIAIGNGSTTT-----RGATNYATYN--DAPONSVEFSGVGDQRQITVVA 1298

Qy 237 GTTASDNVDVRYTDYVEFLSADTKTT-----VNVESK-----DNGKKTEVKIGAKTSV 286

Db 1299 GSADTDAVNVGQLKVTDAQVSQNTQSITNLDNRVTNLDSDRVNIENGICDIVTTGSTKYF 1358

Qy 287 IKEDKGLVTGKKGDENGSSTDEGLVTAKEVIDAVNKAGHRMKTITTAHQGTQGAQKFE 346

Db 1359 KTNFDGVDAQAQKD---SVAIGSGSIAAAD-----N 1387

Qy 347 TVTSGTKVTTPASNGGTTATVSKDDQGNIT-VKYDVNVGDALNVNOLNS---GNWLDSK 402

Db 1388 SVALGTG-SVATEENTISVCSSTNQRRIITVAAGKATDVAVNAQLKSSEAGGVRYDTKA 1446

Qy 403 VAGSGKVISGNVSPSKGMDETVTNAGNNIEITRNCKNIDIIATSWTPQPSVSSVLGAGA 462

Db 1447 -----DGSID-----YSNITLGGGN 1461

Qy 463 DAPTLSDVDDGALNVGSKDANKPVRITNVAPGVKBDVTNVAOLKGVAQ----- 511

Db 1462 GGT-----RISNVSAGVNNVDVYNAQLKQSVQETKYQYTDORMV 1501

Qy 512 NLNRRIDNVGNARAGTAAQIATAGLAQAYLPKGSNMAITGGGTYRGEAGYAIGYSSISDT 571

Db 1502 EMDNKLSTKESLGGSIASAMAWTGLPQAYTPGASMASIGGGTYNGESAVALGVSWYSAN 1561

Qy 572 GNWVYKGTASGNSRGHFHASASVGVQW 598

Db 1562 GRWYKLGQSTNSQGEYSALGAGIQW 1588

RESULT 9

AH0110

probable surface protein (partial) YP00902 [imported] - Yersinia pestis (strain)

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C:Accession: AH0110

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; P. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.;

il, M.; Rutherford, K.; Sammons, M.; Skelton, J.; Stevens, K.; Whitehead, Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB00001; PMID:21470413; PMID:11586360

A:Accession: AH0110

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-658 <KUR>

A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN000

C:Genetics:

A:Gene: YP00902

Query Match	11.0%;	Score 335;	DB 2;	Length 658;
Best Local Similarity	22.3%;	Pred. No. 1e-09;		
Matches 143;	Conservative	87;	Mismatches 255;	Indels 156; Gaps 19
Qy	27	TKRSATVAT-----AVLATLLFATVQ-----ANATDDDDLLPEPVORTAVVLSFRSDK	75	
Db	105	TNLAPATISSSTDVVGSQLYNLVQDGRYFHANSVNPTDSLASGLETIIV-----	156	
Qy	76	ECTGEKETSNNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNNTNTNDSSFTYSL	135	
Db	157	-----GPATVVGSDNGVGIGNATLVGAAATGGIAIGFCT	190	
Qy	136	KDDLTDLTSVET-----EKLSPGANGKNVITSDTKGLNFAKETAGTNG-----	179	
Db	191	QVTAAGATAIGSAQAQAQASIALGAGA----VTQANSIALGAASINTVGAQSSYSAYA	246	





C;Genetics:  
A;Gene: Z12

Query Match	7.3%	Score 222;	DB 2;	Length 1005;
Best Local Similarity	22.7%;	Pred. No. 0.00089;		
Matches 152;	Conservative 89;	Mismatches 263;	Indels 166;	Gaps 32;
Qy	1	MNKYRIIWSALNAAVVVSELTHNTHKSRASATVATATLTLATVQANATDDDDLYLE	60	
Db	61	LNTSYRLVWNHITGLVVVASELARSGRAGVAVALSAAV---TSVPALAAD	110	
Qy	61	PVQRTAVVSPRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNE	120	
Db	111	----KVQAGETVNDGT---LNIHNDQIVFG-----TANGMTISG--LELGPDSSE	153	
Qy	121	NTN-----EN-----TNDSSFTVSLKKDLTDLNSVETEKLSFGA---NGKNVNITS	169	
Db	154	NTGGOWIQNGGIAGNTTVTTRGQVVLVEGGTASDTVIRDGGQGSUNGILAVATVTLNRGEQ	213	
Qy	170	FAKE---TAGT---NGDPTVHLANGISGTLTDTLLTNCATNTVNDVTDDEKKRAASVK	222	
Db	214	WVHGGVATGTIIIRNDGYSQVSKSGLA---TGTIIINTGAEGGPDSDNSYTQOK-----	263	
Qy	223	DVLNAGMNIKGVKPGTASDNVDFVRTY-----DTVEFLSADTK-----TTTVNVESKD	271	
Db	264	-----VQGTAEFTTINKNGRIILFSGLARDTLIYAGGDSVHGRLNNTLN----	310	
Qy	272	NGKTEVKIG--AKYSVIVKEKDKLVTKGKGKDENGSSDTDEGELVTAKEVIDAVNK--AGWR	329	
Db	311	GGYQVYVHRDGLALNTVINEGGQVQVYKAGGAAGTITINQNGELRVHAGGEATVQTGGGA	370	
Qy	330	MKTITA-----NGQTQADKFEETVTSGTKVTFASGNGTATVSKDDQGNIVVK	377	
Db	371	LVTSTAATVICTNRLGNFTVENGKADGV--VLESQGRDLVLESHSAQNTL--VDDGGTLLVS	428	
Qy	378	YDVNVGDALNYQLONGSNWNLDSKAVAGSSGKTSIGNVSPSKGKMDETVNIINAGNIEIT	437	
Db	429	AG---GRATSVT--ITSGG-----ALIASDATVEGTWASGKFSIDGTSGQASGLILLE---	476	
Qy	438	RNGKNIDIATSMTPQFSSVSLGAGADAPTLVSDDGALNV-----GSKDANKPVRITN	490	
Db	477	-NG-----GSFTVWAGQAGQNTTVGHRGTLTLAAGGSLSGRTQLSKGASMYL	522	
Qy	491	VAPVKYEGDVTNVAOLKQVAGQNLNRRIDNVGNARAGIAQAATATAG-----LAQAYLP	543	
Db	523	NGDVYSTGDIVNAGEI-----RFQD--QTPPNAALSRAVAKSNSPVTFHKLTTNTIT	572	
Qy	544	GK-----SMAIGGTYRGEPAGYA---IGYSS---ISDTGNVVIKGTASG	582	
Db	573	QGGGTINMKVRRLDGSNASDQLVINGQATGKTWLTAFTNVGNSNLGVATYTGQIRVVDAQN	632	
Qy	583	NSRHFHGASA	592	
Db	633	GATTEEGAGA	642	

RESULT 14  
AF0394  
probable adhesin hmwA [imported] - *Yersinia pestis* (strain CO92)  
C:Species: *Yersinia pestis*  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AF0394  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0394  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1910 <KUR>

A; Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:g15981183; GSPDB:GN00175  
C; Genetics:  
A; Gene: *hmwA*

Query Match	7.3%	Score 221.5;	DB 2;	Length 1910;
Best Local Similarity	22.2%;	Pred. No. 0.0022;		
Matches 160;	Conservative 85;	Mismatches 259;	Indels 217;	Gaps
Qy	14	NAMVYSELTRNHTKRASATVATVATLFLFATVQANATDDDLLEYVQ-----R	64	
Db	898	NATITANNISMN---GNITANDAVLMTVTFATGDKTD---LTSPTKGLWFRNGGM	950	
Qy	65	TA---VVLSPRDEKGTGKEGTEDSNMAVYFDEKRVLKAGA-ITLKAGDNLKIKQNTN-	119	
Db	951	TAANNILLVANSTSSCETVKINASSN-----KMNITAGKDIISIIAG-NSKTATGPN	10020	
Qy	120	--ENTNENTNDSFTYSLKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGT	177	
Db	1003	NIENVNIETNNGFT-----TNGITSTVSLGVNVSANG--VDITSTVSG-----TGG	1048	
Qy	178	NGDPTVHLNGIGSTLTDLLTGATTNVNDNVNTODEKKRAASVRDV---LNAGWNITKG	233	
Db	1049	VLDTNMLITVGD-----INT-IVTNSSGKGIIWIKSNSTLANSKNDITLVGSAGON-EG	1100	
Qy	234	V--KPGTASDNVDVFRVYDTVEFLSADTKTTTVNVVESKDNKKTEVIG-AKTSVIKE	289	
Db	1101	VIIQGSASARN-----NISAQCNITLIGKMGSGQHLINLGNVSLTS-----	1149	
Qy	290	KDGKLYTGKGDENGSTDEGLVTAKEV-----IDAVNKAGWR	329	
Db	1146	-----SGRNIDLNGSAGTGDVYFNVNLTATAGNVSIYAEKTKALSTLSLNVLSLGN	1199	
Qy	330	MKTTTANG-OTQOADRFETVTSKTVTFASNGTGTATVSKDDQGNITVK-----	377	
Db	1200	NSIKAQNGWLLIGA--FNT-----TQAGIGFRANSLSVDGNILLKGETGVGATRK	1250	
Qy	378	----YDVNVDGALNVQLNSGNLDSKAVAG-----	405	
Db	1251	GIDFYGANTLIINIKGSQLSLLGENKGAQDTAGGNGISYTSLAKLVNNGNSLKMGRSTS	1310	
Qy	406	-----SSGKVLISGVNPSPKGKWD-----	423	
Db	1311	GTGINFPSSNTLVFGDGDGTLIKGSSVAGTGAATSGVVNNSTGPMTEGISTDCAGVHL	1370	
Qy	424	-----ETVINAGN-----NIEITRNKNIDIA-TSMTPOFSSVSLGA--GADAPTL	469	
Db	1371	FSAEHRIDRINVTSSTHABGLRISCNAAIVDTTLTGKSGINGSGVKIDSLPGSSVVTRSV	1430	
Qy	470	DDEGALNVGSKDANKPYRITNVAPVYKEGDVTVNAQLKGAQVNLNRRIDNVGNARAG--	527	
Db	1431	LDNATLN-GSSSGSGKGVKETSIDTINGHSSINGTTGTGTGYGDIGEN-SNVVGTSEADLL	1488	
Qy	528	IAQAIATVAGLAQAY-LPGKSMMAIGGTVYRGBAGYAIQYSS-ISDTGNVVIKGTASGNSR	585	
Db	1489	ILOGVATTGTCTGIKLNGNNDLSNTSLNSAVDGTALDITGPLANQGVNLNGTAGSGSI	1548	
Qy	586	G	586	
Db	1549	G	1549	

RESULT 15  
H83135  
probable adhesin PA4082 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: H83135  
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.;  
Adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; L  
.: Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
.:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa

A;Gene: PA4082

Db 537 TLDGLGNSIGNLSISNTG 554

Search completed: July 3, 2002, 08:38:17  
Job time: 288 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:37:14 ; Search time 29.79 Seconds  
(without alignments)  
777.250 Million cell updates/sec

Title: US-09-771-382-7  
Perfect score: 3044  
Sequence: 1 MNKIYRIIWNALSALNANVVS.....TASGNSRGHFGASASGVQW 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries  
Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Description
1	236	7.8	P39180 escherichia
2	220	7.2	Q03155 escherichia
3	213.5	7.0	P32051 escherichia
4	210	6.9	P15320 serratia ma
5	197	6.5	P15921 rickettsia
6	190	6.2	P16466 proteus mir
7	188	6.2	Q53047 r outer mem
8	187	6.1	Q9kka3 r outer mem
9	184.5	6.1	Q52657 rickettsia
10	183.5	6.0	P14914 rickettsia
11	183	6.0	P18127 ranthomonas
12	182.5	6.0	P33666 escherichia
13	182.5	6.0	Q07833 bacillus su
14	181.5	6.0	P34487 caenorhabdi
15	180	5.9	P52143 escherichia
16	180	5.9	P25927 salmonella
17	178.5	5.9	Q06653 r outer mem
18	175	5.7	P06989 r outer mem
19	174.5	5.7	P35827 campylobact
20	171	5.6	Q08860 shigella fl
21	169.5	5.6	P38536 t amylopull
22	168	5.5	P37710 enterococcu
23	168	5.5	Q53020 r outer mem
24	167	5.5	P35825 bacillus st
25	166	5.5	Q48253 helicobacte
26	165.5	5.4	P45355 haemophilus
27	165	5.4	P35828 caulobacter
28	164.5	5.4	Q09624 caenorhabdi
29	163.5	5.4	P45354 haemophilus
30	163	5.4	P06176 salmonella
31	163	5.4	Q9pjy2 chlamydia m
32	162	5.3	O52959 salmonella
33	162	5.3	Q06982 salmonella

34	162	5.3	1007	1	Y741_CHLMU	Q9pjy2 chlamydia m
35	161	5.3	497	1	FLIC_ECOLI	P04949 escherichia
36	161	5.3	504	1	FLIC_SALMO	Q06983 salmonella
37	161	5.3	1394	1	HAP_HAEIN	P45387 haemophilus
38	160	5.3	504	1	FLIC_SALMO	Q06971 salmonella
39	160	5.3	825	1	GUN3_BACS4	P19570 bacillus sp
40	160	5.3	1702	1	IGA2_HAEIN	P45384 haemophilus
41	160	5.3	1770	1	PMPC_CHLTR	O84419 chlamydia t
42	159.5	5.2	948	1	HP11_DEIRA	P56867 deinococcus
43	159.5	5.2	1200	1	ICEN_PSESV	P06620 pseudomonas
44	159	5.2	1250	1	YFAL_ECOLI	P45508 escherichia
45	159	5.2	1637	1	MRSP_STAUA	P80544 staphylococ

ALIGNMENTS

RESULT 1  
AG43\_ECOLI  
ID AG43\_ECOLI STANDARD; PRT; 1039 AA.  
AC P39180; P76360; P75614; P97241; Q46771;  
DT 01-FEB-1995 (Rel. 31, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Antigen 43 precursor (AG43) (Fluffing protein).  
GN FLU OR B2000.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251358; PubMed=9097040;  
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,  
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,  
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,  
RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,  
RA Sivasubdaram S., Tagami H., Takeda J., Takemoto K., Wada C.,  
RA Yamamoto Y., Horiuchi T.;  
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 40.1-50.0 min region on the linkage map.";  
RL DNA Res. 3:379-392(1996).  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ML 308-225;  
RA Henderson I.R., Owen P.;  
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
RN [4]  
RP PRELIMINARY SEQUENCE OF 53-78.  
RC STRAIN=ML 308-225;  
RX MEDLINE=89291704; PubMed=2661530;  
RA Caffrey P., Owen P.;  
RT "Purification and N-terminal sequence of the alpha subunit of antigen  
43, a unique protein complex associated with the outer membrane of  
Escherichia coli.";  
RL J. Bacteriol. 171:3634-3640(1989).  
RN [5]  
RP SEQUENCE OF 53-63.  
RC STRAIN=K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded





```
CC -----
DR EMBL; X65022; CAA46156.1; .
DR PIR; S28634; S28634.
KW Cell adhesion; Signal; Outer membrane; Plasmid.
FT SIGNAL 1 49
FT CHAIN 50 ? ADHESIN AIDA-I.
FT PROPEP ? 1286
SQ SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;

Query Match
Best Local Similarity 7.2%; Score 220; DB 1; Length 1286;
Matches 160; Conservative 106; Mismatches 290; Indels 362; Gaps 33;

QY 1 MNKIYRIWNSALNAWVYSELTRNH-----TKRASATVATA--VLATLLFATVOANA 51
DB 1 MNKAYSILWHSRQAVIVASELARGHGFVLAKNTLLVAVSTIGNAFVAINSGVSSGG 60
QY 52 TDDDLLYLEPVORTAVVLSFRSDKEGTGEKETE-----
DB 61 TVSSG-----ETQIVYSGRCNSATVNSGGTQIVNNGGKTTATTVNSSGSONVGTSCA 113
QY 86 -----DSNAVYFDEKKVLKAGAIT--- 105
DB 114 TISTVNSGGIQRVSSGGVASATNLSSGAQNTIYNLGHASNTVIFSGNQTIFSGGITDST 173
QY 106 -LKAGDNLKIKO-NTNENNTNENTDSSFTYSLKDL-TDLTSVETEKLSFGANGKNVIT 162
DB 174 NISSGQQRVSSGGVASNTINSSGAQNTLSEGAISTHISGGNQYISAGANATETIVN 233
QY 163 SDTKGLINFAKETAGTNGDPTVHLNG-----IGSLTDLTLN 198
DB 234 SG-----GFORVNSGAVATGTVLSGGTQNVSSGSAISTSVYNSGVQTVFAGATVDTTVN 289
QY 199 TGATNTVNTDNTDDEKKRAASVKQVLNAG-----WNKIG----- 233
DB 290 SGGNQNISSGGIVSETTVNSGTONIYSGGSALSANSGIQAIVNSRGTATNLVSDGGYQ 349
QY 234 -VKPGTASDNDFVRYTDFEFLSADTKTVTVNYESKDKGKTEKIGAKTSVLIKE--K 290
DB 350 HIRNGIASGTIVNSGY-----VNISGGYAEISTINSGGTTLRVLSGDGYA 395
QY 291 DGKLVTKGKD--ENG-----STDEGEGLVTAKREVIDAVNKAG----- 327
DB 396 RGTILNNSGRNVSGVSYNAWINTGGNQYIYSDGEATAAVNTSGFORINSGGTAPVQ 455
QY 328 -----WRNKKTTTANGQ-----TG 340
DB 456 NSVVVTRTVSSAAKPFDAEYVSGGKQTVYLWRGIWYSNFLTAVWSMFPCTASGANVLSG 515
QY 341 QADKFTVTSQT-----KVTASNGTGTATVSKDDQGNITVKYDVNVGDALNVNQLO-- 392
DB 516 RLNFAGNVVGTILNOBGRQYVYSGATATSTVGNNEGREGYVLSGGITDGTVLNSGLQAV 575
QY 393 NSGNWLDKAVAGSSGKVT--SGNYSPSKGMDETWINAGN--NIEITRNGKNIDIAIT 447
DB 576 SSGKASATVINEGGAQFYVDGGQVGTGNIKNGGIRVDSGSALNIALS--SGGNLFTST 634
QY 448 SMT-POFSSV-----SLGAGAD-----APTLSVDDEGALN- 476
DB 635 GATLPELTMAALSVSQNSHASNIVLENGGLLRVTSGGTATDTVNSAGRLRIDGGGTNG 694
QY 477 -----VCSKDANKPVRTNAP----- 493
DB 695 TTTINADGIVAGTNTIQDNGFNLNLAENYDFETELSGSVLVKDNITGIMTYAGTLTQAQG 754
QY 494 -GVKEG-----DVTNVAQLKGVAQN-----LNNRIDNVDCNARA 526
DB 755 VNVKNGGIIFDSAVNVNADMAVNQNAVINISDQATINGSVNNGSIVINNISI--INGNITN 812
QY 527 GIAQAIATAGLAQAYLPGRKSM-----MAIGGGT-----YRGEAGYAIYSSSI--- 568
DB 813 DADLSFGTAKLLSATVNSGSLVNNKNILNPTKESAGNTLTVSNYTTCTPGSVISLGGVLEG 872
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QY 569 --SDTGNWVIKGTASGNS 584
DB 873 DNSLTDRLVVKGNTSQGS 890
RESULT 3
YDEK_ECOLI
ID YDEK_ECOLI STANDARD; PRT: 1325 AA.
AC P32051; P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE Hypothetical lipoprotein ydek precursor (OREF).
GN YDEK OR ORF1 OR BL510.
OS Escherichia coli
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RC SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,
RA Samei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoj P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
RT to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38.";
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
CC (Potential).
CC -!- SIMILARITY: TO E.COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -!- CAUTION: REF. 3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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CC -----
CC EMBL; AF000248; AAC74583.1; .
CC EMBL; D90793; BAAL1590.1; ALT_INIT.
CC EMBL; D90794; BAAL1597.1; ALT_INIT.
CC EMBL; X73295; CAA51730.1; ALT_FRAME.
CC PIR; S34315; S34315.
CC EcoGene; EG11780; ydek.
CC PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.
```

KW Hypothetical protein; Membrane; Lipoprotein; signal;  
KW Complete proteome.  
FT SIGNAL 1 18 POTENTIAL.  
FT CHAIN 19 1325 HYPOTHELICAL LIPOPROTEIN YDEK.  
FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).  
FT CONFLICT 884 N -> K (IN REF. 3).  
FT CONFLICT 1317 M -> S (IN REF. 3).  
SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;

Query Match 7.08; Score 213.5; DB 1; Length 1325;  
Best Local Similarity 22.1%; Pred. No. 0.002;  
Matches 147; Conservative 72; Mismatches 271; Indels 159; Gaps 28;

QY 1 MNRIYIWNALNAAVYVSELTRNHTKRASATVATATLFLPATVQANATDDDDLYLE 60  
DB 1 MNRIYIWNCTLOVFOACSELTRACKTSTVNLKSSGLTTFESRL----- 47  
QY 61 PVQRTAVVLSFRSDKEGTG---EKEGTEDSNWAVYFDEKRY--LKAGAILTKAGDNLKIK 115  
DB 48 ---TLGVLLALSGSASCASLEVDNDQITNIDTDVAYDLVGVGTGVLNLAGGNASLT 104  
QY 116 QNT-----NENTNENTNDSSFYSLAKDLTDLTSVTEKLSFGANGKNYNI--TSDTKGL 168  
DB 105 TITTSVIGANEDSEGTVNVLGGMRL-----YDSGNARPLNVGQSGTGL 150  
QY 169 N-----FAKETAGTNGDPTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKRA 218  
DB 151 NIKQKHVDGGLRLSGTGGTVNVEGEDSVLTTLFELG--SYGTGSLNITD----- 203  
QY 219 ASVKDVLNAGNIKGVKPGTASDNDVFRYDVEFLSADTKTTTVNVESKONGKKTEV 278  
DB 204 -----KG-----YVTSIVA-----ILGYQAGSNGQVVVE 228  
QY 279 KIGAKTSVIEKDGKLVTKGKDENGSTDEGEGLYTAKEVIDAVNKAGRMKTTTANGQ 338  
DB 229 KGG--EWLKNNDSSIEFQIGNQGTGATIREGLVTAENTIIIGNATG----IGTLNVQ 282  
QY 339 TGOADKFTVSGTKVTFASGNGTATVSKDDQGNIVK--YD--VNVGDALN--VNLQNS 394  
DB 283 ----DQDSVITVRLYNGYFGNG---TVNISNGLINNKKEYSLVGVQDGHGVVNVTDKG 335  
QY 395 GWNL-----DSKAVAGSGKVIISGNVSPSKMKMDTVNINAGN----- 432  
DB 336 HWNPLGRGEAFRYIIGDAGDGLNVSSEKGVDSGIITAG---MKET---GTGNITVKDK 389  
QY 433 NIETRNKNIDTATSWTPQFSSVSLGAGADAPTLSDVDEGALNV-----GSKDANKPVR 487  
DB 390 NSVITNLGTLNLYDGHGEMNISNOGLVYVNSGSSLSYGETGVGNVSTITGGMWEVKNVY 449  
QY 488 ITNVAPGVKEGDVNTVAQLKGVAQNLRNIDVNDGNARAGIAOIA---TAGLAAQAYLPG 544  
DB 450 TTIGVAGVGNLNTSDGG--KEVSONITFLDGKASGICITLNLMDATSSFDVINGVNF-G 506  
QY 545 KSMMAIGGGYRGEAGYAI-----GYSSISDTGNWIKGTASGNSR 585  
DB 507 SGIVNVNNGATLNTSGYGTGCGNAGSGIVNISTDSLWNLK--TSSTNAQ 554

## RESULT 4

HLVA\_SERMA STANDARD; PRT; 1608 AA.  
ID HLVA\_SERMA  
AC P15320;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-NOV-1990 (Rel. 16, Last annotation update)  
DE Hemolysin precursor.  
GN SHLA.  
OS Serratia marcescens.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Serratia.  
OX NCBI\_TaxID=615;  
RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.  
RC STRAIN=SN8;  
RX MEDLINE=88257037; PubMed=3290200;  
RA Poole K., Schiebel E., Braun V.;  
RT "Molecular characterization of the hemolysin determinant of Serratia marcescens.";  
RL J. Bacteriol. 170:3177-3188(1988).  
CC -I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.  
CC -I- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.  
CC -I- SUBCELLULAR LOCATION: Outer membrane.  
CC -I- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).  
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CC  
CC EMBL; M22618; AAA50323.1; .  
DR PIR; A28182; A28182.  
KW Hemolysin; Toxin; Outer membrane; signal.  
FT SIGNAL 1 30 HEMOLYSIN.  
FT CHAIN 31 1608  
SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;

Query Match 6.9%; Score 210; DB 1; Length 1608;  
Best Local Similarity 22.1%; Pred. No. 0.0036;  
Matches 159; Conservative 89; Mismatches 275; Indels 196; Gaps 34;

QY 24 RNHTKRASATVATATLTL-----FATVQANATDDDDLYLE---PVQRTAVVLSFRSDK 75  
DB 396 REQLQOAGSTVAASGSAKLSTQEDVLLGANVSADRALSKAARDVHLAGLVEKDKSE 455  
QY 76 EG--TGEKEGTEDSNWAVYFDEKRYLKA-----GAILKAGDNLKIKONTNENTN 127  
DB 456 RGYQRNHTSSLRKTGRWS--NSDESELSKASELSEGLTLKAGRVNS--TQAKVHAQADLT 513  
QY 128 ---DSSFTYSLKDLTDLTSVTEKLSFGANG---NKVNITSDTKGLNFAKETAGTNGDP 181  
DB 514 IDADNQIOGVQK--TANAKAVRDDKTSWGGIGGDKNN--SNRREISHASEL--TSGG-- 567  
QY 182 TVHLNG--IGSTLTDLL--NTGATTNTVNDVNDDEKKRAASKVDVLA---GWNIKGV 234  
DB 568 TRLNCOQGVITGSKARGQKGEVTAHGLRID--NALSTTVDKIDARTGAFNI--- 622  
QY 235 KPGTTASDNDVFRYDVTVEFLSADTKTTTVNVESKD--NGKKT---EVKIGAKTSVIKE 289  
DB 623 ---TSSSHKADNSYQSSTASELSKSDTNLTLSVHKDADVIGSVASGSGELSVESKTGINV 679  
QY 290 KCKLVTKGCKDENGSTDEGEGLVT---AKEVIDAVNKAGWRM-----KTT----- 333  
DB 680 KAA-----ERQNIDEQKALTIVNGYAKAGDKQYRAGLRIEHTRDSEKTRTENS 730  
QY 334 -----TANGOTQADKFTVTSGTKVTFASNGTTA----- 364  
DB 731 ASSLSGGSVKLKAEDKDVTFSGSKLVADKGDASVSGNKVSFLAADDKKTASNETQTKIGGGF 790  
QY 365 -----TVSKDDQGNITVKYDVNVGVALNVQLONS 394  
DB 791 YVTGGIDKLGSGVEAGYENNKTAQSSKAITSGSDVKGNLT-----INARDKLTQQGQSHS 846  
QY 395 GWNLDKSAVAGSGKVIISGNVSPSKMKMDTVNINAGNNTIEITRNKNIDTATSMTPQFS 454  
DB 847 VGGAYQENAGVDHLAAADTASTTTTKTDVGVNI-----GANVDYSATVRPVER 895  
QY 455 SVSLGAGADAPTLSVDEG-----ALNVGSKDANKPVRITN---VAPGVKEGDV----- 500

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Db 896 AVGKAALDA-TGVINDIGGAPNVGLDIGAOGSSSEKRSQAVSSVQAGSIDINA 954
QY 501 -----TNAOLKCAVONLN-----NRIDVGNARAGIAQAATAGLAQAYL 542
Db 955 KGEVRDQGTQYQASK-AYNLADSRHSRAAANDEQSDRTGSGVRVYTTTGSDLTV 1013
QY 543 PKSMMAIGGGTYRGAGYAIGYSSISDTGNW-----VIKGTASGNSRGHFGASA 592
Db 1014 DAKG-----EGGTQRSSSSASQAVTGSIDAANGINNVKKDAIYQGTALNGRGRKTAVNA 1068

RESULT 5
OMPA_RICRI
ID OMPA_RICRI STANDARD; PRT; 2249 AA.
AC P1592L;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
  antigen) (rOmpA) (rOmpA).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
  repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -I- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
  S-LAYER WITH HEXAGONAL SYMMETRY.
CC -I- PTM: GLYCOSYLATED (PROBABLE).
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC
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  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31227; AAA26380.1; -
DR PIR; A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.
FT SIGNAL 1 28 POTENTIAL.
FT CHAIN 29 2249 OUTER MEMBRANE PROTEIN A.
FT DOMAIN 212 1180 13 X APPROXIMATE TANDEM REPEATS.
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE II).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;
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Query Match 6.5%; Score 197; DB 1; Length 2249;
Best Local Similarity 22.3%; Pred. No. 0.023;
Matches 143; Conservative 71; Mismatches 261; Indels 166; Gaps 29;

QY 34 VATAVLATLLFATVOANATDDDDLYLEPQRTAVVLSFRSDKECTGKECTEDSNNAVYF 93
Db 39 VATGVATNNNAAFSNNVGNNN---WNEITAAGV-----ANGTPAGGPONNAFTY 86
QY 94 D-----EKRLKA-----GAI-----TLKAGDNLKIKQ 116
Db 87 GGDYTVTADAADRIKAINVAGTTPVGLNITQNTVGSIIKGNLLPVLNAGKSLTNG 146
QY 117 NTNENTNENTSSFTYSLKKDLTDLTSVETEKLSFGANG-----NKVNITS--DT 165
Db 147 NNAVAANHGFADAPDNY-----TGLGNIALG-----GANAALIQAAPSKITLAGNIDG 196
QY 166 KGLNFAKETAGTNGDPTVHLNGIGSTLTDLTLLNTGATTNVTNDNV---TDDEKKRAASYK 222
Db 197 GGIIVTKTDAAINGT-----IGTNALATVNVAGTATLGGAIVKATTKLTNAASVL 249
QY 223 DVLNAGWNKGVKPGTITASDNVDFVRTYDTVEFLSADTKTT---TVNVESKD---NG-- 273
Db 250 TLTNANAVLTGAIDNTTGGDNVGLNLNGALSQVTDGIGNTNSLATISVGAGTATLGGAV 309
QY 274 -KTEVKIGAKTSVIEKDKGLVTG---KGDENGSTDEGEGLVTAK----EVIDAVN 324
Db 310 IKATTTKLTDAASAVKFTNPVVVTGAIDNTGNANNGIVTFTGNSVTGNVGNNTALATVN 369
QY 325 KAGWRMKTITANGQTQOAKFETVTSKVTTFASGNGTATATVSKDDQGNIT---VKYDVN 381
Db 370 VGAGLLQ---VOGGVVKANTINLTDNASAVTFT--NPVVVTGAIDNTGNANNGIVTFTGN 424
QY 382 ---VGDAANVNOLNSGWNLDKAVAGSSGKVIISGNVSPSKGKMDFTVNINA--GNNIEI 436
Db 425 STVTGIDGNTNALTATVNVGAGTATLGGAIVKATTKLTNAASVLTLT--NANAVLTGAIDN 483
QY 437 TRNGKNIDIAI-----SMTPOQSSVSLGAGADAPTLSVDDEGALNVGSKDANK 484
Db 484 TTGSDNVGLNLNGALSQVTDGIGNTNSLATISVGAG--TATLGGAVIKATTTKLTDAAS 541
QY 485 PVRTINVAPGKEDVTNVAQLKGVQNLNNRIDNVGDNARA-----GIAQAIATAGLAQA 540
Db 542 AVKFTN--PVVVTGAIDNTG-----NANNGIVTFTGNSVTGTDGIGNTNSLAT----- 586
QY 541 YLPCKSMATGGCTGYRGEAGYAIGYSSISDTGNWIKGTAS 581
Db 587 -----ISVGAGT-----ATLGGAVIKATTT 606

RESULT 6
HLVA_PROMI
ID HLVA_PROMI STANDARD; PRT; 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN=ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
  hemolysin genes (hpmA and hpmB) reveals sequence similarity with the
  Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -I- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
  CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
```

CC DEFINED.  
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM  
CC ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA  
CC REQUIRES HPMB FUNCTION.  
CC -!- SUBCELLULAR LOCATION: Outer membrane.  
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA  
CC MAY BE RESPONSIBLE FOR PORE FORMATION.  
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; M30186; AAA25657.1; --  
DR PIR; A35140; A35140.  
DR Hemolysis; Toxin; Outer membrane; Signal.  
FT SIGNAL 1 29  
FT CHAIN 30 1577 HEMOLYSIN.  
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;  
  
Query Match 6.2%; Score 190; DB 1; Length 1577;  
Best Local Similarity 20.1%; Pred. No. 0.034;  
Matches 142; Conservative 101; Mismatches 227; Indels 238; Gaps 35;  
  
QY 23 TRNITKASATVATA-----VLAYLLFATVQANATDDDDLLKLEPVQRTAVVLSF 71  
DB 619 TNKQTSGLSELISAQTLTVSGNDVNVIGSLKSAKGLHLSGLDINVKSAQQVTKIDDE 678  
QY 72 RSDREGTGEKGTEDSNVAVFDEKRVLKAGAITLKAGDNLKIKONTNENTNENTDSSF 131  
DB 679 KTSIAITGHAKVEKQYSAGF-----HITHTKNKNTSTTEQANS 719  
QY 132 TYS-----LKKDLT-----DL-----TSVETKLSFGANGKVNITSDTKGLNFAKET 174  
DB 720 TISGANVDLOANKDVTAGSLDKTTAGNASITGDNVAFVSTENK-----KQT 766  
QY 175 AGTNGDPTVH-----LNGIGS-----TLDTLLNTGATNTVND----- 208  
DB 767 --DNTDTTISGGFSYTGVDKVGSKADFDYDKOHTQTEVTNKRGSQTEVAGDLTITANKD 824  
QY 209 -----NVTDEKKRAASKVDVLNAGWNI-----KGV 234  
DB 825 LHEGASHHVEGRYQESGENIQHLAVNDSETSKTDSLNVGIDVGNLDYSGVTPVKKAI 884  
QY 235 KPG-----TTASDNVDF-----VRTYDFVEFLSADTKTTTVNVESKDKGKKTEVKIGAKTSVIK 288  
DB 885 EDGVNTTKPGNNTDLTKKVTARDAIANLA-----NLSNLETTPNVGVEVIGKGG--SQQS 937  
QY 289 EKDKGLVT-----GKKG-----DENGSTDEGGLVTAKEVIDAVNKAQWTKMTTANGQTGQA 342  
DB 938 QTDQAVSTSNAGKIDIDSNKHLHQGTHYQSTQEG-----SLTANTHTSEA 986  
QY 343 --DRFEVTVSTGK-----VTFASGNGTTATVSKDDQGNITVKYDVNVGDALNVLQNSGW 396  
DB 987 TLDKHQHTFTHETKGGGQIGVSTKGTSDITVAIKEGQTT-----DNALMETHKAKGSQF 1039  
QY 397 --NLDSKAVAGSSGKVISGNVSPSKMDTEVTNINAGNNIEITR-----NGK- 441  
DB 1040 TSNGDISINVENGAHVEGAQFDQKKGK--TV-INAGGDLTLAQATDTHSESQSNVNGSA 1095  
QY 442 NIDATSWTQFQSSVSLGACADPTL-SVDDEGALNVGSKDANKPVKITVAPCVKGGDV 500  
DB 1096 NLKVGK--TPE--SKDYGGFNAGTTHHSKEQTTAKVGTITGSQIGELNAGHNLTLQG-- 1149  
QY 501 TNVAOLKGVANLNRIY-----NVDGNARAGTAQ-----ATATAGLAQAYL 542  
DB 1150 THLSSEODIALNATNKVDLQASASSEHTEKGNLSSGVQAGFGKKMTDASSVNGL----- 1204

QY 543 PGKSMMAIG-----GGTYRGEAGYAIGYSSISDGTGNWIKGTA 580  
DB 1205 -GSAQFAIGKQDEKSVSREGT-----INNSGNLTNGNS 1238  
  
RESULT 7  
OMPB\_RICRI  
ID OMPB\_RICRI STANDARD; PRT; 1654 AA.  
AC Q53047;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)  
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
GN OMPB.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=92167802; PubMed=1724278;  
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;  
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia  
RT rickettsii is encoded by an unusually long open reading frame:  
RT evidence for protein processing from a large precursor.";  
RL Mol. Microbiol. 5:2361-2370(1991).  
RN [2]  
RP SEQUENCE OF 279-1654 FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=90136087; PubMed=2515418;  
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
RT "Cloning, expression and sequence analysis of the gene encoding the  
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";  
RL Mol. Microbiol. 3:1579-1586(1989).  
CC -!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR  
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
CC LAYER WITH HEXAGONAL SYMMETRY.  
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
CC -----  
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CC -----  
DR EMBL; X16353; CAA34403.1; --  
DR InterPro; IPR003858; rOmpA\_rOmpB.  
DR Pfam; PF02708; rOmpA\_rOmpB; 1.  
KW Antigen; S-layer; Cell wall.  
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.  
FT DOMAIN 1181 1188 POLY-THR.  
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;  
  
Query Match 6.2%; Score 188; DB 1; Length 1654;  
Best Local Similarity 21.9%; Pred. No. 0.045;  
Matches 159; Conservative 85; Mismatches 285; Indels 198; Gaps 36;  
  
QY 15 AVWVSELTNRHTKRA-----SATVATVATL-----LFATVQA-NATDDD 55  
DB 181 ASTLVFNLANPTTQKAPLILGDNAVINGVNTLVNTGTFQVSNKSFATVKAINIADGQ 240  
QY 56 DLYLEPVQRTAVVLSFSDKGEKGTEDSNVAVFDEKRVLKAGAITLKAGDNLK-- 113

Db 241 GIIFNTDANNANLNLQAGGT-TINFGTGDTGRLVLLSKHAAATNFNITSLGGNKG 299  
QY 114 IKONT-----NENTNENTND-----SFTYSLKLDLTDLTSVETEKLSFGANG 156  
Db 300 IEFNVAVDQGLTANAGANAVIGNNGAGRAAGFVSV-----NG 341  
QY 157 NKVNITSPTKGLNFAKETAGTAGNDPTV-HLNGIGSTLTDLTLLNTGATTVNTNDN--VTDD 213  
Db 342 KVATIDGOVYAKDMVQSANATQVNFRIHVDVGADGTTAFKTAASKVITITQDSNFGNTD 401  
QY 214 EKKRAASVK--DVLNAGNWK--VKPGTASDNVDFVRYD---TVEPLSADTKTTTVN 266  
Db 402 FGNLAQIKVPNAITLTGNTGDASNPGTAG-----VITFDANGTLESADANAVTN 456  
QY 267 ---VESKDNG-----KKTETVKIGAKTSVIKEXDKLVTKG-----CKDENGSGT 307  
Db 457 NITAIERSAGVQVLSGTHAEELRLGNAGSIFKLADGTVINQVKTALVGGALAGTIT 516  
QY 308 DEGEGLVTAKEVIDAVNKAGWRMKTITANGOTQADKFETVTSKTVTFASNGT----- 362  
Db 517 LOGSATITGD--IGNAGGAALQRITLAN-----DAKKTLLGGAIIIGAGGTIDLQA 568  
QY 363 -----TATVSKDDGNTTVKYDV-----NVGDALNVNQLNSGWN-----LDSK 401  
Db 569 NGGTIKLTST-----QNNIVVDFDLAIAITDQTCGVVDASSLTNAQTILTKIGTIGANNK 623  
QY 402 AVA---GSSGKVIS-GNV-----SPSKGKMDTETVNLN 429  
Db 624 TLQFNIGSKSVLNSGNVAINELVINGDGAQVFAHDTYLIITRTNAAOGGKIIFNPVN 683  
QY 430 AGNIEITRNGKNIDATSMTPQFSVSLGAGADAPTLSDVDEG-----ALNVGSKDANKP 485  
Db 684 NGTTLAA---GTNLGSATNPLAEINFGSKGVNVD--VLNV-GEVNLXATNTITTDANVG 738  
QY 486 VRI-----TNVAPGV---KEGDTVNVQALKG---VAONLNRRDN-----VDGN 523  
Db 739 SEFVNAGGTNIYSGTVGGQGNKFNVALENGTTVKFLGNATFNNGNTTIAANSTLQIGGN 798  
QY 524 ARAGIAQAIATAGLAQAYLPKSMMAIGGTYRGEAGYAIYSSISDTCNWNKIGTASGN 583  
Db 799 YTADCVASADGTGIVEFVNTGITVTL---NKQAPVNAKQITVSGPGNVVI--NEIGN 853  
QY 584 SRGHFGA 590  
Db 854 AGNHGCA 860  
RESULT 8  
ID OMPA\_RICCN STANDARD; PRT: 2021 AA.  
AC Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;  
AC Q52670; Q52674;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOmpA) (rOmp A).  
GN OMPA OR RC1273.  
OS Rickettsia conorii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiae; Rickettsia.  
OX NCBI\_TaxID=781;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Mallish 7;  
RX MEDLINE=94171067; PubMed=8125327;  
RA Croquet-Valdes P.A., Weiss K., Walker D.H.;  
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Mallish 7 strain).";  
RL Gene 140:115-119(1994).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-Mallish 7;  
RX MEDLINE=21442074; PubMed=11557893;  
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;  
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii."; Science 293:2093-2098(2001).  
RL [3]  
RP SEQUENCE OF 8-204 FROM N.A.  
RC STRAIN-Indian tick typhus, M1, Malish 7, and Moroccan;  
RX MEDLINE=97015921; PubMed=8862558;  
RA Roux V., Fournier P.E., Raoult D.;  
RT "Differentiation of spotted fever group rickettsiae by sequencing and analysis of restriction fragment length polymorphism of PCR-amplified DNA of the gene encoding the protein rOmpA."; J. Clin. Microbiol. 34:2058-2065(1996).  
RL [4]  
RP SEQUENCE OF 953-2012 FROM N.A.  
RC STRAIN-Indian tick typhus, M1, Malish 7, and Moroccan;  
RA Raoult D., Fournier P.E., Roux V.;  
RT "Phylogenetic analysis of spotted fever group rickettsiae by study of the outer surface protein rOmpA."; Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.  
RL  
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY (BY SIMILARITY).  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -!- PTM: GLYCOSYLATED (BY SIMILARITY).  
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
CC  
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CC  
CC EMBL: U01028; AAA17405.1; -  
DR EMBL: AE008674; AAL03811.1; -  
DR EMBL: U43794; ABA9549.1; -  
DR EMBL: U43798; ABA9550.1; -  
DR EMBL: U43806; ABA9551.1; -  
DR EMBL: U45244; ABA9566.1; -  
DR EMBL: U46918; ABA8666.1; -  
DR EMBL: U83440; AAC35176.1; -  
DR EMBL: U83443; AAC35179.1; -  
DR EMBL: U83448; AAC35184.1; -  
DR EMBL: U83453; AAC35189.1; -  
DR InterPro: IPR003858; rOmpA\_rOmpB.  
DR Pfam: PF02708; rOmpA\_rOmpB; 1.  
DR Antigen: Repeat; Signal; Cell wall; S-layer; Glycoprotein; Complete proteome.  
KW  
FT SIGNAL 1 38  
FT CHAIN 39 2021  
FT DOMAIN 238 946  
FT DOMAIN 1424 1528  
FT VARIANT 60 60  
FT VARIANT 76 76  
FT VARIANT 86 137  
FT VARIANT 126 133  
FT VARIANT 953 954  
FT VARIANT 1245 1245  
FT VARIANT 1308 1308  
FT VARIANT 1877 1877  
FT CONFLICT 10 10  
FT CONFLICT 92 92  
FT CONFLICT 126 126  
FT CONFLICT 137 137  
FT CONFLICT 157 157  
FT CONFLICT 369 369  
FT CONFLICT 374 388  
FT CONFLICT 640 640  
FT CONFLICT 1  
FT N -> D (IN REF. 1).  
FT N -> H (IN STRAIN MOROCCAN).  
FT M -> I (IN STRAIN INDIAN TICK TYPHUS).  
FT Q -> K (IN REF. 1).  
FT I -> V (IN REF. 1).  
FT V -> I (IN REF. 1).  
FT T -> N (IN REF. 1).  
FT G -> D (IN REF. 1).  
FT IS -> VN (IN REF. 1).  
FT KATLGAIKATTK -> LLOVQGVVKANTIN (IN REF. 1).  
FT N -> D (IN REF. 1).

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FT CONFLICT 669 669 V -> I (IN REF. 1).
FT CONFLICT 793 793 N -> D (IN REF. 1).
FT CONFLICT 803 804 VN -> IS (IN REF. 1).
FT CONFLICT 809 823 LLRVGGVKSNTIN -> KATLGGAIIKATTK (IN
REF. 1).
FT CONFLICT 898 898 D -> Y (IN REF. 1).
FT CONFLICT 908 908 P -> N (IN REF. 1).
FT CONFLICT 985 985 N -> K (IN REF. 1).
FT CONFLICT 1009 1009 L -> S (IN REF. 1).
FT CONFLICT 1013 1013 Y -> S (IN REF. 1).
FT CONFLICT 1182 1182 K -> Q (IN REF. 1).
FT CONFLICT 1314 1314 N -> Y (IN REF. 4).
FT CONFLICT 1451 1451 H -> N (IN REF. 1).
FT CONFLICT 1624 1624 G -> D (IN REF. 1).
FT CONFLICT 1628 1628 E -> G (IN REF. 1).
FT CONFLICT 1872 1872 A -> V (IN REF. 1).
FT CONFLICT 1875 1875 T -> P (IN REF. 1).
FT CONFLICT 1878 1878 MS -> LP (IN REF. 1).
FT CONFLICT 1936 1936 E -> A (IN REF. 1).
FT CONFLICT 1965 1970 MTAFLP -> ITPLS (IN REF. 1).
FT CONFLICT 1997 1997 G -> R (IN REF. 1).
FT CONFLICT 2021 AA; 203328 MW; 327FC42D7CB24668 CRC64;
SQ SEQUENCE

Query Match 6.1%; Score 187; DB 1; Length 2021;
Best Local Similarity 21.6%; Pred. No. 0.064;
Matches 176; Conservative 86; Mismatches 287; Indels 264; Gaps 40;

QY 10 NSALNANVVVSELTRN-HTKRASATVAT-AVLATLLFATVQANATDDDD-----LYLEPV 62
DB 415 NNGVITFGDSTVGTGNTGNATATISVGAGKATLGGAIIKATTKLTDNASAVTFNPV 474
QY 63 QRTAV-----VLSFRSDKGEKTEKEDSNNVAVFDEKRVLKAGAI-----TLKA 108
DB 475 VVTAIDNTGNANNGVITFGDSTVGTG-NIGNTNALATISVGAGKATLGGAIIKATTKL 533
QY 109 GDNLIKIKONTN-----ENT-NEN-----TNDSSFTYSL-KKDLTDLTSVETEKLSF 152
DB 534 TDNASAVTFNPVVVTVGAIDNTGNANNGVITFGDSTVGTGNTGNATATISVGAGKATL 593
QY 153 GA-----NGKNVITSDTKGLNFAKETAGTN-----GDPVHLNGIGSTLT 193
DB 594 GGAIKATTKLTLDNASAVTFNPVVVTVGAIDNTGNANNGVITFGTGNSTVTGN-IGNTNA 652
QY 194 DTLLNTGA-----TTVNTDNDVTDDEKRAASVKDVLNAGNKGKPGTTA 240
DB 653 LATVNVGAGIATLEGAVIKATTKLTN-----AASVLTITNNNAVLTGAIDNTG 702
QY 241 SDNVDFVRYTDVFEFLSADTKTT-----TVNV-----ESKDNG---KKTEVKIGAKTSVIEK 290
DB 703 VDNVGVNLNGALSQVTGNTGNATATISVGAGKATLGGAIIKATTKLTLDNASAVTF 762
QY 291 DGKLVGTG---KGDENGSSTDEGEGLVTAK-----EVIDAVNKA-----GWRMKTTTA 335
DB 763 NPVVVTVGAIDNTGNANNGIATFTGDSVGTGNTGNATATVNVGAGLLRVGGVYKNTI 822
QY 336 N-----GOTGQADK-FETVTSKTKTFASGN-GTTATVS-----367
DB 823 NLTDNASAVTFNPVVVTVGAIDNTGNANNGVITFGDSTVGTGNTGNATATISVGAGKA 882
QY 368 -----KDDOGNITKYIDYVNGDALNVNLQNSGWNLDKAVAGSSGKVI 413
DB 883 TLGGAIKATTKLTLDNASAVTFNPVVVTVGAID-----NTG-NANNGVITFGDSTVGTG 936
QY 414 NVSPSKMDETNYINAGNIEI---TRNGKNIDTATSKTQFSSVSLGACADAP-----T 466
DB 937 NIGNTNAL--ATVNVGAGVTLQAGSLDANNIDFGARSTLEFNGLDGGGNAIPIYFKGA 994
QY 467 LSVDEGALNVGSK-----DANK-PVIRTN-----490
DB 995 IANGNNAILNVNTKLLTAYHLTIGTVAEINIGAGNLFAIDASAGDVITLNAQDTHFRALD 1054
QY 491 -----VAPGVKEGDV-----TNVAQLKGVAQNLNRR 516
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DB 1055 SALVLSNLTGVGVNNILLAADLVAPGVDEGTVFDDGGVNGNLNIGSNVA---GAARN-----1107
QY 517 IDNVGDNA-----RAGIAQATATAGLAQAYLPK-----SMMAIGGTYR-GEAGYAI 563
DB 1108 IGVGGKRFNLLLYNAVITDDVNLGIONVLINNADFTSSTAFNAGTIQINDATYTI 1167
QY 564 -----GYSSISDGTGNWIKGTASGNSR 585
DB 1168 DANNGLNIPAGNIKFAHADQAQLILQNSSGND 1200
RESULT 9
OMP_B_RICCN
ID OMP_B_RICCN STANDARD; PRT; 1655 AA.
AC O9KKA3; O9KKA98; O9XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Scas) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Orata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissbach J., Claverie J.-M.,
RA Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
[2]
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT "Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein rOmpB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
[3]
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases
CC -/- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -/- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -/- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -/- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC EMBL; AE008659; AL03623.1; -.
CC EMBL; AF123721; AAF34124.1; -.
CC EMBL; AF123726; AAF34129.1; -.
-----
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DR EMBL; AF149110; RAD39533.1; --  
DR InterPro; IPR003858; rOmpA\_rOmpB.  
DR Pfam; PF02708; rOmpA\_rOmpB; 1.

KW Antigen; S-layer; Cell wall; Complete proteome.

FT CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.

FT CHAIN 1335 1655 32 KDA BETA PEPTIDE.

FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).

FT VARIANT 353 354 KD -> GH (IN REF. 3).

FT CONFLICT 776 776 F -> S (IN REF. 3).

FT CONFLICT 1159 1159 E -> D (IN REF. 3).

FT CONFLICT 1177 1177 G -> S (IN REF. 3).

FT CONFLICT 1492 1492 H -> R (IN REF. 3).

SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;

Query Match 6.1%; Score 184.5; DB 1; Length 1655;

Best Local Similarity 22.1%; Pred. No. 0.067;

Matches 147; Conservative 76; Mismatches 292; Indels 149; Gaps 30;

QY 10 NSALNAWVVSELTNRHTKRASATATAVLATLLEFATVOANATDDDDLLLEPVQRTAVVL 69

Db 211 NGTLN-----VTNGFIKVSRSFATVNVINGDGGIMFNFDADNVNTLNQANGATI 263

QY 70 SFRSDKEGTGEKEDSNWVYFDEKRVLKAGAILKAGDNLK-----IKQ 116

Db 264 TF-----NGDTGRLVLLSKNAATDENVTGSLGGNLKGIIEFTVAVNQLKA 313

QY 117 NTNEN-----TNENTNDSS-FYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNF 170

Db 314 NAGANAAVTGTNNGAGRAAGFVVSVD-----NGKVATIDQGVYAKDM 355

QY 171 AKETACTNGDPT---VHLNGTGLSTLDTLLNTGATNTVNDVNDTDEKKRAASVKD--- 223

Db 356 VQSANAVGQVFRHIVDGTGTGTAFAKVAASKVAITQNSFGTTDFGNLAAQIIVPNTM 415

QY 224 VLNAGNIRKVKPGTTASDNVDFRTYD---TVEFLSADTKTTTVN---VESKDNG--- 273

Db 416 TLNGNFTGDSNPGNTAG-----VTFDANGTLASASADANAVTNITTAIESAGAGVQ 470

QY 274 ----KTEVKIGAKTSVIEKDGKLVTKG-----GKDENGSSDTDEGLVTAKEVID 321

Db 471 LSGTHAAELRLGNAGSVFKLADGTVINGKVQNTALYGGALAAAGTITLDGSATITG---D 526

QY 322 AVNKGWRMKTITANGOTGOADKFEVTVT-----SGTKVTFASGNGTTATVSKDDQG 372

Db 527 IGNAGG-----AALQGITLANDATKTLTGGANIIGANGGTINFGANGTITKITS--TON 580

QY 373 NITVKYDV-----NVGDALNVNQLQNSGWNLDKSAVAGSGKVIAGNVPSPKGM-DE 424

Db 581 NIVVDFDLAIAITDQGVVDASSLTNAQTITINGKITGVANNKTLQFNIGSKTVLSDG 640

QY 425 TVNIN---AGNN---IEITRNGKNIDIATSMTPQ-----FSSV-----SLGAGADAPTLSDV 470

Db 641 DVAINELVINGNAGVQFAHNTYLTITRNAAGQGIENFPVNNNTTLATGTNLGS-ATN 699

QY 471 DEGALNVGSKDANKPVRIINVPAGVKEGDTNVQAQLKVAQNLNLRIDNVDG-NARAGTIA 529

Db 700 PLAIEINFGSKGANVDTVLNVGKGNL-YATNITTTTDA-----NVGSPFIKAGGTNIVSG-- 753

QY 530 QALATAGLAQ-----AYLPKSMMAIGGGTVRGEAGVAIGYSSISDGTGNVIKGTASG 582

Db 754 ----TVGGQGGKFNFTVLDNGTTFVFLGNATFNNGNTTAAAN-STLQIGGNVYADFVASA 808

QY 583 NSRG 586

Db 809 DGTG 812

RESULT 10

120K\_RICRI STANDARD; PRT; 1300 AA.

AC P14914;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE 120 kDa surface-exposed protein.

GN P120.

OS Rickettsia rickettsii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiella; Rickettsia.

OX NCBI\_TaxID=783;

RN [1]

SEQUENCE FROM N.A.

RC STRAIN=R;

RX MEDLINE=90136087; PubMed=2515418;

RA Gilmore R.D. Jr., Joste N., McDonald G.A.;

RT "Cloning, expression and sequence analysis of the gene encoding the

RT 120 kDa surface-exposed protein of Rickettsia rickettsii.";

RL Mol. Microbiol. 3:1579-1586(1989).

CC -!- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS

CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A

CC S-LAYER WITH HEXAGONAL SYMMETRY.

CC -!- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES

CC CONFERRING ANTIGENICITY TO THE PROTEIN.

CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

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entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

CC EMBL; X16353; CAA34402.1; --

DR PIR; S07575; S07575.

DR InterPro; IPR003858; rOmpA\_rOmpB.

DR Pfam; PF02708; rOmpA\_rOmpB; 1.

KW Antigen; Glycoprotein; Cell wall; S-layer.

FT CARBOHYD 7 7 N-LINKED (POTENTIAL).

FT CARBOHYD 66 66 N-LINKED (POTENTIAL).

FT CARBOHYD 86 86 N-LINKED (POTENTIAL).

FT CARBOHYD 103 103 N-LINKED (POTENTIAL).

FT CARBOHYD 147 147 N-LINKED (POTENTIAL).

FT CARBOHYD 268 268 N-LINKED (POTENTIAL).

FT CARBOHYD 330 330 N-LINKED (POTENTIAL).

FT CARBOHYD 375 375 N-LINKED (POTENTIAL).

FT CARBOHYD 415 415 N-LINKED (POTENTIAL).

FT CARBOHYD 424 424 N-LINKED (POTENTIAL).

FT CARBOHYD 430 430 N-LINKED (POTENTIAL).

FT CARBOHYD 436 436 N-LINKED (POTENTIAL).

FT CARBOHYD 444 444 N-LINKED (POTENTIAL).

FT CARBOHYD 515 515 N-LINKED (POTENTIAL).

FT CARBOHYD 547 547 N-LINKED (POTENTIAL).

FT CARBOHYD 593 593 N-LINKED (POTENTIAL).

FT CARBOHYD 655 655 N-LINKED (POTENTIAL).

FT CARBOHYD 698 698 N-LINKED (POTENTIAL).

FT CARBOHYD 710 710 N-LINKED (POTENTIAL).

FT CARBOHYD 799 799 N-LINKED (POTENTIAL).

FT CARBOHYD 800 800 N-LINKED (POTENTIAL).

FT CARBOHYD 826 826 N-LINKED (POTENTIAL).

FT CARBOHYD 844 844 N-LINKED (POTENTIAL).

FT CARBOHYD 861 861 N-LINKED (POTENTIAL).

FT CARBOHYD 879 879 N-LINKED (POTENTIAL).

FT CARBOHYD 920 920 N-LINKED (POTENTIAL).

FT CARBOHYD 926 926 N-LINKED (POTENTIAL).

FT CARBOHYD 1116 1116 N-LINKED (POTENTIAL).

FT CARBOHYD 1128 1128 N-LINKED (POTENTIAL).



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FT CARBOHYD 1140 1140 N-LINKED (POTENTIAL).
FT CARBOHYD 1146 N-LINKED (POTENTIAL).
FT CARBOHYD 1211 1211 N-LINKED (POTENTIAL).
SQ SEQUENCE 1300 AA; 132801 MW; E09E52C3F647243D CRC64;

Query Match 6.0%; Score 183.5; DB 1; Length 1300;
Best Local Similarity 21.8%; Pred. No. 0.056;
Matches 161; Conservative 93; Mismatches 273; Indels 213; Gaps 37;

QY 30 ASATVATAVLATLFAVQAN--ATDDDLVLEVPQVAVV--SPRSDKEGTEKEGTE 85
DB 22 ADGTAFTKATKATVITQDSNFGNFCNLAQAQIKVPNAITLTCNFTGCDASNPONTAG-- 79

QY 86 DSMNAVYFDEKRVLKAGAILKAGDNLKIKONTN--ENTNENTNDSSFTYSLKXDLADLT 143
DB 80 ----VITFDANGTLESAS----ADANVAVTNNITAEASGAGVVQLSGTHAAELRLGNAG 131

QY 144 SVETEKLSFGA--NGNKVNITSDTKGLNFAKETAGTNGDPTVHLNGIGSLTLDLTLNAGA 201
DB 132 SI--FKLADGTIVNG-KVNQTA-----LVGGALAAGTITLDG-SATITGDIGNAG 178

QY 202 TTNVTNDNVTDDEKRAASVKVDNLNAGNKGKPGT-----TASDN---VDF 246
DB 179 AALQRTLANDAK-----KTLPLGGANIIGAGGGTIDLOANGGTTIKLSTQNNIVVDF 232

QY 247 ---VRTYDT-----VEFLSADTKTTTVNVESKDNGK-----KT-----E 277
DB 233 DLATDQTVGDVDASSLTNAQTLTKINGKIGTIGANNKTLQGFNIGSSKTVLSNGVAIN 292

QY 278 VKIGAKTSVTEKDKGLVT-----GKKG-----DENGSTG----- 308
DB 293 LVIGNDGAVOFAHDTYILTRTNAAGOGKIIFNPVNVNGTTLAAGTNLGSATNPLAEINF 352

QY 309 --EGEGLVTAKEVIDANKAGWRMKTAN-----GQTG--QADKFEVT 349
DB 353 GSKGVNDVTVLNVEGYNLYATNITTTDANVGSFVNAGTNIVSGVGGQGNKFNTVA 412

QY 350 --SGTKVTF---ASNGGTTATVSKDD---QGNITVKVDVNVGDALNVNLQNSG---WNL 398
DB 413 LENGTTVKFLGNATFNNGNTTIAANSTLIQIGNYATDC-VASADGTGIVEFVNTGPIVT 471

QY 399 DSKA-----VAGSSKVIS--CNVSPSKMDVETNI----- 428
DB 472 NKQAPVNALQITVSGVPGNVINEIGNAGNHGAVDTTIAFENSLSGAVVFLPRGIPFN 531

QY 429 MAGNNIET-----RNGKNIDIATSWT-----POFSSVSLGAGAD--- 463
DB 532 DAGNTPLTIKSTVGNKTAQGFVPSVVVLGVDSVIADGQVIGQNNIVGLGSDNGII 591

QY 464 --APTLSV-----DREGALNVGSKDANKPVRIITNVPAGVKEGVTNVAQLKGVAQNLN 515
DB 592 VNATTLVAGISTLNNQGTVTLSGVPNTPGTVYGLGTIGASKFKQVT-----FTTDYNN 647

QY 516 RIDNVGDNARAGIAQATATAGLAQAYLPGKSWMAIGGTVRGEAGYAGYSSIDTGNV 575
DB 648 LGNIATNATINDGVTVTTGGIAGIGDFGK--ITLGSVNGNGNVRFDGILSNST--M 702

QY 576 IKGTFASGNSRGHFCASASV 595
DB 703 IGTTKANNGVTVYLGNAFVG 722

RESULT 11
ICEN_XANCT STANDARD; PRT; 1567 AA.
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
```

```
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-X56S;
RX MEDLINE-91080859; PubMed-2259339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
RT Xanthomonas campestris pv. translucens.";
RL Mol. Gen. Genet. 223:163-166(1990).
CC -I- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CC -I- CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -I- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -I- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -I- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -I- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC FAMILY.
CC -----
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CC -----
CC EMBL; X52970; CAA37140.1; -.
CC PIR; S11672; S11672.
CC HSP; P06620; IINA.
CC InterPro: IPR000258; Ice_nucleatn.
CC Pfam: PF00818; Ice_nucleation; 81.
CC PRINTS; PR00327; ICENUCLNATN.
CC DR PROSITE; PS00314; ICE_NUCLEATION; 57.
KW Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; CBB451D959ECAD63 CRC64;

Query Match 6.0%; Score 183; DB 1; Length 1567;
Best Local Similarity 20.2%; Pred. No. 0.074;
Matches 115; Conservative 83; Mismatches 274; Indels 98; Gaps 19;

QY 77 GTGKEGTEDSNAVYFDEKRVLKAGAILKAGDNLKIKONTN-----ENTNENTNDSSF 131
DB 735 GSTQTSKSDSSLTAGYGTQTARKGSDVYTAGYGTGTAGADSTLIAGYGTQTSGSDSL 794
QY 132 TYSLKDLT-----DLTSVETEKLSFGA-----NGKNVITSDTKGLNFAKE 173
DB 795 TAGYGTQTARKGSDITAGYGTGTAGADSTLIAGYGTQTSGSDSLTAGYGTQTARE 854

QY 174 -----TAGTNGDPTVHLNGIGSTLT---DTLLATGATTVNTDNDVDEKRAASV 221
DB 855 GSDVYTAGYGTGTAGADSTLIAGYGTQTAGSDSLTAGYGTQTARKGSD----- 905

QY 222 KDVLNAGWNKIGVKPGTASDNVDFVRYDTVEFLSADTKTTTVNVESKONGKTEVKIG 281
DB 906 ---VTAGYGTG-----TAGADSTLIAGYGTQTSGSDSLTAGYGTQTARKGSDMTAG 957

QY 282 AKTSVIREKDGKLVTKGKDENGSSTDEGELVTAKEVIDAVNKGAWRMKTTTANGQTG 341
DB 958 YGSGTGTAGADSTLIAGYGTQTSGS-----DSSLTAGYGTQTAREGSDVT 1003

QY 342 ADKEFTVTSKTKVTFASNGCTTATVSKDDQGNITVKYDVNVGDALNVNOLNSGNLDSK 401
DB 1004 AGYGTGTAGADSTLIAGYGTQTAGSD---SSLTAGY-----GSTQARQSGDVTAGYGT 1057

QY 402 AVAGSSKGVISGNVSPSKMDVETNINAGNIEITRNGKNIDIATSMTPQFSSVSLGAG 461
DB 1058 GTAGADSTLIAGYGTQTAGSDSLTAGYGT--QTARQGSDI-----TAGYGTGT--AG 1109
```





OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OX Bacillus/Staphylococcus group; Bacillus.  
RN NCBI\_TaxID=1423;  
RP [1]  
RC SEQUENCE FROM N.A.  
RX STRAIN=168;  
RA MEDLINE=93302506; PubMed=8316082;  
RA Foster S.J.;  
RT "Molecular analysis of three major wall-associated proteins of  
RT Bacillus subtilis 168: evidence for processing of the product of a  
RT gene encoding a 258 kDa precursor two-domain ligand-binding  
RT protein.";  
RL Mol. Microbiol. 8:299-310(1993).  
RN [2]  
RN SEQUENCE FROM N.A.  
RP STRAIN=168 / BGSC1A1;  
RX MEDLINE=95219088; PubMed=7704263;  
RA Yoshida K.-I., Sano H., Seki S., Oda M., Fujimura M., Fujita Y.;  
RT "Cloning and sequencing of a 29 kb region of the Bacillus subtilis  
RT genome containing the hut and wpa loci.";  
RL Microbiology 141:337-343(1995).  
RN [3]  
RP SEQUENCE FROM N.A.  
RX STRAIN=168 / BGSC1A1;  
RX MEDLINE=97124196; PubMed=8969509;  
RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,  
RA Miwa Y., Fujita Y.;  
RT "Sequencing of a 65 kb region of the Bacillus subtilis genome  
RT containing the lic and cel loci, and creation of a 177 kb contig  
RT covering the gnt-sacX region.";  
RL Microbiology 142:3113-3123(1996).  
CC -!- FUNCTION: STILL UNKNOWN. NOT INVOLVED IN CELL MEMBRANE METABOLISM,  
CC MOTILITY, SECRETION OR DIFFERENTIATION.  
CC -!- SUBCELLULAR LOCATION: MEMBRANE-ASSOCIATED. MAY BE RELEASED  
CC INTO THE MEDIUM.  
CC -!- DOMAIN: HAS TWO LIGAND-BINDING DOMAINS; THE N-TERMINUS, HAS THREE  
CC 101 AA REPEATS WHICH ARE RESPONSIBLE FOR CELL WALL BINDING; THE  
CC C-TERMINUS CONSISTS OF TWO BLOCKS OF RESIDUES WITH A CONSERVED  
CC MOTIF REPEATED 31 TIMES.  
CC -!- SIMILARITY: THE REPEATED MOTIF IN THE C-TERMINUS HAS SOME  
CC SIMILARITY TO THE REPEAT IN E. COLI RHS GROUP OF PROTEINS (RHS-A-D).  
CC -----  
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CC -----  
DR EMBL; L05634; AAA22883.1; -  
DR EMBL; D31856; BAA06656.1; -  
DR EMBL; D29985; BAA06260.1; -  
DR EMBL; D83026; BAA11683.1; -  
DR EMBL; Z99124; CAB15959.1; -  
DR PIR; S32920; S32920.  
DR Subtilisin; BG10797; wapa.  
DR InterPro; IPR003305; CBD\_6.  
DR Pfam; PF02018; CBD\_6; 1.  
KW Cell wall; Repeat; Signal; Complete proteome.  
FT SIGNAL 1 28  
FT CHAIN 29 2334  
FT DOMAIN 504 869  
FT REPEAT 504 869  
FT REPEAT 504 869  
FT REPEAT 636 736  
FT REPEAT 769 869  
FT DOMAIN 1021 2139  
FT REPEAT 1021 1040  
FT REPEAT 1042 1061  
FT REPEAT 1063 1082  
FT REPEAT 1083 1102  
FT REPEAT 1109 1128  
FT REPEAT, 2-1.  
FT REPEAT 2-2.  
FT REPEAT 2-3.  
FT REPEAT 2-4.  
FT REPEAT 2-5.  
FT REPEAT, 31 X 21 AA APPROXIMATE TANDEM REPEATS OF  
FT X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).  
FT REPEAT, 3 X 101 AA APPROXIMATE TANDEM REPEATS.  
FT 1-1.  
FT 1-2.  
FT 1-3.  
FT 31 X 21 AA APPROXIMATE TANDEM REPEATS OF  
FT X(4)-G-X(4)-[YF]-X-D-X(2)-G-X(4).  
FT REPEAT 2-1.  
FT REPEAT 2-2.  
FT REPEAT 2-3.  
FT REPEAT 2-4.  
FT REPEAT 2-5.

FT REPEAT 1148 2-6.  
FT REPEAT 1150 2-7.  
FT REPEAT 1174 2-8.  
FT REPEAT 1199 2-9.  
FT REPEAT 1219 2-10.  
FT REPEAT 1238 2-11.  
FT REPEAT 1646 2-12.  
FT REPEAT 1667 2-13.  
FT REPEAT 1690 2-14.  
FT REPEAT 1711 2-15.  
FT REPEAT 1732 2-16.  
FT REPEAT 1753 2-17.  
FT REPEAT 1795 2-18.  
FT REPEAT 1820 2-19.  
FT REPEAT 1840 2-20.  
FT REPEAT 1861 2-21.  
FT REPEAT 1887 2-22.  
FT REPEAT 1908 2-23.  
FT REPEAT 1929 2-24 (APPROXIMATE).  
FT REPEAT 1969 1982  
FT REPEAT 1983 2002  
FT REPEAT 2008 2027  
FT REPEAT 2028 2047  
FT REPEAT 2051 2070  
FT REPEAT 2071 2090  
FT REPEAT 2093 2112  
FT REPEAT 2120 2139  
SQ SEQUENCE 2334 AA; 258329 MW; B75138CCD278BAA3 CRC64;

Query Match 6.08; Score 182.5; DB 1; Length 2334;  
Best Local Similarity 21.3%; Pred. No. 0.13;  
Matches 151; Conservative 90; Mismatches 270; Indels 199; Gaps 30;

QY 24 RNHTKRASAVATVATLTLFATVQANATDDDDLLYLPVQRTAVVLFSRSDKGTGEGK 83  
DB 7 RNKRFTAALVLVLAIMLSLPADVLAKSTEE-----ENGRIAA-----DDPETLOREQ 56  
QY 84 TEDSNWAVYFDEKRVLKAGAITLKAGDNLKI-----KQ-----NTNENTNENTND 128  
DB 57 TEE---AVPEDPKDINKEGETSERTENTKLYBEGDGVYKQEVYLDPIHTTKETPDADWED 113  
QY 129 SSFTYSKLKDLTDLTS--VETEK-----LSFGANGKNVNT--SDTKGLN 169  
DB 114 -----ISPELKESTKQVETENAILNSDFQOMKNGLYATFEHNDHKVITYSLAEAKGN 167  
QY 170 FAKET-AGTNGDPVHLNGIGSTLTDLTLNTGATTNTNDNVTD-----E 214  
DB 168 KTSLTPKDTSADYKTDSENI--VYDPVFPNIDLQTFTEFNENIKEDLVHLHYNGYNTFTFQ 225  
QY 215 KKRAASVYKVDVLNAGWNIKGVKPGTTASDNVDVFTYDTVEFLSADTKIT---TVNVESKO 271  
DB 226 LKTDLOAKEQEDGSDISDFDEKGVVFSVPKPFM-TDSKLDLSGEVERSDKVSYLEKNE 284  
QY 272 NG-----KKTE-----VKIGAKTSVIKEKDKLVTKGKDKDNGSDTDEGLVT 315  
DB 285 EGYLLHLTADENWLKDPERYVPSIDPSTLSVSDTFVMSAYPTTNYASSQKWDANLK 344  
QY 316 AKEVIDAVNAGWNRKMTTANGOTGOADKPE-----TVTSGTKVTEASGN--GTTAT--- 365  
DB 345 A-----YVLKTYGYDKTGTGTYAFMKFNENLKPIOMNMTVTRATLKYVAHSYTGKATGLW 399  
QY 366 ----VSXDDQGNIT-----VKYDVNVGDALNVNQLNSGNWLDISK 401  
DB 400 LDTVNSYDNAKVTWNTKPKASKNIGKADVHKQWASVDVTA-----VKSWSNGGANYGFK 455  
QY 402 AVAGSSG-----KVISGNVSPSKGMDVETNINAGN--NIEITRNGKN---IDTATSWTP 451  
DB 456 LHTNGNGKEYKKLLISSANSANKPYIEVTVTPKNGTPTTKAYHNGDSTGYFDIS----- 510  
QY 452 QFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVPAGVKGDVTNVAOLKGVQAO 511  
DB 511 -WKKVEGAKGVYWIYNGKEYQQAISAG-----NVTISWSTKGGKIWPTSAETASK 558

	Qy	512	NLNRIRDVNGNRRAGTAAQTATGAAQAAYLPCKSWMAIGGGTYRGEAGYAIGYSSISDT	571
	Dt	:	:   :	
	Db	559	RYLKHLDDKGDC-----AELADSPVKYKNKGSGSYATSKNWGWGVSAIFDQ	603
	Qy	572	GNNWVI-----KGTASGNRSRGHE-----CASASVGQY	597
	Dt	:	:   :	
	Db	604	GEGAMSAPAKPVIPNVGKAQAPSAGKYNNNGNATGYFDLSWKAVSGATGYK	653
	AC	P34487;	STANDARD; PRT; 918 AA.	
	ID	YMJB_CAEEL		
	DT	01-FEB-1994 (Rel. 28, Created)		
	DT	01-FEB-1995 (Rel. 31, Last sequence update)		
	DE	01-MAR-2002 (Rel. 41, Last annotation update)		
	DE	Hypotheetical 96.6 kDa protein F59B2.12 in chromosome III.		
	GN	F59B2.12.		
	OS	Cenorhabditis elegans.		
	OC	Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditiida; Rhabditoidea;		
	OC	Rhabditiidae; Peloderinae; Caenorhabditis.		
	OX	NCBI_TaxID=6239;		
	RN	[1]		
	RC	SEQUENCE FROM N.A.		
	RP	STRAIN-BRISTOL N2;		
	RX	MEDLINE=94150718; PubMed=7906398;		
	RA	Wilson R., Alnscough R., Anderson K., Baynes C., Berks M., Coulson A., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Fraser A., Craxton M., Dear S., Du Z., Durbin R., Favetto A., Hillier L., Jier M., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laister N., Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkhen R., Sims M., Smaldon N., Smith A., Smith M., Sonhammer E., Staden K., Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J., Wooldman P.; "2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans"; Nature 368:32-38(1994).		
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	DR	EMBL: Z11505; CAA77581.1; -		
	DR	PIR: S31132; S31132.		
	DR	Wormpep; F59B2.12; CE01024.		
	KW	Hypotheetical protein.		
	SQ	SEQUENCE 918 AA; 96566 MW; E464FD86B14945DE CRC64;		

Query Match	6.08;	Score 181.5;	DB 1;	Length 918;
Best Local Similarity	22.18;	Presd. No. 0.047;		
Matches 130;	Conservative 87;	Mismatches 227;	Indels 145;	Gaps 29;
Qy	65	TAVVLSFRSDKEGTGEGTSDSNWVYDFDKRYLKAGAITLTKAGDNLTKIQ-----NT 118		
		:   :   :           :   :		
Db	91	TVVGADGKNITENSEKDG-----YNKESV-----DEANETWKIKSADGSVIET 135		
Qy	119	NENTNENTNDSFYSLKKDLDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAG-T 177		
		:   :   :   :   :   :   :   :   :   :   :   :   :		
Db	136	GKSHNKSDDAS--SVGLEK--SSKTYADKNGTLMLSNTNKINNOSSAALDEGEFVNNQ 192		
Qy	178	NGDPTVHLNGTSLTD-----TLLNTGATNTVNDVTDDEKRAASVRYDLNAGNLIK 232		
		:   :   :   :   :   :   :   :   :   :		
Db	193	NADGTFLRNNTGHKNITDEHLSHNVLDNAQMSIGADGTSNHTNWKGSVGDSHNA----- 247		
Qy	233	GVKEGTTASDNVDVRYTDVTFEFLSADTKTTTVNVEKDNKGKKTVEIGARTSV----- 286		

Db	248	 ---ASD-----AHSNFESLDAQG---  :::     ::
Qy	287	IKEKDGKLVTKGKDENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKPE 346   ::
Db	290	LKNADGTSMNSNGFNNTSYDK----ATAEEVMS-----KKVNADG-TSSWEASH 336   ::
Qy	347	TVTSGTKVTFASG-----NG--TTATVSKDDQ-----GNITVKYDVNVGD 384 ::: ::
Db	337	AGNSSKINSASGGSDLSVMVGPNGIKSHSTSNKTNYALDEANQSAGSISEQIGNKGQR 396   ::
Qy	385	ALNVNQLONGWNLDSK--AVASSGKV-LSGVNVPSPKGMDETVINAGNN-----433   ::
Db	397	SLNESSIE-SGRKAESRNRNTAADTLDSVDANGTVSSHKSASGTSLDENHNKTHALQAS 455   ::
Qy	434	TEITRNCKNTDIATS-----MTPOFSSVSLGA---GADAPLTVSDDEGALNVGSKDANKPV 486   ::
Db	456	VDEHGNNKNHISIDGSYRNKKTGFEGENSEMSASTKNADCTMSQVNVKNDTRNTTYAEKSA 515   ::
Qy	487	RITNVAPGVREGDVTNVAQLKGVAAQNLRNDRINVDGNARAGIAQAATAGLAQAYLPGKS 546   ::
Db	516	LEKN---HEKNSDGT----FKDESKGSRVRNTDGGSNLAVG-----SYSVGK- 557   ::
Qy	547	MMAITGGTTYGEAGYATGYSSISDTGNWVIKGTASGNSRGHFCSASVSG 595   ::
Db	558	-----GGVSSNE---TIASNAFNTSD-----AESNQFDHLHQKTANG 592   ::

RESULT 15

YPJA\_ECOLI STANDARD; PRT: 1569 AA.

ID YPJA\_ECOLI

AC P52143; P76610; P77017; P77019;

DT 01-OCT-1996 (Rel. 34, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Hypothetical outer membrane protein YPJ\_A.

GN YPJ\_A OR B2647.

OS Escherichia coli.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OX Escherichia

OX NCBI\_TaxID=562;

[1]

RN SEQUENCE FROM N.A.

RP STRAIN-K12 / MG1655;

RC MEDLINE=97439980; PubMed=9278503;

RX Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,

RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,

RA Mau B., Shao Y.

RA "The complete genome sequence of Escherichia coli K-12.";

RL Science 277:1453-1474(1997).

RN [2]

RN SEQUENCE FROM N.A.

RC STRAIN-K12;

RA MEDLINE=97439980; PubMed=9205837;

RX Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K.,

RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,

RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H.,

RA Oshima T., Oyama S., Saito N., Sampei G., Satoh Y., Sivasubram S.,

RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,

RA Yamagata S., Horiiuchi T.

RT "Construction of a contiguous 874-Kb sequence of the Escherichia coli

RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and

RT analysis of its sequence features.";

RL DNA Res. 4:91-113(1997).

CC -! SUBCELLULAR LOCATION: Outer membrane (Potential).

CC -! SIMILARITY: STRONG, TO BORDETELLA PERTACTIN.

CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL Outstat-

CC the European Bioinformatics Institute. There are no restrictions on

CC use by non-profit institutions as long as its content is in no

CC modified and this statement is not removed. Usage by and for comm-





QY	477	VGSDANKAPVITVAVGVEKEDVTNTAOLKGYAONLNRRIDVDGNAGIAOLAATAG	536
Db	470	VGSKDKNKPRRITVAVGVEKEDVTNTAOLKGYAONLNRRIDVDGNAGIAOLAATAG	529
QY	537	LAQAVLPKSSMAIGGTYGREGAGYAIGVSSISDTONWYIKGTASGNSRGHGASASVGY	596
Db	530	LVAQAVLPKSSMAIGGTYGREGAGYAIGVSSISDGNWIIKGTASGNSRGHGASASVGY	589
QY	597	QW 598	
Db	590	QW 591	
RESULT	15		
Q9JRI8			
ID	Q9JRI8	PRELIMINARY:	PRT: 591 AA.
AC	Q9JRI8:		
DT	01-OCT-2000 (TREMblrel. 15, Created)		
DT	01-OCT-2000 (TREMblrel. 15, Last sequence update)		
DT	01-DEC-2001 (TREMblrel. 19, last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE PROTEIN).		
DE	GNA992 OR NMB0992 OR NHHA.		
GN	Neisseria meningitidis, and		
OS	Neisseria meningitidis (serogroup B).		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487, 491;		
NP			
RP	SEQUENCE FROM N.A.		
RC	STRAIN-MC58 / SEROGROUP B, B2169, B283, AND H44/76;		
RX	MEDLINE=20175755; PubMed=10710308;		
RA	Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Sallini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappunli R.;		
RT	"Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing."		
RL	Science 287:1816-1820(2000).		
RP			
RP	SEQUENCE FROM N.A.		
RC	STRAIN-MC58 / SEROGROUP B;		
RX	MEDLINE=20175755; PubMed=10710307;		
RA	Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,		
RA	Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,		
RA	Nelson W.C., Gwyn M.L., Deboy R., Peterson J.D., Hickey E.R.,		
RA	Halt D.H., Salberg S.L., White O., Fleischmann R.D., Dougherty B.A.,		
RA	Mason T., Cleebo A., Parksey D.S., Blair E., Clifton H., Clark E.B.,		
RA	Cotton M.D., Uittenback T.R., Khouri H., Qin H., Vamathevan J.,		
RA	Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,		
RA	Smith H.O., Fraser C.M., Moxon E.R., Rappunli R., Venter J.C.;		
RT	"Complete genome sequence of Neisseria meningitidis serogroup B strain		
RT	MC58."		
RL	Science 287:1809-1815(2000).		
RN			
RP	SEQUENCE FROM N.A.		
RC	SPECIES=N.meningitidis; STRAIN=PMC21;		
RA	Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	"Identification and Characterisation of a gene encoding a novel outer		
RT	membrane protein of Neisseria meningitidis."		
RL	Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.		
DR	EMBL: AF226375; AAF42524.1;		
DR	EMBL: AF002450; AAF41395.1;		
DR	EMBL: AF226367; AAF42516.1;		
DR	EMBL: AF226370; AAF42519.1;		
DR	EMBL: AF226374; AAF42523.1;		
DR	EMBL: AF157611; AAK68872.1;		
DR	TIGR: NMB0992;		
KW	Complete proteome.		
QO	SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;		

Query Match	89.5%;	Score 2725.5;	DB 16;	Length 591;
Best Local Similarity	91.0%;	Pred. No. 1.1e-106;		
Matches 548;	Conservative 12;	Mismatches 27;	Indels 15;	Gaps 4;

Qy	1	MNKITRIIMNSALNAWVVSSELTNRHNRKRAATVAATALATLEPATVOANMTE---	DDDL	57
Db	1	MNKITRIIMNSALNAWVVSSELTNRHNRKRAATVAATALATLEPATVOANMTE---	DDDL	57
Qy	58	YLEPVQRTAVVLSFRSDKEGTGEKEGTED-SNMAVYFDEKRVLKAGAITLKAGDNLKIKO		118
Db	61	YLDPEQRTAVVLAIVNSDEGEKEKEKEENSDMAFENEKGVLFAREITTLKAGDNLKIKO		120
Qy	117	NTNENNTNNTNDSSFPYSLKKDLDTLSVEFEKLSFPGANGKVVITSDDTGLNFAKKTAG		176
Db	121	-----NGTNEFYTSLKKDLDTLSVTEKLSFSGANGKVVITSDDTGLNFAKKTAG		170
Qy	177	TNGDPYVHALNGIGSTLDDTLNTGATTNVTNDNTYTDDEKKRAASVKKVULNAGNMRIKVKP		236
Db	171	TNGDTYVHALNGIGSTLDDTLNTGATTNVTNDNTYTDDEKKRAASVKKVULNAGNMRIKVKP		230
Qy	237	GTTASDNDVDFVRYDYVEELSDAKTKTTTVNYESKDNGKRTKEVKTIGAKTSYIKEDGKLVY		296
Db	231	GTTASDNDVDFRFTDYVEELSDAKTKTTTVNYESKDNGKRTKEVKTIGAKTSYIKEDGKLVY		290
Qy	297	GKGDENGSSSTDEBEGVLTAKVEIDAYNKAQWRRKTTTANGQOQAKPFTVYSGTWT		356
Db	291	GKDGEMSSSTDEBEGVLTAKVEIDAYNKAQWRRKTTTANGQOQAKPFTVYSGTWT		350
Qy	357	ASGNGTATVYASKDDOGNTVYVYDVGDALVNOLONSGNLDSKAVAGSSGKVISGNVS		416
Db	351	ASGKGTTATVYASKDDOGNTVYVYDVGDALVNOLONSGNLDSKAVAGSSGKVISGNVS		410
Qy	417	PSKGMDETVIINAGNNIETIRNKNKNDIATSMTPPOSSVSLGAGAPPLSYDDBEALN		476
Db	411	PSKGMDETVIINAGNNIETIRNKNKNDIATSMTPPOSSVSLGAGAPPLSYDDBEALN		469
Qy	477	VGSKDANKPVKITVNAVCPVEKEDGDTNVAOLKGVANQNNRNDRDNDVGNARAGIAQALITAG		536
Db	470	VGSKDKDKPVAITVNAVCPVEKEDGDTNVAOLKGVANQNNRNDRDNDVGNARAGIAQALITAG		529
Qy	537	LAQAVLPEKSSMAITGGGTYRGEAGVYAIGYSSISDPTGMVWIKGTASGNSRQHFGASASVGY		596
Db	530	LVQAVLPEKSSMAITGGGTYRGEAGVYAIGYSSISDGMWIIKGTASGNSRQHFGASASVGY		589
Qy	597	QW 598		
Db	590	QW 591		

Search completed: July 3, 2002, 08:48:08  
Job time: 699 sec

RP SEQUENCE FROM N.A.  
RC SPECIES=N.meningitidis; STRAIN=PMC21;  
RA Peak I.R., Srikhanta Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226375; AAF42524.1; -  
DR EMBL: AF002450; AAF41395.1; -  
DR EMBL: AF226367; AAF42516.1; -  
DR EMBL: AF226370; AAF42519.1; -  
DR EMBL: AF226374; AAF42523.1; -  
DR EMBL: AF157611; AAF68872.1; -  
DR TIGR: NMB0992; -  
KW Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAEF773BC6 CRC64;

Qy 598 W 598  
Db 599 W 599

## RESULT 13

Q9JPS7 PRELIMINARY: PRT: 598 AA.  
AC Q9JPS7;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=SM2107;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226385; AAF42534.1; -  
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 89.9%; Score 2736; DB 2; Length 598;  
Best Local Similarity 90.8%; Pred. No. 3.9e-107;  
Matches 545; Conservative 16; Mismatches 35; Indels 4; Gaps 2;

Qy 1 MNKIRIINWSALNMAVVSSELTNRHNRKASATVATVATLLEFATVQANATDDDDLTLE 60  
Db 1 MNKIRIINWSALNMAVVSSELTNRHNRKASATVATVATLLEFATVQANATDDDDLTLE 60  
Qy 61 PVORTAVVLSFRSDKEGTEGEGEDSNMAYVFEDEKRVLKAGATLKAGDNLKIQNTNE 120  
Db 61 PVORTAVVLSFRSDKEGTEGEGEDSNMAYVFEDEKRVLKAGATLKAGDNLKIQNTNE 120  
Qy 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNGD 180  
Db 121 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAGTNGD 180  
Qy 181 PTYHNGISLTLDLMTGATNTNNDVYDDEKKRAASVYDVLAACMNKIGVAPGTA 240  
Db 181 PTYHNGISLTLDLMTGATNTNNDVYDDEKKRAASVYDVLAACMNKIGVAPGTA 240  
Qy 241 --SDNVDFVRYDYEFESADTKTTTVNESKDNKTEVKIGAKTSVYKEKDGKLVYK 298  
Db 241 --SDNVDFVRYDYEFESADTKTTTVNESKDNKTEVKIGAKTSVYKEKDGKLVYK 298  
Qy 239 GQSEKVDVRRYDYEFESADTKTTTVNESKDNKTEVKIGAKTSVYKEKDGKLVYK 298  
Db 239 GQSEKVDVRRYDYEFESADTKTTTVNESKDNKTEVKIGAKTSVYKEKDGKLVYK 298  
Qy 239 GKDENGSSSTDEGEGLVYAKVIDAVNKAQWRKTTTANGQTQADKFEETVSGTVTFAS 358  
Db 239 GKDENGSSSTDEGEGLVYAKVIDAVNKAQWRKTTTANGQTQADKFEETVSGTVTFAS 358  
Qy 359 GNGTATATVSKDQGNITVYKDVNVDALNVNOLNSGWNLSKAAVAGSSGKIVSNNVSPS 418  
Db 359 GNGTATATVSKDQGNITVYKDVNVDALNVNOLNSGWNLSKAAVAGSSGKIVSNNVSPS 418  
Qy 419 KGKMDETVNNNGNIIETRNKNKIDITSMTPQFSSVSLGAGADAPLTVSYDEGALVNG 478  
Db 419 KGKMDETVNNNGNIIETRNKNKIDITSMTPQFSSVSLGAGADAPLTVSYDEGALVNG 478  
Qy 479 SKDANKPVRTINVAQVGEQDVNTVAQLKGAQNLNRIQNDVGNARAGIAQAIATAGLA 538  
Db 479 SKDANKPVRTINVAQVGEQDVNTVAQLKGAQNLNRIQNDVGNARAGIAQAIATAGLA 538

Db 479 SKDANKPVRTINVAQVGEQDVNTVAQLKGAQNLNRIQNDVGNARAGIAQAIATAGLA 538  
Qy 539 QAYLPKSKMAIIGGTYGEGAGYAIQYSSISDTGMMVYIKGTASGNSRCHFGASASVGYQW 598  
Db 539 QAYLPKSKMAIIGGTYGEGAGYAIQYSSISDTGMMVYIKGTASGNSRCHFGASASVGYQW 598

## RESULT 14

Q9JPS7 PRELIMINARY: PRT: 591 AA.  
AC Q9JPS7;  
DT 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226386; AAF42515.1; -  
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 89.5%; Score 2725.5; DB 2; Length 591;  
Best Local Similarity 91.0%; Pred. No. 1.1e-106;  
Matches 548; Conservative 12; Mismatches 27; Indels 15; Gaps 4;

Qy 1 MNKIRIINWSALNMAVVSSELTNRHNRKASATVATVATLLEFATVQANATDD--DDL 57  
Db 1 MNKIRIINWSALNMAVVSSELTNRHNRKASATVATVATLLEFATVQANNEBOEDL 60  
Qy 58 YLEPVORTAVVLSFRSDKEGTEGEGED--SNMAYVFEDEKRVLKAGATLKAGDNLKIQ 116  
Db 61 YLDPVORTAVVLSFRSDKEGTEGEGEDSNMAYVFEDEKRVLKAGATLKAGDNLKIQ 120  
Qy 117 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAG 176  
Db 117 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAG 170  
Qy 121 -----KQNTNTYSLKKDLTDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAG 170  
Db 121 -----KQNTNTYSLKKDLTDLTSVETEKLSFGANGKRVNITSDTKGLNFAKETAG 170  
Qy 177 TNGDPTVHLNGISLTLDLMTGATNTNNDVYDDEKKRAASVYDVLAACMNKIGVAP 236  
Db 177 TNGDPTVHLNGISLTLDLMTGATNTNNDVYDDEKKRAASVYDVLAACMNKIGVAP 230  
Qy 237 GTTASDNDVRYTYVTEFLSADPTTTVNESKDNKTEVKIGAKTSVYKEKDGKLVY 296  
Db 237 GTTASDNDVRYTYVTEFLSADPTTTVNESKDNKTEVKIGAKTSVYKEKDGKLVY 290  
Qy 297 GKDENGSSSTDEGEGLVYAKVIDAVNKAQWRKTTTANGQTQADKFEETVSGTVTF 356  
Db 297 GKDENGSSSTDEGEGLVYAKVIDAVNKAQWRKTTTANGQTQADKFEETVSGTVTF 350  
Qy 359 ASGNGTATVSKDQGNITVYKDVNVDALNVNOLNSGWNLSKAAVAGSSGKIVSNNVSPS 416  
Db 359 ASGNGTATVSKDQGNITVYKDVNVDALNVNOLNSGWNLSKAAVAGSSGKIVSNNVSPS 410  
Qy 417 PSKGMDETVINNGNIIETRNKNKIDITSMTPQFSSVSLGAGADAPLTVSYDEGALN 476  
Db 417 PSKGMDETVINNGNIIETRNKNKIDITSMTPQFSSVSLGAGADAPLTVSYDEGALN 469

AC Q9JPS8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -;  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 91.1%; Score 2772; DB 2; Length 590;  
Best Local Similarity 92.3%; Pred. No. 1.2e-108;  
Matches 554; Conservative 10; Mismatches 24; Indels 12; Gaps 3;

QY 1 MNKIYRIINMSALNANWVSELTRNHTKRASATVATVATLTLFATVQANATD-DDLY-L 59  
DB 1 MNKIYRIINMSALNANWVSELTRNHTKRASATVATVATLTLFATVQANATDDEEDL 60  
QY 60 EPVQRTAVVLSPRSDEKGEKTEGTEDED-SNMAVYFDEKRVLKAGATLTKAGDNLIKONT 118  
DB 61 DPVQRTAVVLSPRSDEKGEKTEGTEKESNDMAVYFNEKGVLFAGTITLTKAGDNLIKIQ-- 118  
QY 119 NENTNENTNDSSFTYSLKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTN 178  
DB 119 -NCTNFTYSLKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTN 170  
QY 179 GDPVHLNGIGSTLTDLTLMTGATNTNTNDVDEKKRAASVKDVLNAGMNIKGVPQT 238  
DB 171 GDTVHLNGIGSTLTDLTLMTGATNTNTNDVDEKKRAASVKDVLNAGMNIKGVPQT 230  
QY 239 TASDNVDFRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIREKDGKLVTK 298  
DB 231 TASDNVDFRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIREKDGKLVTK 290  
QY 299 GKRENGSSSTDEBEGGLVTAKEVIDAVNKAQRKMTTANGOTGADKFEVTSCTKVTFA 358  
DB 291 KKGGENSSSTDEBEGGLVTAKEVIDAVNKAQRKMTTANGOTGADKFEVTSCTKVTFA 350  
QY 359 GNGTATVASKDDOGNTTVKDVNVGDALNVNOLQNSGMNLDKRAVAGSSGKVIISGNVSP 418  
DB 351 GNGTATVASKDDOGNTTVKDVNVGDALNVNOLQNSGMNLDKRAVAGSSGKVIISGNVSP 410  
QY 419 KGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVDEGALNVG 478  
DB 411 KGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVDEGALNVG 470  
QY 479 SKDANKPVRTITNVAPEGVKGDTVNTVAQLKGVAONLNRRIDNDVGNARAAGIAQAIATAGLA 538  
DB 471 SKDANKPVRTITNVAPEGVKGDTVNTVAQLKGVAONLNRRIDNDVGNARAAGIAQAIATAGLA 530  
QY 539 QATLPKSMMAIGGTYRGAGYAIGYSSISDPTGMNVIKGTASGNSRGHGASASVGYQ 598  
DB 531 QATLPKSMMAIGGTYRGAGYAIGYSSISDPTGMNVIKGTASGNSRGHGASASVGYQ 590

RESULT 12

Q9JPS8  
ID Q9JPS8 PRELIMINARY; PRT; 599 AA.  
AC Q9JPS8;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A22;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scariato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226364; AAF42513.1; -;  
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 90.5%; Score 2755.5; DB 2; Length 599;  
Best Local Similarity 91.7%; Pred. No. 6e-108;  
Matches 551; Conservative 15; Mismatches 30; Indels 5; Gaps 3;

QY 1 MNKIYRIINMSALNANWVSELTRNHTKRASATVATVATLTLFATVQANATD-DDLY-L 59  
DB 1 MNKIYRIINMSALNANWVSELTRNHTKRASATVATVATLTLFATVQANTDDEDEYL 60  
QY 60 EPVQRTAVVLSPRSDEKGEKTEGTEGSHGVYFDEKRVLKAGATLTKAGDNLIKONT 119  
DB 61 EPVQRTAVVLSPRSDEKGEKTEGTEGSHGVYFDEKRVLKAGATLTKAGDNLIKONT 120  
QY 120 ENTNENTNDSSFTYSLKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTN 179  
DB 121 ENTNENTNDSSFTYSLKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTN 180  
QY 180 DPTVHLNGIGSTLTDLTLMTGATNTNTNDVDEKKRAASVKDVLNAGMNIKGVPQT 239  
DB 181 DPTVHLNGIGSTLTDLTLMTGATNTNTNDVDEKKRAASVKDVLNAGMNIKGVPQT 238  
QY 240 A--SDNVDFRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIREKDGKLVTK 297  
DB 239 TGOSENVDFRTYDVEFLSADTKTTTVNVESSKNGKTEYKIGAKTSVIREKDGKLVTK 298  
QY 298 KGDENSSSTDEBEGGLVTAKEVIDAVNKAQRKMTTANGOTGADKFEVTSCTKVTFA 357  
DB 299 KKGGENSSSTDEBEGGLVTAKEVIDAVNKAQRKMTTANGOTGADKFEVTSCTKVTFA 358  
QY 358 GNGTATVASKDDOGNTTVKDVNVGDALNVNOLQNSGMNLDKRAVAGSSGKVIISGNVSP 417  
DB 359 GNGTATVASKDDOGNTTVKDVNVGDALNVNOLQNSGMNLDKRAVAGSSGKVIISGNVSP 418  
QY 418 SKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVDEGALNV 477  
DB 419 SKGMDETVINAGNNIEITRNKNIDIASMTPOFSSVSLGAGADAPTLVDEGALNV 478  
QY 478 GSKDANKPVRTITNVAPEGVKGDTVNTVAQLKGVAONLNRRIDNDVGNARAAGIAQAIATAGLA 537  
DB 479 GSKDANKPVRTITNVAPEGVKGDTVNTVAQLKGVAONLNRRIDNDVGNARAAGIAQAIATAGLA 538  
QY 538 QATLPKSMMAIGGTYRGAGYAIGYSSISDPTGMNVIKGTASGNSRGHGASASVGYQ 597  
DB 539 QATLPKSMMAIGGTYRGAGYAIGYSSISDPTGMNVIKGTASGNSRGHGASASVGYQ 598



RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.,  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.",  
RL Science 287:1816-1820(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H38;  
RA Peak I.R., Strikhanova Y., Dieckelman M., Moxon R., Jennings M.P.,  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*.",  
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF226383; AAF42532.1; -  
DR EMBL: AF157608; AAK68869.1; -  
SQ SEQUENCE 599 AA; 62844 MW; BBA16BF53C1970C CRC64;

Query Match 92.8%; Score 2824.5; DB 2; Length 599;  
Best Local Similarity 92.7%; Pred. No. 7.9e-111;  
Matches 555; Conservative 14; Mismatches 29; Indels 1; Gaps 1;

OY 1 MNKIRIITNSALNANWVYSELTRNHTKRASATVATVATLTLFATVOANATD-DDDLYL 59  
DB 1 MNKIRIITNSALNANWVYSELTRNHTKRASATVATVATLTLFATVOANATDEDEEEL 60  
OY 60 EPVQTAVALVSRSDKEGEGEEDSNMAYFDEKRVLKAGATTLKAGDNLKTKONTN 119  
DB 61 EPVNSALVLFQMDKEGENESGNIIGWYLYDNHNTLHGATVTLKAGDNLKTKONTN 120  
OY 120 ENTNENTDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGINFKEATGNG 179  
DB 121 KNTNENTDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGINFKEATGNG 180  
OY 180 DPTVHLNGIGSTLDTLNTGATNTVNDNVTDEKKRAASVYKDVNLNAGWNIKVPCTT 239  
DB 181 DTTVHLNGIGSTLDTLNTGATNTVNDNVTDEKKRAASVYKDVNLNAGWNIKVPCTT 240  
OY 240 ASDNDVFRYDVEFLSADRTKTTVNVESKDNKKEVKGAKTSVIREKDGKLVTKG 299  
DB 241 ASDNDVFRYDVEFLSADRTKTTVNVESKDNKKEVKGAKTSVIREKDGKLVTKG 300  
OY 300 KDENGSSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSCTKVTFA 359  
DB 301 KGENSSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTSCTKVTFA 360  
OY 360 NGTATVSKDDOGNITVRYDVNVGDALNVNOLQNSGMNLSKAVAGSSGKVISGVS 419  
DB 361 KGTATVSKDDOGNITVRYDVNVGDALNVNOLQNSGMNLSKAVAGSSGKVISGVS 420  
OY 420 GKMDVTVINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLTSDVDEG 479  
DB 421 GKMDVTVINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLTSDVDEG 480  
OY 480 KDANKPVRITVNAAPGVKEDGVTNVNQLKGVANLNNRIDNVGNRAGIAQIAIATAG 539  
DB 481 KDANKPVRITVNAAPGVKEDGVTNVNQLKGVANLNNRIDNVGNRAGIAQIAIATAG 540  
OY 540 AYLPGKSMMAIGGTYRGAGAGTAIGSSISDTGNVNIKGTASGNSRGHFGASASV 598  
DB 541 AYLPGKSMMAIGGTYRGAGAGTAIGSSISDTGNVNIKGTASGNSRGHFGASASV 599

RESULT 10  
O9JPS6 PRELIMINARY; PRT; 600 AA.  
AC O9JPS6;  
DT 01-OCT-2000 (Tremblrel. 15, Created)  
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.

OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzo M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartoloni E., Capocchi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.,  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.",  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226371; AAF42520.1; -  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 91.4%; Score 2781; DB 2; Length 600;  
Best Local Similarity 91.7%; Pred. No. 5.2e-109;  
Matches 555; Conservative 14; Mismatches 24; Indels 12; Gaps 3;

OY 1 MNKIRIITNSALNANWVYSELTRNHTKRASATVATVATLTLFATVOANATD 53  
DB 1 MNKIRIITNSALNANWVYSELTRNHTKRASATVATVATLTLFATVOASADNVASADN 60  
OY 54 DDDLYLEPVQTAVALVSRSDKEGEGEEDSNMAYFDEKRVLKAGATTLKAGDNLK 113  
DB 61 EEEVLEPVQTAVALVSRSDKEGEGEEDSNMAYFDEKRVLKAGATTLKAGDNLK 120  
OY 114 IKONTNENTDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGINFKE 173  
DB 121 IKONTNENTDSSFTYSLKDLTDLTSVETEKLSFGANGKNVNTSDTKGINFKE 176  
OY 174 TAGTGDPTVHLNGIGSTLDTLNTGATNTVNDNVTDEKKRAASVYKDVNLNAGWNI 233  
DB 177 TAGTGDPTVHLNGIGSTLDTLNTGATNTVNDNVTDEKKRAASVYKDVNLNAGWNI 236  
OY 234 VKPGTTASDNVDFRTYDVEFLSADRTKTTVNVESKDNKKEVKGAKTSVIREKDGK 293  
DB 237 VKPGTTASDNVDFRTYDVEFLSADRTKTTVNVESKDNKKEVKGAKTSVIREKDGK 296  
OY 294 LVTGKGRKENGSSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTS 353  
DB 297 LVTGKGRKENGSSSTDEGEGLVTAKEVIDAVNKAQMRKTTTANGOTGOADKFEVTS 356  
OY 354 VTFASGNGTATVSKDDOGNITVRYDVNVGDALNVNOLQNSGMNLSKAVAGSSGKVIS 413  
DB 357 VTFASGNGTATVSKDDOGNITVRYDVNVGDALNVNOLQNSGMNLSKAVAGSSGKVIS 416  
OY 414 NVSPSKGKMDVTVINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLTSDV 473  
DB 417 NVSPSKGKMDVTVINAGNNEITRNKGNIDATSMTPQFSSVSLGAGADAPTLTSDV 475  
OY 474 ALNVGSKRANKPVRITVNAAPGVKEDGVTNVNQLKGVANLNNRIDNVGNRAGIAQIA 533  
DB 476 ALNVGSKRANKPVRITVNAAPGVKEDGVTNVNQLKGVANLNNRIDNVGNRAGIAQIA 535  
OY 534 TAGLQAVLTPGKSMMAIGGTYRGAGAGTAIGSSISDTGNVNIKGTASGNSRGHFGAS 593  
DB 536 TAGLQAVLTPGKSMMAIGGTYRGAGAGTAIGSSISDTGNVNIKGTASGNSRGHFGAS 595

RESULT 11  
O9JPS3 PRELIMINARY; PRT; 590 AA.  
ID O9JPS3

RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storti E., Zuo P.,  
 RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.T., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226376; AAF42525.1; -  
 DR EMBL: AF226369; AAF42518.1; -  
 SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B9D04B46 CRC64;

Query Match 94.8%; Score 2887; DB 2; Length 594;  
 Best Local Similarity 95.5%; Pred. No. 1.9e-113;  
 Matches 571; Conservative 5; Mismatches 18; Indels 4; Gaps 1;

QY 1 MNKIRIIMNSALNANWVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
 DB 1 MNKIRIIMNSALNANWVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60  
 QY 61 PVORTAVVLSFRSDKEGTGEGTESNMAVYDEKRYLKAGAITTLKAGNLKIKONTNE 120  
 DB 61 PVORTAVVLSFRSDKEGTGEGTESNMAVYDEKRYLKAGAITTLKAGNLKIKONTNE 120  
 QY 121 NTNENTDSSFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKLNAKETAETNGD 180  
 DB 121 NTNENTDSSFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKLNAKETAETNGD 180  
 QY 121 NTNA-----SFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKLNAKETAETNGD 176  
 DB 121 NTNA-----SFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKLNAKETAETNGD 176  
 QY 181 PTVHLNGIGSTLPTDLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGNMIKGVKPGTTA 240  
 DB 177 TTVHLNGIGSTLPTDLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGNMIKGVKPGTTA 236  
 QY 241 SDNVDFRYTDYVEFLSADTKTTTVNESKDNCKTEVKIGAKTSVIREKDGKLVYTGSK 300  
 DB 237 SDNVDFRYTDYVEFLSADTKTTTVNESKDNCKTEVKIGAKTSVIREKDGKLVYTGSK 296  
 QY 301 DENGSSTDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVYTGKTFTFASGN 360  
 DB 297 GENGSSSTDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVYTGKTFTFASGN 356  
 QY 361 GTTATVSKDDOGNTTVYDVNVDGALNVNOLQNSGNMLDRAVAGSSGKVISGNVSPSKG 420  
 DB 357 GTTATVSKDDOGNTTVYDVNVDGALNVNOLQNSGNMLDRAVAGSSGKVISGNVSPSKG 416  
 QY 421 KMETVINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 480  
 DB 417 KMETVINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 476  
 QY 481 DANKPVRITVAPGVKRGDVTNVAOLKGVANONLNRIIDNDVGNARAGIAAIAATAGLAA 540  
 DB 477 DANKPVRITVAPGVKRGDVTNVAOLKGVANONLNRIIDNDVGNARAGIAAIAATAGLAA 536  
 QY 541 YLPKSMMAIGGTYRGEAGYAGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYOM 598  
 DB 537 YLPKSMMAIGGTYRGEAGYAGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYOM 594

RESULT 8  
 Q930Y4 PRELIMINARY; PRT; 594 AA.  
 AC Q930Y4;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE NHHA OUTER MEMBRANE PROTEIN.  
 GN NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN (1)  
 RP SEQUENCE FROM N.A.

RC STRAIN-EG327;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 membrane protein of Neisseria meningitidis.";  
 RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF157605; AAK68866.1; -  
 SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8BA2 CRC64;

Query Match 93.8%; Score 2855; DB 2; Length 594;  
 Best Local Similarity 94.6%; Pred. No. 4.2e-112;  
 Matches 566; Conservative 6; Mismatches 22; Indels 4; Gaps 1;

QY 1 MNKIRIIMNSALNANWVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60  
 DB 1 MNKIRIIMNSALNANWVSELTRNHTKRASATVATVATLTLFATVQASTDDDDLYLE 60  
 QY 61 PVORTAVVLSFRSDKEGTGEGTESNMAVYDEKRYLKAGAITTLKAGNLKIKONTNE 120  
 DB 61 PVORTAVVLSFRSDKEGTGEGTESNMAVYDEKRYLKAGAITTLKAGNLKIKONTNE 120  
 QY 121 NTNENTDSSFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKLNAKETAETNGD 180  
 DB 121 NTNENTDSSFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKLNAKETAETNGD 176  
 QY 121 NTNA-----SFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKLNAKETAETNGD 176  
 DB 121 NTNA-----SFTYSLKRDLDLTSVETEKLSFGANGKKNVITSDTKLNAKETAETNGD 176  
 QY 181 PTVHLNGIGSTLPTDLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGNMIKGVKPGTTA 240  
 DB 177 TTVHLNGIGSTLPTDLTNTGATTNVTNDNTDDEKKRAASVKDVLNAGNMIKGVKPGTTA 236  
 QY 241 SDNVDFRYTDYVEFLSADTKTTTVNESKDNCKTEVKIGAKTSVIREKDGKLVYTGSK 300  
 DB 237 SDNVDFRYTDYVEFLSADTKTTTVNESKDNCKTEVKIGAKTSVIREKDGKLVYTGSK 296  
 QY 301 DENGSSTDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVYTGKTFTFASGN 360  
 DB 297 GENGSSSTDEEGGLVTAKEVIDAVNKAAGRMKTTTANGOTQADKFEVYTGKTFTFASGN 356  
 QY 361 GTTATVSKDDOGNTTVYDVNVDGALNVNOLQNSGNMLDRAVAGSSGKVISGNVSPSKG 420  
 DB 357 GTTATVSKDDOGNTTVYDVNVDGALNVNOLQNSGNMLDRAVAGSSGKVISGNVSPSKG 416  
 QY 421 KMETVINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 480  
 DB 417 KMETVINAGNNIETIRNKNIDIASMTPOFSSVSLGAGADAPTLVSDEGALNVGSK 476  
 QY 481 DANKPVRITVAPGVKRGDVTNVAOLKGVANONLNRIIDNDVGNARAGIAAIAATAGLAA 540  
 DB 477 DANKPVRITVAPGVKRGDVTNVAOLKGVANONLNRIIDNDVGNARAGIAAIAATAGLAA 536  
 QY 541 YLPKSMMAIGGTYRGEAGYAGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYOM 598  
 DB 537 YLPKSMMAIGGTYRGEAGYAGYSSISDPTGMNVIKGTASGNSRGHFGASASVGYOM 594

RESULT 9  
 Q9JPR8 PRELIMINARY; PRT; 599 AA.  
 AC Q9JPR8;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA92 (NHHA OUTER MEMBRANE PROTEIN).  
 GN GNA92 OR NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-NGH38;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Piza M., Scariato V., Masiagnan V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Iuzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of *Neisseria meningitidis*."  
RT Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226368; AAF42517.1; -  
DR EMBL: AF226368; AAF42507.1; -  
DR EMBL: AF157604; AK68865.1; -  
SQ SEQUENCE 594 AA: 62361 MW: 4368DEDD6826365C CRC64;

Query Match 97.6%; Score 2971; DB 2; Length 594;

Best Local Similarity 98.0%; Pred. No. 5.9e-117;  
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

```

QY 1 MNKYYRIIMNSALNAAWVSELTFRNHTRKASATATATLTLFATYQANATDDDDLYLE 60
    1 MNKYYRIIMNSALNAAWVSELTFRNHTRKASATATATLTLFATYQANATDDDDLYLE 60
DB 1 MNKYYRIIMNSALNAAWVSELTFRNHTRKASATATATLTLFATYQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTEGEKTEDSNMAYVFDEKRYLKAATLTKAGDNLKIKONTNE 120
    61 PVORTAVVLSFRSDKEGTEGEKTEDSNMAYVFDEKRYLKAATLTKAGDNLKIKONTNE 120
DB 61 PVORTAVVLSFRSDKEGTEGEKTEDSNMAYVFDEKRYLKAATLTKAGDNLKIKONTNE 116
QY 121 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
    121 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
DB 121 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
QY 117 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
    117 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
DB 117 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
QY 181 PTYHLNGIGSLTDLTLNTGATNTVNDVDEKKRAASVDVNLNAGMNIKGVKPGTTA 240
    181 PTYHLNGIGSLTDLTLNTGATNTVNDVDEKKRAASVDVNLNAGMNIKGVKPGTTA 240
DB 177 PTYHLNGIGSLTDLTLNTGATNTVNDVDEKKRAASVDVNLNAGMNIKGVKPGTTA 236
QY 241 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGRKTEVKIGAKTSVIEKDKGLVTGKG 300
    241 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGRKTEVKIGAKTSVIEKDKGLVTGKG 300
DB 237 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGRKTEVKIGAKTSVIEKDKGLVTGKG 296
QY 301 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKYTFASGN 360
    301 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKYTFASGN 360
DB 297 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKYTFASGN 356
QY 361 GTTATVSKDDGDNITVKKDVAVNGDALNVNOLONGSMNDSKAVAGSSGKVSIGNVSPSKG 420
    361 GTTATVSKDDGDNITVKKDVAVNGDALNVNOLONGSMNDSKAVAGSSGKVSIGNVSPSKG 420
DB 357 GTTATVSKDDGDNITVKKDVAVNGDALNVNOLONGSMNDSKAVAGSSGKVSIGNVSPSKG 416
QY 421 KMDETVNIAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 480
    421 KMDETVNIAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 480
DB 417 KMDETVNIAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 476
QY 481 DANKPVRTITNAPGVKESDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 540
    481 DANKPVRTITNAPGVKESDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 540
DB 477 DANKPVRTITNAPGVKESDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 536
QY 541 YLPCKSMAAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRGRHFGASASVGYOW 598
    541 YLPCKSMAAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRGRHFGASASVGYOW 598
DB 537 YLPCKSMAAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRGRHFGASASVGYOW 594
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RESULT 6

09JPS2 PRELIMINARY; PRT; 594 AA.

AC 09JPS2;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OC NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Galeonucci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeonucci C.L., Iuzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelein H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT *Meningococcus* by Whole-Genome Sequencing."  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1; -  
SQ SEQUENCE 594 AA: 62114 MW: 1E2A63A78F53D256 CRC64;

Query Match 95.0%; Score 2891; DB 2; Length 594;

Best Local Similarity 95.7%; Pred. No. 1.3e-113;  
Matches 572; Conservative 5; Mismatches 17; Indels 4; Gaps 1;

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QY 1 MNKYYRIIMNSALNAAWVSELTFRNHTRKASATATATLTLFATYQANATDDDDLYLE 60
    1 MNKYYRIIMNSALNAAWVSELTFRNHTRKASATATATLTLFATYQANATDDDDLYLE 60
DB 1 MNKYYRIIMNSALNAAWVSELTFRNHTRKASATATATLTLFATYQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTEGEKTEDSNMAYVFDEKRYLKAATLTKAGDNLKIKONTNE 120
    61 PVORTAVVLSFRSDKEGTEGEKTEDSNMAYVFDEKRYLKAATLTKAGDNLKIKONTNE 120
DB 61 PVORTAVVLSFRSDKEGTEGEKTEDSNMAYVFDEKRYLKAATLTKAGDNLKIKONTNE 120
QY 121 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
    121 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
DB 121 NTNNTNDSSFTYSLKDLIDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
QY 181 PTYHLNGIGSLTDLTLNTGATNTVNDVDEKKRAASVDVNLNAGMNIKGVKPGTTA 240
    181 PTYHLNGIGSLTDLTLNTGATNTVNDVDEKKRAASVDVNLNAGMNIKGVKPGTTA 240
DB 177 PTYHLNGIGSLTDLTLNTGATNTVNDVDEKKRAASVDVNLNAGMNIKGVKPGTTA 236
QY 241 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGRKTEVKIGAKTSVIEKDKGLVTGKG 300
    241 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGRKTEVKIGAKTSVIEKDKGLVTGKG 300
DB 237 SDNVDFVRYDTVEFLSADTKTTTVNVESSKDNKGRKTEVKIGAKTSVIEKDKGLVTGKG 296
QY 301 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKYTFASGN 360
    301 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKYTFASGN 360
DB 297 DENSSSTDEGGLYTAKEVIDAVNKAAGRMKTTTANGOTGADKFEYVTSCTKYTFASGN 356
QY 361 GTTATVSKDDGDNITVKKDVAVNGDALNVNOLONGSMNDSKAVAGSSGKVSIGNVSPSKG 420
    361 GTTATVSKDDGDNITVKKDVAVNGDALNVNOLONGSMNDSKAVAGSSGKVSIGNVSPSKG 420
DB 357 GTTATVSKDDGDNITVKKDVAVNGDALNVNOLONGSMNDSKAVAGSSGKVSIGNVSPSKG 416
QY 421 KMDETVNIAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 480
    421 KMDETVNIAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 480
DB 417 KMDETVNIAGNNIEITRNKNIDIAITSMTPQFSSVSLGAGADAPTLISVDEGALNVGSK 476
QY 481 DANKPVRTITNAPGVKESDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 540
    481 DANKPVRTITNAPGVKESDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 540
DB 477 DANKPVRTITNAPGVKESDVTNVAOLKGVNOLNRRIDNVGNARAGIAQAIAATAGLVA 536
QY 541 YLPCKSMAAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRGRHFGASASVGYOW 598
    541 YLPCKSMAAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRGRHFGASASVGYOW 598
DB 537 YLPCKSMAAIGGTYRGAGYAIGYSSISDPTGNVYIKGTASGNSRGRHFGASASVGYOW 594
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RESULT 7

09JPI3 PRELIMINARY; PRT; 594 AA.

AC 09JPI3;  
DT 01-OCT-2000 (TREMBLrel. 15, Created)  
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.

OC NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, AND B2232;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizsa M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,

Query Match	98.7%;	Score 3005;	DB 2;	Length 598;
Best Local Similarity	98.7%;	Pred. No. 2.3e-118;		

[illegible]

Best Local Similarity 100.0%; Pred. No. 5.3e-120;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MNKIRIIMNSALNMMVVSSELTFRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
Db 1 MNKIRIIMNSALNMMVVSSELTFRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
OY 61 PVORTAAVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120  
Db 61 PVORTAAVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120  
OY 121 NTNENTNDSSTFYSLKQDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
Db 121 NTNENTNDSSTFYSLKQDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
OY 181 PTVHLNGISGLTDLTLMTGATNTNDNTDDEKKRAASVYKDVLMAGMNIKGVKPGTTA 240  
Db 181 PTVHLNGISGLTDLTLMTGATNTNDNTDDEKKRAASVYKDVLMAGMNIKGVKPGTTA 240  
OY 241 SDNVDFVFTYDVEFLSADTKTTTVNVESKDKNGKTEVKGAKTSVIEKDGKLVTKGK 300  
Db 241 SDNVDFVFTYDVEFLSADTKTTTVNVESKDKNGKTEVKGAKTSVIEKDGKLVTKGK 300  
OY 301 DENGSTDEGEGLYTAKVDAVNAKAGRMKTTTANGOTGADKEFTVTSKTYTFASGN 360  
Db 301 DENGSTDEGEGLYTAKVDAVNAKAGRMKTTTANGOTGADKEFTVTSKTYTFASGN 360  
OY 361 GTTATVSKDDGQNTVKKYDVNVGDLNVOLONSGMNLSKRAVAGSSKRVISGNVSPSKG 420  
Db 361 GTTATVSKDDGQNTVKKYDVNVGDLNVOLONSGMNLSKRAVAGSSKRVISGNVSPSKG 420  
OY 421 KMDETVINAGNIEITFRNGKNIDTATSMTPQFSSVSLGAGADAPTLVDEGALNVSK 480  
Db 421 KMDETVINAGNIEITFRNGKNIDTATSMTPQFSSVSLGAGADAPTLVDEGALNVSK 480  
OY 481 DANKVRITTNAPVKGEDVTNVQOLKGAONLNRINDVGNARAGIAQAIATAGLAQA 540  
Db 481 DANKVRITTNAPVKGEDVTNVQOLKGAONLNRINDVGNARAGIAQAIATAGLAQA 540  
OY 541 YLPKSMMAIGGGTYRGAGYAGTSSISDTGNMVIKGTASGNSRGRHGFASASVGYOW 598  
Db 541 YLPKSMMAIGGGTYRGAGYAGTSSISDTGNMVIKGTASGNSRGRHGFASASVGYOW 598

RESULT 2  
O9JPT0 PRELIMINARY; PRT: 598 AA.  
AC O9JPT0; 01-OCT-2000 (TREMblrel. 15, Created)  
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GMA992.  
GN GMA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-2996;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Piza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brooker M., Hunt E., Knapp B., Blair E., Hanson T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing."  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226359; AAF42508.1;  
SQ SEQUENCE 598 AA: 62763 MW: 63A6A3BD7F0F2EE3 CRC64;

Query Match 99.5%; Score 3030; DB 2; Length 598;  
Best Local Similarity 99.5%; Pred. No. 2.1e-119;  
Matches 595; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 1 MNKIRIIMNSALNMMVVSSELTFRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
Db 1 MNKIRIIMNSALNMMVVSSELTFRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
OY 61 PVORTAAVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120  
Db 61 PVORTAAVLSFRSDKEGEGTEGEGEDSNMAYFDEKRYLKAGATLTKAGDNLIKQNTNE 120  
OY 121 NTNENTNDSSTFYSLKQDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
Db 121 NTNENTNDSSTFYSLKQDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
OY 181 PTVHLNGISGLTDLTLMTGATNTNDNTDDEKKRAASVYKDVLMAGMNIKGVKPGTTA 240  
Db 181 PTVHLNGISGLTDLTLMTGATNTNDNTDDEKKRAASVYKDVLMAGMNIKGVKPGTTA 240  
OY 241 SDNVDFVFTYDVEFLSADTKTTTVNVESKDKNGKTEVKGAKTSVIEKDGKLVTKGK 300  
Db 241 SDNVDFVFTYDVEFLSADTKTTTVNVESKDKNGKTEVKGAKTSVIEKDGKLVTKGK 300  
OY 301 DENGSTDEGEGLYTAKVDAVNAKAGRMKTTTANGOTGADKEFTVTSKTYTFASGN 360  
Db 301 DENGSTDEGEGLYTAKVDAVNAKAGRMKTTTANGOTGADKEFTVTSKTYTFASGN 360  
OY 361 GTTATVSKDDGQNTVKKYDVNVGDLNVOLONSGMNLSKRAVAGSSKRVISGNVSPSKG 420  
Db 361 GTTATVSKDDGQNTVKKYDVNVGDLNVOLONSGMNLSKRAVAGSSKRVISGNVSPSKG 420  
OY 421 KMDETVINAGNIEITFRNGKNIDTATSMTPQFSSVSLGAGADAPTLVDEGALNVSK 480  
Db 421 KMDETVINAGNIEITFRNGKNIDTATSMTPQFSSVSLGAGADAPTLVDEGALNVSK 480  
OY 481 DANKVRITTNAPVKGEDVTNVQOLKGAONLNRINDVGNARAGIAQAIATAGLAQA 540  
Db 481 DANKVRITTNAPVKGEDVTNVQOLKGAONLNRINDVGNARAGIAQAIATAGLAQA 540  
OY 541 YLPKSMMAIGGGTYRGAGYAGTSSISDTGNMVIKGTASGNSRGRHGFASASVGYOW 598  
Db 541 YLPKSMMAIGGGTYRGAGYAGTSSISDTGNMVIKGTASGNSRGRHGFASASVGYOW 598

RESULT 3  
O93OY5 PRELIMINARY; PRT: 598 AA.  
AC O93OY5; 01-DEC-2001 (TREMblrel. 19, Created)  
DT 01-DEC-2001 (TREMblrel. 19, Last sequence update)  
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
DE NHIA OUTER MEMBRANE PROTEIN.  
GN NHIA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-B210;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis."  
RL Submitted (JUN-1999) to the EMBL/Genbank/DBJ databases.  
DR EMBL: AF157603; AAK6864.1;  
SQ SEQUENCE 598 AA: 62687 MW: 18CEFFE6410A15DF CRC64;

Query Match 99.2%; Score 3021; DB 2; Length 598;  
Best Local Similarity 99.3%; Pred. No. 4.9e-119;  
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:36:29 ; Search time 100.13 Seconds  
(without alignments)  
1033.167 Million cell updates/sec

Title: US-09-771-382-7  
Perfect score: 3044  
Sequence: 1 MNKIYRILIMNSALNAMYVS.....TASGNSRGHFGASASVGYOW 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapept 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

SPREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_virus:\*  
16: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	3044	100.0	598	2	Q9JPS0	Q9JPS0 neisseria m
2	3030	99.5	598	2	Q9JPT0	Q9JPT0 neisseria m
3	3021	99.2	598	2	Q9JPT5	Q9JPT5 neisseria m
4	3005	98.7	598	2	Q9JPR9	Q9JPR9 neisseria m
5	2971	97.6	594	2	Q9JPH7	Q9JPH7 neisseria m
6	2891	95.0	594	2	Q9JPS2	Q9JPS2 neisseria m
7	2887	94.8	594	2	Q9JPT3	Q9JPT3 neisseria m
8	2855	93.8	594	2	Q9JPT4	Q9JPT4 neisseria m
9	2824.5	92.8	599	2	Q9JPR8	Q9JPR8 neisseria m
10	2781	91.4	600	2	Q9JPS6	Q9JPS6 neisseria m
11	2772	91.1	590	2	Q9JPS3	Q9JPS3 neisseria m
12	2755.5	90.5	599	2	Q9JPS8	Q9JPS8 neisseria m
13	2736	89.9	598	2	Q9JPR7	Q9JPR7 neisseria m
14	2725.5	89.5	591	2	Q9JPS7	Q9JPS7 neisseria m
15	2725.5	89.5	591	16	Q9JRI8	Q9JRI8 neisseria m
16	2718	89.3	592	2	Q9AQF0	Q9AQF0 neisseria m

17	2706.5	88.9	591	2	Q93QY3	Q93QY3 neisseria m
18	2705	88.9	600	2	Q9JPS5	Q9JPS5 neisseria m
19	2675	87.9	592	2	Q9JPS9	Q9JPS9 neisseria m
20	2667	87.6	592	2	Q93QY2	Q93QY2 neisseria m
21	2637.5	86.6	595	2	Q9JPH0	Q9JPH0 neisseria m
22	2621.5	86.1	589	2	Q9JPH0	Q9JPH0 neisseria m
23	2610.5	85.8	592	2	Q93QY1	Q93QY1 neisseria m
24	2524	82.9	592	16	Q9JQW4	Q9JQW4 neisseria m
25	2501.5	82.2	596	2	Q9JPS4	Q9JPS4 neisseria m
26	2493.5	81.9	530	2	Q9JPS1	Q9JPS1 neisseria m
27	2418.5	43.3	2353	2	P71401	P71401 haemophilus
28	1057	34.7	1098	2	Q48152	Q48152 haemophilus
29	450	14.8	1299	16	Q9F3X6	Q9F3X6 pasteurella
30	402	13.2	2059	16	Q9PD50	Q9PD50 xylella fas
31	395	13.0	1107	2	Q9F2D8	Q9F2D8 salmonella
32	382.5	12.6	1190	16	Q9PC04	Q9PC04 xylella fas
33	360	11.8	2712	16	Q9F3X5	Q9F3X5 pasteurella
34	269.5	8.9	1291	16	Q92KQ7	Q92KQ7 rhizobium m
35	257.5	8.5	1953	16	Q98HJ2	Q98HJ2 rhizobium l
36	257.5	8.5	2276	2	Q93TY6	Q93TY6 staphylococ
37	254	8.3	1004	16	Q9PD63	Q9PD63 xylella fas
38	236	7.8	1039	2	Q9L6T7	Q9L6T7 escherichia
39	230.5	7.6	832	2	Q54356	Q54356 moraxella c
40	226	7.4	1040	2	Q9AL50	Q9AL50 shigella fl
41	225.5	7.4	1039	2	Q9L6T8	Q9L6T8 escherichia
42	222.5	7.3	1265	2	Q9FPA0	Q9FPA0 xanthomonas
43	221	7.3	989	2	Q9XBD4	Q9XBD4 escherichia
44	221	7.3	1018	16	Q9HW06	Q9HW06 pseudomonas
45	221	7.3	2747	2	Q91800	Q91800 aeromonas s

## ALIGNMENTS

RESULT 1  
ID Q9JPS0 PRELIMINARY; PRT; 598 AA.  
AC Q9JPS0;  
DT 01-OCT-2000 (TREMBL) 15, Last sequence update)  
DE 01-DEC-2001 (TREMBL) 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria: Proteobacteria; beta subdivision: Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH15;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B., Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capechi B., Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S., Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P., Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H., Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C., Moxon E.R., Grandi G., Rappuoli R.;  
RA "Identification of Vaccine Candidates Against Serogroup B Meningococcus by Whole-Genome Sequencing";  
RT Science 287:1816-1820(2000).  
RL [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H15;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer membrane protein of Neisseria meningitidis";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL, AF26381; AAF42530.1; -;  
DR EMBL, AF157607; AAF68668.1; -;  
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0BBA63CB CRC64;

Query Match 100.0%; Score 3044; DB 2; Length 598;

GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:36:22 ; Search time 104.77 Seconds  
(without alignments)  
533.980 Million cell updates/sec

Title: US-09-771-382-8  
Perfect score: 3042  
Sequence: 1 MNKISRIWNSALNAWVVS.....TASGNSRGHFGTSASGVQW 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT.\*  
3: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT.\*  
4: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1983.DAT.\*  
5: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1984.DAT.\*  
6: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1985.DAT.\*  
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18: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1997.DAT.\*  
19: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1998.DAT.\*  
20: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA1999.DAT.\*  
21: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
22: /SIDS1/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	3042	100.0	598	20 AAY23738	A surface protein
2	3042	100.0	598	22 AAU06178	N. meningitidis B2
3	3021	99.3	598	20 AAY23742	A surface protein
4	3021	99.3	598	22 AAU06177	N. meningitidis H1
5	2948	96.9	594	20 AAY23739	A surface protein
6	2948	96.9	594	22 AAU06179	N. meningitidis B2
7	2852	93.8	594	20 AAY23740	A surface protein
8	2852	93.8	594	21 AAY57044	BASB029 amino acid
9	2852	93.8	594	22 AAU06174	N. meningitidis EG
10	2821.5	92.8	599	20 AAY23743	A surface protein
11	2821.5	92.8	599	22 AAU06176	N. meningitidis H3

12	2732.5	89.8	591	21 AAY57045	BASB029 amino acid
13	2716.5	89.3	591	20 AAY27202	Amino acid sequenc
14	2716.5	89.3	591	20 AAY23746	A surface protein
15	2716.5	89.3	591	22 AAU06171	N. meningitidis PM
16	2709	89.1	592	20 AAY23737	A surface protein
17	2705.5	88.9	591	20 AAY23741	A surface protein
18	2705.5	88.9	591	22 AAU06175	N. meningitidis EG
19	2658	87.4	592	20 AAY23744	A surface protein
20	2658	87.4	592	22 AAU06172	N. meningitidis H4
21	2616.5	86.0	589	20 AAY23745	A surface protein
22	2616.5	86.0	589	22 AAU06173	N. meningitidis P2
23	2521	82.9	592	22 AAU06180	N. meningitidis Z2
24	2485	81.7	592	20 AAY27203	Amino acid sequenc
25	2451.5	80.6	513	22 AAU06183	N. meningitidis H4
26	2418	79.5	512	22 AAU06182	N. meningitidis PM
27	2335	76.8	502	22 AAU06186	N. meningitidis PM
28	2235	73.5	604	22 AAU06181	N. meningitidis su
29	2001.5	65.8	433	22 AAU06185	N. meningitidis PM
30	1855.5	61.0	407	22 AAU06184	N. meningitidis PM
31	1312.5	43.1	2353	17 AAR9393	Haemophilus adhesi
32	1286.5	42.3	2411	21 AAB23860	Haemophilus influe
33	1066	35.0	1094	21 AAB23858	Haemophilus influe
34	1054	34.6	1098	17 AAR9392	Haemophilus adhesi
35	1038	34.1	245	20 AAY27201	Amino acid sequenc
36	1004.5	33.0	679	17 AAR9394	Haemophilus adhesi
37	1004.5	33.0	679	21 AAB23855	Haemophilus influe
38	762	25.0	1002	21 AAB23854	Haemophilus influe
39	753	24.8	1004	21 AAB23857	Haemophilus influe
40	703	23.1	1104	21 AAB23856	Haemophilus influe
41	703	23.1	1104	21 AAB23859	Haemophilus influe
42	583	19.2	116	21 AAB37832	Neisseria conserv
43	412.5	13.6	2314	22 AAB69136	M. catarrhalis les
44	395.5	13.0	2123	22 AAE00701	Moraxella catarrha
45	392.5	12.9	1992	17 AAW04505	Moraxella 200 kDa

## ALIGNMENTS

RESULT 1  
AAY23738  
ID AAY23738 standard; Protein; 598 AA.  
XX  
AC AAY23738;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85790.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections







QY 1 MNKISRIIWNLSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATDDDDLYLE 60  
DB 1 mnkiirilwnsalnawvvseltnrhtrkrasatvatvatltilfatvqanaddddlyle 60  
QY 61 PVQRTAVLSFSDKEGTEGTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
DB 61 pvrqtavlsfksdtegektegdsnwavyfdekrvllkagaitlkagdnlikqntne 120  
QY 121 NTNENTNDSSFTYSLKDLTDLTSLVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
DB 121 ntntentndssffyslkkdltdltsveteklsfgangknvntsdtkglnfaketagntgd 180  
QY 181 PRVHLNGIGSTLDTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNINIKVPGTTA 240  
DB 181 prvhlingigstltdlntgattntvndvtddekkraasvkdvlalnagninikvpgttta 240  
QY 241 SDNVDFVRYDVEFLSADTKTTNVNVEKDKNGKRTVEKIGAKTSVIREKDGKLVTKGK 300  
DB 241 sdnvdfvrydveflsadtktttvnveskdngkrtvekgikaktsvirekdgklvtgk 300  
QY 301 GENGSTDEGEGLVTAKEVIDAVNKAQWVMTTANGOTQADKPFETVTSKVTTFASGN 360  
DB 301 gengstdegeglvtakevdaavnkagwvmttngotqadkpfetvtskvttfasgn 360  
QY 361 GTTATVSKDDQGNITVKYDVNVGDLNVLNQLNSGWNLDKSAVAGSSGKVISGNVSPSKG 420  
DB 361 gttatvskddqgnitvkydvnvgdlnvlnqlnsgwnldskavagssgkvisgnvpskg 420  
QY 421 KMDETVNIAGNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
DB 421 kmdevtninagnnieitrngknidatsmtpqfssvslgagadaptlsvddegalnvsgk 480  
QY 481 DANKPVRITNVAPGKGVGTNNVAQLKGVAQNLNRRIDNVGDNARAGIAQATAGLAQA 540  
DB 481 dankpvrilnvapgvkgegdvtnvaqlkgvaqnlrridnvdgnaraglaqataglaqa 540  
QY 541 YLPGKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVVIKGTASGNSRGHFGTSAVGYQW 598  
DB 541 ylpgksmmaigggtyrgeagyaigyssisdgtgnwvvikgtasgnsrghfgtsasvgyqw 598

## RESULT 3

AAV23742  
ID AAV23742 standard; Protein; 598 AA.

AC AAV23742;

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; infection; vaccine;  
immunoreactive peptide.

OS Neisseria meningitidis.

PN W09031132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYQU ) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

DR N-PSDB; AAX85794.

PT Neisseria meningitidis surface proteins useful for treating N.

PT meningitis infections

PS Claim 1; Page 108-110; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

SQ Sequence 598 AA;

Query Match 99.3%; Score 3021; DB 20; Length 598;  
Best Local Similarity 99.3%; Pred. No. 1e-174;  
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNKISRIIWNLSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATDDDDLYLE 60

DB 1 mnkiirilwnsalnawvvseltnrhtrkrasatvatvatltilfatvqanaddddlyle 60

QY 61 PVQRTAVLSFSDKEGTEGTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120

DB 61 pvrqtavlsfksdtegektegdsnwavyfdekrvllkagaitlkagdnlikqntne 120

QY 121 NTNENTNDSSFTYSLKDLTDLTSLVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180

DB 121 ntntentndssffyslkkdltdltsveteklsfgangknvntsdtkglnfaketagntgd 180

QY 181 PRVHLNGIGSTLDTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNINIKVPGTTA 240

DB 181 prvhlingigstltdlntgattntvndvtddekkraasvkdvlalnagninikvpgttta 240

QY 241 SDNVDFVRYDVEFLSADTKTTNVNVEKDKNGKRTVEKIGAKTSVIREKDGKLVTKGK 300

DB 241 sdnvdfvrydveflsadtktttvnveskdngkrtvekgikaktsvirekdgklvtgk 300

QY 301 GENGSTDEGEGLVTAKEVIDAVNKAQWVMTTANGOTQADKPFETVTSKVTTFASGN 360

DB 301 gengstdegeglvtakevdaavnkagwvmttngotqadkpfetvtskvttfasgn 360

QY 361 GTTATVSKDDQGNITVKYDVNVGDLNVLNQLNSGWNLDKSAVAGSSGKVISGNVSPSKG 420

DB 361 gttatvskddqgnitvkydvnvgdlnvlnqlnsgwnldskavagssgkvisgnvpskg 420

QY 421 KMDETVNIAGNIEITRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480

DB 421 kmdevtninagnnieitrngknidatsmtpqfssvslgagadaptlsvddegalnvsgk 480

QY 481 DANKPVRITNVAPGKGVGTNNVAQLKGVAQNLNRRIDNVGDNARAGIAQATAGLAQA 540

DB 481 dankpvrilnvapgvkgegdvtnvaqlkgvaqnlrridnvdgnaraglaqataglaqa 540

QY 541 YLPGKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVVIKGTASGNSRGHFGTSAVGYQW 598

DB 541 ylpgksmmaigggtyrgeagyaigyssisdgtgnwvvikgtasgnsrghfgtsasvgyqw 598

## RESULT 4

AAU06177  
ID AAU06177 standard; Protein; 598 AA.

AC AAU06177;

DT 24-OCT-2001 (first entry)

XX N. meningitidis H15 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain H15.  
 XX FH Key Location/Qualifiers  
 XX FT Region 1..50  
 XX FT /label= C1  
 XX FT /note= "Conserved region 1"  
 XX FT 51..104  
 XX FT /label= V1  
 XX FT /note= "Variable region 1"  
 XX FT 105..116  
 XX FT /label= C2  
 XX FT /note= "Conserved region 2"  
 XX FT 117..130  
 XX FT /label= V2  
 XX FT /note= "Variable region 2"  
 XX FT 131..194  
 XX FT /label= C3  
 XX FT /note= "Conserved region 3"  
 XX FT 195..216  
 XX FT /label= V3  
 XX FT /note= "Variable region 3"  
 XX FT 217..235  
 XX FT /label= C4  
 XX FT /note= "Conserved region 4"  
 XX FT 236..242  
 XX FT /label= V4  
 XX FT /note= "Variable region 4"  
 XX FT 243..598  
 XX FT /label= C5  
 XX FT /note= "Conserved region 5"  
 XX FT WO20015182-A1.  
 XX PN 02-AUG-2001.  
 XX XX 25-JAN-2001; 2001WO-AU000069.  
 XX XX 25-JAN-2000; 2000US-0177917.  
 XX XX (UYQU ) UNIV QUEENSLAND.  
 XX PI Peak IRA, Jennings MP;  
 XX XX WPI: 2001-488774/53.  
 XX DR N-PSDB; AAS09167.  
 XX XX New Nhha surface antigen polypeptides and polynucleotides from  
 PT Neisseria meningitidis, useful in producing vaccines for treating or  
 PT preventing broad spectrum of Neisseria meningitidis -  
 XX Claim 9; Fig 1; 91pp; English.  
 XX CC The present invention relates to the isolation of novel Neisseria  
 CC meningitidis mutant polypeptides of the surface antigen Nhha  
 CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
 CC characterised by deletions of non-conserved amino acids, particularly  
 CC the deletion of variable regions. The deletion mutants are useful in  
 CC diagnostics, therapeutic and prophylactic vaccines against a broader  
 CC spectrum of N. meningitidis, and in designing and/or screening of  
 CC medicaments. The mutant proteins when used as a vaccine can effectively  
 CC immunise against a broader spectrum of N. meningitidis strains than  
 CC would be expected from a corresponding wild-type surface antigen.  
 CC The present sequence representing the wild type surface antigen Nhha  
 CC from N. meningitidis strain H15 is 1 of 10 Nhha polypeptide sequences  
 CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
 CC the present invention.  
 XX SQ Sequence 598 AA;  
 Query Match 99.3%; Score 3021; DB 22; Length 598;  
 Best Local Similarity 99.3%; Pred. No. 1e-174;

Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLALLFATVOANATDDDDLYLE 60  
 DB 1 mkiyriiwsalnawvvsseletrnhtrkrasatvatvatlatllfatvqanatdddlyle 60  
 QY 61 PVQRTAVVLSFRSDKEGTGEGTSDSNWAVYFDEKRVLRKAGAITLKGADNMLTKQNTNE 120  
 DB 61 pvqrtavvlsfrsdegtgegtedsnwavyfdekrvlrkagaitlkagdnmlkikqntne 120  
 QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTISDTKGLNFAKETAGTNGD 180  
 DB 121 ntentndssftyllkdltdltsveteklsfgangknvnitsdtkglnfaketagcngd 180  
 QY 181 PTVHLNGIGSTLTDLTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240  
 DB 181 ptvhlngigstltdlntgattnvtndvtddekkraasvkdvlngwnikgvkpgtta 240  
 QY 241 SDNVDFVRYTDTVEFLSADTKTTTNNVESKDNGKRTVEKIGAKTSVKEKDKLVTGKKG 300  
 DB 241 sdnvdfvrytdtveflsadtktttnnveskdngkrtvekgikgtsvkekdglvtgkkg 300  
 QY 301 GENGSSDTDEGECLVTAKEVIDAVNKAGWRMKTTPANGQTGOADKFEFTVTSCTKVTFPASGN 360  
 DB 301 dengsstdegeclvtakevidavnkagwrmtttangqtgoadkfeftvtsctkvtfasgn 360  
 QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNOLNSGWNLDSKAVAGSSGKVISGNVSPSKG 420  
 DB 361 gttatvskddqgnitvkvdyvngdnlvnlqnswnldskavagsggkvisgnvpskg 420  
 QY 421 KMDETVNINAGNIEITRNGKNIDIIATSMTPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 480  
 DB 421 kmdetvninagnieitrngknidiatsmtptqfssvslgagadaptilsvddegalnvsgk 480  
 QY 481 DANKPVRIITNVAPGVKEGDTNVNAQLKGVAQNLNRRDNDGNARAGIAQAIATAGLAQA 540  
 DB 481 dankpvritnvapgvkegdtnvnaqlkgvaqnlrrdnndgnaraglaiaataglaqa 540  
 QY 541 YLPQKSMMAIGGTYRGEAGYAIYSSISDTGNMVKGTASGNSRGHFGTSASVGYQW 598  
 DB 541 ylpqksmmaiggytyrgeagyaiyssi sdtgnmwkgtasgnsrghfgtasasvgyqw 598  
 RESULT 5  
 AAY23739  
 ID AAY23739 standard; Protein; 594 AA.  
 XX AC AAY23739;  
 XX DT 08-SEP-1999 (first entry)  
 XX DE A surface protein of Neisseria meningitidis.  
 XX KW Surface protein; surface glycoprotein; infection; vaccine;  
 KW Immunoreactive peptide.  
 OS Neisseria meningitidis.  
 PN WO9931132-A1.  
 XX PD 24-JUN-1999.  
 XX PF 14-DEC-1998; 98WO-AU01031.  
 XX PR 12-DEC-1997; 97GB-0026398.  
 XX PA (ISIS-) ISIS INNOVATION LTD.  
 XX PA (UYQU ) UNIV QUEENSLAND.  
 XX PI Jennings MP, Moxon ER, Peak IRA;  
 XX WPI; 1999-418754/35.  
 DR N-PSDB; AAX85791.



Query Match 96.9%; Score 2948; DB 22; Length 594;  
Best Local Similarity 97.3%; Pred. No. 2.7e-170;  
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

QY 1 MNKISRIIWSALNAAVWVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
DB 1 mnklyriiwsalnawvseltrnhkkrasatvatavlatllfatvqanatdddddyle 60

QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVKAGAITLKAGDNLIKQNTNE 120  
DB 61 pvqrtavvlsfrsdektegtegsdsnwavfyfdekrvklagaitlkagdnlikqntne 116

QY 121 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
DB 117 ntentndssftyslkkdltdltsveteklsfgangknvitsdtkglnfaketagntgd 176

QY 181 PTVHLNGIGSTLTLTGATTNVDVNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240  
DB 177 ptvhlngigstltdlntgattnvndvndvtddekkraasvkdvlagnwnlkgvpgtta 236

QY 241 SDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKRTEVKIGAKTSVKEKDGKLVTKGK 300  
DB 237 sdnvdfvrtvdtveflsadtktttnnveskdngkrtvkgaktsvikekgklvtgk 296

QY 301 GENGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFEVTSCTKVTFA 360  
DB 297 dengsstdegeglvtakevidavnkgawrmktttangotgqadkfetvtsctnvtf 356

QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSP 420  
DB 357 gttatvskddqgnitvkydvnnvgdnlvnnqlqnsqwnldskavagssgkvlsnvsp 416

QY 421 KMDETVINAGNNIEITRNKNIDIAISMTPOQSSVSLGAGADAPTLSVDDEGALNV 480  
DB 417 kmdetvinagnnieitrnkniidiatsmpqpfssvslgagadaptsvdddegaln 476

QY 481 DANKPVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLA 540  
DB 477 dtnkpvritnvapgvkggdvtnvvaqlkgvaqnlrnidnvdgnaraglaiaiatagl 536

QY 541 YLPCKSMMAIGGGTYRGEAGYAGYSSISDTGNMVIKGTASGNSRGHFGTSASVGY 598  
DB 537 ylpcksmmaigggtyrgeagayagysisdsdgnwilkgtasgnsrghfgtsasvgy 594

## RESULT 7

AAAY23740  
ID AAY23740 standard; Protein; 594 AA.

AC AAY23740;

DT 08-SEP-1999 (first entry)

DE A surface protein of *Neisseria meningitidis*.

KW Surface protein; surface glycoprotein; infection; vaccine;  
immunoreactive peptide.

OS *Neisseria meningitidis*.

PN WO9931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

PA (UYU ) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX

DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85792.  
XX *Neisseria meningitidis* surface proteins useful for treating *N.*  
PT *meningitidis* infections  
XX Claim 1; Page 100-101; 132pp; English.  
XX The present sequence represents a surface protein of *Neisseria*  
CC *meningitidis* which is approximately 62 kDa. The *N. meningitidis*  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of *N. meningitidis* infection in humans.  
CC The *N. meningitidis* surface glycoproteins can also be used to  
CC prevent or treat *N. meningitidis* infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX Sequence 594 AA;

Query Match 93.8%; Score 2852; DB 20; Length 594;  
Best Local Similarity 94.6%; Pred. No. 1.7e-164;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;

QY 1 MNKISRIIWSALNAAVWVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
DB 1 mnklyriiwsalnawvseltrnhkkrasatvatavlatllfatvqastdddddyle 60

QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVKAGAITLKAGDNLIKQNTNE 120  
DB 61 pvqrtavvlsfrsdektegtegsdsnwavfyfdekrvklagaitlkagdnlikqntne 120

QY 121 NTNENTNDSSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
DB 121 ntntndssftyslkkdltdltsveteklsfgangknvitsdtkglnfaketagntgd 176

QY 181 PTVHLNGIGSTLTLTGATTNVDVNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 240  
DB 177 ptvhlngigstltdlntgattnvndvndvtddekkraasvkdvlagnwnlkgvpgtta 236

QY 241 SDNVDFVRTYDTVEFLSADTKTTTNNVESKDNKRTEVKIGAKTSVKEKDGKLVTKGK 300  
DB 237 sdnvdfvrtvdtveflsadtktttnnveskdngkrtvkgaktsvikekgklvtgk 296

QY 301 GENGSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFEVTSCTKVTFA 360  
DB 297 gendsstdegeglvtakevidavnkgawrmktttangotgqadkfetvtsctnvtf 356

QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSP 420  
DB 357 gttatvskddqgnitvkydvnnvgdnlvnnqlqnsqwnldskavagssgkvlsnvsp 416

QY 421 KMDETVINAGNNIEITRNKNIDIAISMTPOQSSVSLGAGADAPTLSVDDEGALNV 480  
DB 417 kmdetvinagnnieitrnkniidiatsmpqpfssvslgagadaptsvdddegaln 476

QY 481 DANKPVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLA 540  
DB 477 dankpvritnvapgvkggdvtnvvaqlkgvaqnlrnidnvdgnaraglaiaiatagl 536

QY 541 YLPCKSMMAIGGGTYRGEAGYAGYSSISDTGNMVIKGTASGNSRGHFGTSASVGY 598  
DB 537 ylpcksmmaigggtyrgeagayagysisdsdgnwilkgtasgnsrghfgtsasvgy 594

## RESULT 8

AAAY57044

ID AAY57044 standard; Protein; 594 AA.

XX AAY57044;

XX 21-FEB-2000 (first entry)

XX BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
XX  
XX  
KW BASB029; *Neisseria meningitidis*; surface fibril protein; HSF; diagnosis;  
KW Infection; treatment; prevent; antibacterial drug.  
XX  
XX  
OS *Neisseria meningitidis*.  
XX  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 104  
FT /note= "Encoded by AATC"  
XX  
XX  
PN W09958683-A2.  
XX  
XX  
PD 18-NOV-1999.  
XX  
XX  
PF 07-MAY-1999; 99WO-EP03255.  
XX  
XX  
PR 13-MAY-1998; 98GB-0010276.  
XX  
XX (SMK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA  
XX Ruelle J;  
PI  
XX  
XX  
DR WPI; 2000-053103/04.  
DR N-PSDB; AAZ39864.  
XX  
XX  
PT New polypeptide from *Neisseria meningitidis* useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal .  
XX  
XX  
PS Claim 4; Fig 2; 74pp; English.  
XX  
XX This is the *Neisseria meningitidis* BASB029 amino acid sequence from  
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AAZ39864-Z39865) and  
CC polypeptide sequences (AAZ39864-Z39865) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a *Neisseria*  
CC meningitidis infection in a mammal. Compositions containing a BASB029  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with *Neisseria*  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
XX  
SQ Sequence 594 AA;  
  
Query Match 93.8%; Score 2852; DB 21; Length 594;  
Best Local Similarity 94.6%; Pred. No. 1.7e-164;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;  
  
QY 1 MKKISRIIWSALNAWVYSELTRNHTKRASATVATVATLILFATVQANATDDDLYLE 60  
DB 1 mkiyriiwnsalnawvseltrnhtkrasatvatvatlilfatvqastdddlyle 60  
  
QY 61 PVQRTAVLSFRSDKEGTEGSDSNWAVYFDEKRVILKAGAITLKAGDNLKIKQNTNE 120  
DB 61 pvqrtavlsfrsdkegtegsdswvfyfdekrvilkagaitlkgadnlkikqntne 120  
  
QY 121 NTNENTNDSFFYSLKKDLTDLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
DB 121 ntne-----sftyslkkdltdltsvetklsfgangknvntsdtkglnfaketaetngd 176  
  
QY 181 PTVHLNGIGSTLTDLTLLNTGATTNTVNDNVTDDKKRAASVKDVLNAGWNIGVKPGTTA 240  
XX

DB 177 tcvhlingistltdtllntgattntvndnvtddkkraasvkdvlmagvniqvkpgttca 236  
QY 241 SDNVDFVRYDYVEFLSADTKTTTNNVESKDNGKRTVEKIGAKTSVKEKDGKLVTKGCK 300  
DB 237 sdnvdfvrydyveflsadtktttvneskdngkrtvekgigaktsvkekdgklvtgkdk 296  
QY 301 GENGSSTDEGLVTAKEVIDAVNKAQWRMKTTTANGOTGOADKFETVTSCTKVTFTASGN 360  
DB 297 gendstdkgeglvtakevldavnkagwmktttangqtgqadkfetvtsctnvtftasgk 356  
QY 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLQNSGNWLDKSAVAGSSGVISGNVSPSKG 420  
DB 357 gttatvskddqgnitvmydvnygdalnvnyqlqnsqwnldskavagssgkvvisgnvpskg 416  
QY 421 KMDETVNIAGNNIEITRNGKNIDTATSMTPQPSVSLGAGADAPTLSDVDDGALNVGSK 480  
DB 417 kmdetvniagnnieitrngknidiatmtptqfssvslgagadaptlsvddgalnvsgk 476  
QY 481 DANKPVRITNVAPGVKQEGDVTNVAOLKGAONLNRRIDNVGNARAGIAQAIATAGLAQA 540  
DB 477 dankpvrilnvapgvkqegdvtnvaqlkgvaqnlnnhldnvgnaragiqaiaataglvqa 536  
QY 541 YLPGKSMMAIGGTYRGEAGYATGYSSISDTGNWVTKGTASGNSRGHFGTASVGYQW 598  
DB 537 ylpgksmmaiggytyrgeagyaigyssisdggnwllkgtasgnsrghfgaasvgyqw 594  
  
RESULT 9  
AAU06174  
ID AAU06174 standard; Protein; 594 AA.  
XX  
AC AAU06174;  
XX  
DT 24-OCT-2001 (first entry)  
DE N. meningitidis EG327 surface antigen Nhha polypeptide sequence.  
XX  
KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.  
XX  
OS *Neisseria meningitidis* strain EG327.  
XX  
FH Key Location/Qualifiers  
FT Region 1..50 /label= C1  
FT /note= "Conserved region 1"  
FT Region 51..104 /label= V1  
FT /note= "Variable region 1"  
FT Region 105..116 /label= C2  
FT /note= "Conserved region 2"  
FT Region 117..126 /label= V2  
FT /note= "Variable region 2"  
FT Region 127..190 /label= C3  
FT /note= "Conserved region 3"  
FT Region 191..212 /label= V3  
FT /note= "Variable region 3"  
FT Region 213..231 /label= C4  
FT /note= "Conserved region 4"  
FT Region 232..238 /label= V4  
FT /note= "Variable region 4"  
FT Region 239..594 /label= C5  
FT /note= "Conserved region 5"  
XX  
PN WO200155182-A1.  
XX

PD 02-AUG-2001.  
XX  
PF 25-JAN-2001; 2001WO-AU00069.  
XX  
PR 25-JAN-2000; 2000US-0177917.  
XX  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
XX  
PI Peak IRA, Jennings MP;  
XX  
XX WPI: 2001-488774/53.  
DR N-PSDB; AAS09164.  
XX  
XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
XX Claim 9; Fig 1; 91pp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX  
XX Sequence 594 AA;  
SQ

Query Match 93.8%; Score 2852; DB 22; Length 594;  
Best Local Similarity 94.6%; Pred. No. 1.7e-164;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;  
QY 1 MNKISRIWNSALNAWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
Db 1 mnkiyriiwnsalnawvavseltrnhkkrasatvatavlatilfatvgastdddddlyle 60  
QY 61 PVQRTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120  
Db 61 pvqrtavvlsfrsdektegekednsnwavyfdekrvklagaitlkgadnlkikqntne 120  
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
Db 121 ntne----ssftyslkkdltldtsvgtelksfsgangknvntsdtkglnfaketaetngd 176  
QY 181 PTVHLNGIGSTLTDTLLTNGATTNTVNDVTDDEKKRAASVKDVLNAGWNITKGVKPGTTA 240  
Db 177 ttvhlngigstltdlntgattntvndvtddekkraasvkdvlngwnitkgvkgpgtta 236  
QY 241 SDNYDVRTYDTVEFLSADRTTNNVYESKDNKRTVEKIGAKTSVKEKDKGLVTGKGK 300  
Db 237 sdnydvrttydtveflsadtkttnvveskdngrtevkigaktsvkekgklvtgkdk 296  
QY 301 GENGSSSTDEGEGLYTAKEVIDAVNKAQWRMKTNTTANGQTGOADRFETVTSQTKVTFASGN 360  
Db 297 gendsstdekgeglvtakevidavnkagwrmtnttngqgtgqadkfetvtsqtnvtfasgk 356  
QY 361 GTTATVSKDDOGNTVYKVDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVTSGNVSFSKG 420  
Db 357 gttatvskddognitvnykvdvngdnlvqnlqnsqwnldskavagssgkvtsngvnvpskg 416  
QY 421 KMDETVNIAGNNTIEITRNKNIDIAITSMTPQFSSVSIAGADAPTLSVDDDEGALNVGSK 480  
Db 417 kmdetvniagnntieitrnknidiaitcsmtpqfssvsiagadaptilsvdddegalnvgsk 476

-QY 481 DANKPVRITNVAPGVKEGDVTNVQAQLKGAQNLNRRIDNVGNARAGIAQAIATAGLAQA 540  
Db 477 dankpvritnvapgvkegdvtnvqagqlnlnhhdvndgnaragiagataglvqa 536  
QY 541 YLPKSNMAWIGGGTYRGEAGYAIGYSSISDPTGNVVIKVTASGNSRGHFGTSASVYQW 598  
Db 537 ylpksmmaigggtyrgeagyaigysisdsdgnwllkgtasgnsrghfgasvgyqw 594  
RESULT 10.  
AA23743  
ID AAY23743 standard; Protein; 599 AA.  
XX  
XX AAY23743;  
AC AC  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
XX Neisseria meningitidis.  
OS  
XX WO9931132-A1.  
PN  
XX 24-JUN-1999.  
PD  
XX 14-DEC-1998; 98WO-AU01031.  
PF  
XX 12-DEC-1997; 97GB-0026398.  
PR  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
PI  
XX WPI: 1999-418754/35.  
DR N-PSDB; AAX85795.  
DR  
XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
PT  
XX  
PS Claim 1; Page 114-115; 132pp; English.  
XX  
XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX Sequence 599 AA;  
SQ

Query Match 92.8%; Score 2821.5; DB 20; Length 599;  
Best Local Similarity 92.7%; Pred. No. 1.2e-162;  
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;  
QY 1 MNKISRIWNSALNAWVVSSELTRNHTKRASATVATVATLTLFATVOANATD-DDDLYL 59  
Db 1 mnkiyriiwnsalnawvavseltrnhkkrasatvatavlatilfatvqanatdedeeel 60  
QY 60 EPVORTAVVLSFRSDEKTEGEGEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN 119  
Db 61 epvortavvlsfrsdektegekednsnwavyfdekrvklagaitlkgadnlkikqntn 120  
QY 120 ENTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179  
Db 121 kntnentndssftyslkkdltldtsveteklsfgangknvntsdtkglnfaketaetng 180

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QY 180 DPTVHLNGIGSTLDTLLNTGATTNTVNDVDEKKRAASVKDVLNAGWNKIGVKPGTT 239
Db 181 dtvhlngigstltdtllntgattntvndvddkkrasvkdvlndagwnlkgvkgpgtt 240
QY 240 ASDNVDFVRYDTVEFLSADTKTTTVNVSCKONGRTEYKIGAKTSVKEKDGKLVTKGK 299
Db 241 asdnvdfvrydtveflsadtktttvnvsckongrteykgaktsvikekdgklvtgk 300
QY 300 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTTANGOTGQADKFEETVSGTKVTFASG 359
Db 301 kgengsstdegglvtakevidavnkagwrmttttangtqgqadkfetvtsgtnvtfasg 360
QY 360 NGTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 419
Db 361 kgttatvskddognitvkydvnvgdnlvnlqnsqwnldskavagsgkvisgnvspk 420
QY 420 GKMDETVNTNAGNNIEITRNGKNIDIATSMTPQFSVSLGAGADAPTLVSDDGALNVGS 479
Db 421 gkmdetvnnagnnieitrngknidiatsmtqpfssvslgagadaptlsvddkgalnvgs 480
QY 480 KDANKPVRITNVAPGKVEDVTNVAQLKGVAQNLRIDVNDGNARAGTAQAIAATAGLAQ 539
Db 481 kdankpvrirtnvapgkvedvtnvvaqlkgvaqnlnridvndgnaragtaqaiaataglvq 540
QY 540 AYLPGKSMMAIGGTYRGAGYAIGYSSISDGTGNWIKGTASGNSRGHFGTASVGYQW 598
Db 541 aylpgksmmaiggytyrgagyaigyssisdgtgnwlikgtasgnsrghfgasvgyqw 599

RESULT 11
AAU06176
ID AAU06176 standard; Protein; 599 AA.
XX AC AAU06176;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis H38 surface antigen Nhha polypeptide sequence.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain H38.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..50 /label= C1
XX FT 51..105 /note= "Conserved region 1"
XX FT /label= V1
XX FT /note= "Variable region 1"
XX FT 106..117 /label= C2
XX FT /label= V2
XX FT /note= "Variable region 2"
XX FT 118..131 /label= C3
XX FT /label= V3
XX FT /note= "Conserved region 3"
XX FT 132..195 /label= C4
XX FT /label= V4
XX FT /note= "Variable region 4"
XX FT 196..217 /label= C5
XX FT /label= V5
XX FT /note= "Conserved region 5"
```

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PN WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYOU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09166.
XX New Nhha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhha
XX from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX Sequence 599 AA;
```

```
Query Match 92.8%; Score 2821.5; DB 22; Length 599;
Best Local Similarity 92.7%; Pred. No. 1.2e-162;
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;
QY 1 MNKISRIIWSNALNAWVVSSELTNRHTKRASATVATVATLTLFATVQANATD-DDDLXL 59
Db 1 makiyriiwnsalnawvavseiltnrhtkrasatvcvkatlilfatvqanadedeeel 60
QY 60 EPVQRTAVVLSFRSDKEGTGEGTDSNNAVYFDEKRVLKAGAITLKAGDNLKIKQNTN 119
Db 61 epvrsalvlqfmidkegenestgnigswydydnhtlghatvltkagdnlikqntn 120
QY 120 ENTNENTNDSSFTYSLKDLTLTTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 179
Db 121 kntnentndssftyslkkdltdltsveteklsfgangknvntsdtkglnfaketagting 180
QY 180 DPTVHLNGIGSTLDTLLNTGATTNTVNDVDEKKRAASVKDVLNAGWNKIGVKPGTT 239
Db 181 dtvhlngigstltdtllntgattntvndvddkkrasvkdvlndagwnlkgvkgpgtt 240
QY 240 ASDNVDFVRYDTVEFLSADTKTTTVNVSCKONGRTEYKIGAKTSVKEKDGKLVTKGK 299
Db 241 asdnvdfvrydtveflsadtktttvnvsckongrteykgaktsvikekdgklvtgk 300
QY 300 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTTANGOTGQADKFEETVSGTKVTFASG 359
Db 301 kgengsstdegglvtakevidavnkagwrmttttangtqgqadkfetvtsgtnvtfasg 360
QY 360 NGTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 419
Db 361 kgttatvskddognitvkydvnvgdnlvnlqnsqwnldskavagsgkvisgnvspk 420
QY 420 GKMDETVNTNAGNNIEITRNGKNIDIATSMTPQFSVSLGAGADAPTLVSDDGALNVGS 479
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Db 421 gkmdetvnnagnnieitrngknidiatmtptqfssvslgagadaptsldkgalnvgs 480  
QY 480 KDANKPVRIITNAPGVKEGSDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAGLAQ 539  
|||||  
Db 481 kdankpvritnvpvgvkegdvtnvaqlkgvaqlnnrldnvdnragiaqaiataglvq 540  
QY 540 AYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVKGVTASGNSRCHFGTSASVGYQW 598  
|||||  
Db 541 ayipgksmmaiggytyrgeagyaigyssisdggnwliikgtasgnsrghfgasasvgyqw 599

## RESULT 12

AAV57045

ID AAV57045 standard; Protein: 591 AA.

XX AC AAV57045;

XX DT 21-FEB-2000 (first entry)

XX DE BASB029 amino acid sequence from N. meningitidis strain H44/76.

XX KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;

XX QY infection; treatment; prevent; antibacterial drug.

XX OS Neisseria meningitidis.

XX FH Key Location/Qualifiers

XX FT Misc-difference 90 /note= "Encoded by AAT"

XX FT Misc-difference 92 /note= "Encoded by GAT"

XX FT Misc-difference 98 /note= "Encoded by AAC"

XX FT Misc-difference 108 /note= "Encoded by AATC"

XX FT Misc-difference 123 /note= "Encoded by ACA"

XX FT Misc-difference 269 /note= "Encoded by AAA"

XX FT Misc-difference 389 /note= "Encoded by CGT"

XX PN W09958683-A2.

XX PD 18-NOV-1999.

XX PF 07-MAY-1999; 99WO-EP03255.

XX PR 13-MAY-1998; 98GB-0010276.

XX PA (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.

XX PI Ruelle J;

XX DR WPI; 2000-053103/04.

XX DR N-PSDB; AA239865.

XX PT New polypeptide from neisseria meningitidis useful for diagnosis,

XX PS treatment or prevention of bacterial infections in mammal

XX PS Claim 4; Fig 2; 74pp; English.

XX CC This is the Neisseria meningitidis BASB029 amino acid sequence from

XX CC serogroup B strain H44/76. The BASB029 protein is homologous to the

XX CC Haemophilus influenzae surface fibril (HSF) protein. The invention

XX CC relates to BASB029 polynucleotide sequences (AA239864-239865) and

XX CC polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.

XX CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria

XX CC meningitidis infection in a mammal. Compositions containing an immune

XX CC polynucleotides and polypeptides are useful for generating an immune

XX CC response in an animal. A therapeutic composition comprising an antibody

XX CC directed against BASB029 is useful in treating humans with Neisseria

XX CC meningitidis disease. The polynucleotide is useful in the diagnosis of

CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes,  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
XX receiving the protein.

XX QY Sequence 591 AA;

QY 1 MNKISRIIWNALNAWVVSSELTRNHTKRASATVATAVLATLTLFATVOANATD---DDDL 57

Db 1 mnkiyriiwnsalnawvavseltrnhtkrasatvktavlatlflfatvqasannee 60

QY 58 YLEPVORTAVVLSFRSDKECTGEKGT-EDSNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116

Db 61 yldpvqrtvavlivnsdkektgekeveedsnwavyfdekgvltareitlkagdnkikq 120

QY 117 NTNENTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVNIITSDTKGLNFAKETAG 176

Db 121 -----ngsnftyyslkkdltdltsvgteteklsfsangknvniitdtkglnfaketag 170

QY 177 TNGDPTVHLNGIGSTLTDLTLNTGATNTVNDVNDVDEKRAASVDKVLNAGNLIKGVKP 236

Db 171 tngdptvhlngigstltdlntgattvndvndvndvdekkraasvdkvlnagwnikgvkp 230

QY 237 GTTASDNVDFVRYDYTVFELSDTKTTNVNVEKDNKRTVEVIGAKTSVIKEDGKLVT 296

Db 231 gttasdnvdfvrydytveflsadtkttnvnveskdngkrtevkigaktsvikekdgklvt 290

QY 297 GKKGENGSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTGQADKFTETVTSGTKVTF 356

Db 291 gkdkgengsstdegeglvtakevidavnkagwrmktttangtqgqdkfetvtsgtntvf 350

QY 357 ASNGTITATVSKDDQGNITVRYDVNVGDALNVNQLQSNWLNDSKAVAGSGKVISGNVS 416

Db 351 asggtttatvskddqgnitvrydvnvvgdalinvnqlqsgwnlkskavagsgkvvisgnvs 410

QY 417 PSKGKMDETVINAGNIEITRNGKNIDIAITSMTPQFSSVSLGAGADAPTLSVDEGALN 476

Db 411 pskgkmdetvinagnieitrngknidiatmtptqfssvslgagadaptsldkgalnv 469

QY 477 VGSKDANKPVRIITNAPGVKEGSDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAATAG 536

Db 470 vgskkdnkpvrirtnvapgvgkdvtnvaqlkgvaqlnnrldnvdnragiaqaiatag 529

QY 537 LAQAYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVKGVTASGNSRCHFGTSASVGY 596

Db 530 lvdaylpkksmmaiggytyrgeagyaigyssisdggnwliikgtasgnsrghfgasasvgy 589

QY 597 QW 598

Db 590 qw 591

RESULT 13

AAV27202

ID AAV27202 standard; Protein: 591 AA.

XX AC AAV27202;

XX DT 24-SEP-1999 (first entry)

XX DE Amino acid sequence of N. meningitidis protein ORF40-1.

XX QY Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;

XX KW



bacterial infection; treatment.

OS Neisseria meningitidis.  
PN WO9936544-A2.  
XX 22-JUL-1999.  
PD 14-JAN-1999; 99WO-IB00103.  
PF 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX (CHIR-) CHIRON SPA.  
XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;  
PI WPI; 1999-444400/37.  
DR N-PSDB; AAX99124.  
XX New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing Neisseria  
PT meningitidis infections  
XX Claim 1; Page 62; 123pp; English.  
PS The invention provides proteins (AAY27201-245) from Neisseria  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to Neisseria  
CC bacteria, especially Neisseria meningitidis.  
XX Sequence 591 AA;  
SQ

Query Match 89.3%; Score 2716.5; DB 20; Length 591;  
Best Local Similarity 90.7%; Pred. No. 2.6e-156;  
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKISRIIWNLSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
DB 1 mnkiyriiwnsalnawvyseltrnhtkrasatvktavlatllfatvqasanneeedl 60  
QY 58 YLEPVQRTAVLSFRSDKEGTGEKTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116  
DB 61 yldpvqrtvavliivnsdkegtgekeveensdwavyfnekglvtareitlkagdnlikq 120  
QY 117 NTNENTNTNDSSFTYSLKKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKETAG 176  
DB 121 -----ngunfyslkkdltltsvgteklsfsgangknvntsdtkglnfaketag 170  
QY 177 TGGDPTVHLNGIGSTLTLTLLTGATNTVNDVDEKRAASVADVLNAGWNKIGKVP 236  
DB 171 tngdptvhlingstltdlntgattntvndvdekkraasvkdvnagwnikgvp 230  
QY 237 GTTASNDVFRTYDVEFLSADTKTTTVNVEKNGKRTVEKIGAKTSVIEKDGKLV 296  
DB 231 gttasndvfrtydvtelnsadtkttvnsveskdngkktveikgtsviekdgklvt 290  
QY 297 GKKGNGSGSTDEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKEETVTSKTVP 356  
DB 291 gkkgngsgstdegeglvtakevdaavnkgwrmtnttngqgqadketvtsgtnvtf 350  
QY 357 ASGNGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNVS 416  
DB 351 asgngtatvskddqgnitvmydvngdnlvnlqnsqwnldskavagssgkvisgnvs 410  
QY 417 PSKGMDEVTNINAGNIEITRNGKNIDIASMTPOFSSVSLGAGADAPTLSDVDDGALN 476  
DB 411 pskgmdetvniagnnieitrngknidiatmtpqfssvslgagadaptlsvdgd-ain 469

QY 477 VGSKDANKPVRITNVAPGVKEGDTNVQAQLKGVAQNLRNDRIDNVGNARAGIAQAIATAG 536  
DB 470 vgskdankpvrntnvpagvkegdvtnvaqlkgvaqnlmrdrdnvgnaragiatatag 529  
QY 537 LAQAYLPKGSMAIGAIGGTYRGEAGYAIGYSSISDSTGNWIKGTASGNSRCHFTSASVGY 596  
DB 530 lvqaylpkgksmmaiggytyrgeagyaigyssisdsgnwiikgtasgnsrghfgasasvgy 589  
QY 597 QW 598  
DB 590 qw 591  
RESULT 14  
AAY23746  
ID AAY23746 standard; Protein; 591 AA.  
XX  
AC AAY23746;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-Al.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
XX WPI; 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 127-128; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
SQ Sequence 591 AA;

Query Match 89.3%; Score 2716.5; DB 20; Length 591;  
Best Local Similarity 90.7%; Pred. No. 2.6e-156;  
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKISRIIWNLSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
DB 1 mnkiyriiwnsalnawvyseltrnhtkrasatvktavlatllfatvqasanneeedl 60  
QY 58 YLEPVQRTAVLSFRSDKEGTGEKTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116  
DB 61 yldpvqrtvavliivnsdkegtgekeveensdwavyfnekglvtareitlkagdnlikq 120

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Db 61 yldpvqrtavlivnsdkegtkekeveensdwavyfnekvgltareitlkagdnllkq 120
Qy 117 NTNENTNENTNDSTFTYSLKDLTDLTSVTEKLSFGANGKNVNITSDTKGLNFAKETAG 176
Db 121 -----ngntftysllkldtldsvgteklfsfngknvnitsdtkglnfaketag 170
Qy 177 TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDVDDDEKKRAASVKDVLNAGWNKIGVKP 236
Db 171 tngdttvhlngigstltdtllntgattenvndndvdddekkraasvkdvlagnwnikgvkp 230
Qy 237 GTTASDNVDFVRYDTVEFLSADTKTTNNVESKDNKRTVEKIGAKTSVIKEKDGKLYT 296
Db 231 gttasdnvdfvrydtveflsadtkttnvneskdngkttevkigaktsvikekdglvt 290
Qy 297 GKRGENGSSDDEGLVTAKEVIDAYNKAGWRMKTTTANGQTGOADKFETVTSGTKVTF 356
Db 291 qdkgengsstdeglivtakevidavnkagwrnktttangqtgqadkfetvtsgtvtf 350
Qy 357 ASGNGTTATVSKDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSGKVISGNVS 416
Db 351 asgngttatvskddqgnitvmydvngdalnvnglqnswnldskavagsgkvisgnvs 410
Qy 417 PSKGMDETVNNAGNIEITRNCKNIDTATSPQSSVSLGAGADAPTLSVDDEGALN 476
Db 411 pskgmdetvnnagnnleitrngknidiatsmtpqfssvslgagadapltlsvdgd-aln 469
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Qy 537 LAQAYLPKSNMATTGGTYRGEAGYATGYSSISDTGNWIKNGTASGNSRGHFGTSASVGY 596
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Qy 597 QW 598
Db 590 qw 591

RESULT 15
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ID AAU06171 standard; Protein: 591 AA.
XX AC AAU06171;
XX DT 24-OCT-2001 (first entry)
XX XX
DE N. meningitidis PMC21 surface antigen Nhha polypeptide sequence.
XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain PMC21.
XX FH
XX Key Location/Qualifiers
FT Peptide 1..51
FT FT /label= Signal_peptide
FT Region 1..50
FT FT /label= C1
FT FT /note= "Conserved region 1"
FT Region 51..108
FT FT /label= V1
FT FT /note= "Variable region 1"
FT Protein 52..591
FT FT /label= Mature_Nhha
FT FT /note= "Predicted mature protein, specifically
FT 109..120
FT FT /label= C2
FT FT /note= "Conserved region 2"
FT Region 121..124
FT FT /label= V2
FT FT /note= "Variable region 2"
FT Region 125..188
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FT FT /note= "Conserved region 3"
FT Region 189..210
FT FT /label= V3
FT FT /note= "Variable region 3"
FT Region 211..229
FT FT /label= C4
FT FT /note= "Conserved region 4"
FT Region 230..236
FT FT /label= V4
FT FT /note= "Variable region 4"
FT Region 237..591
FT FT /label= C5
FT FT /note= "Conserved region 5"
XX WO200155182-A1.
PN 02-AUG-2001.
XX XX
XX 25-JAN-2001; 2001WO-AU00069.
XX PR 25-JAN-2000; 2000US-0177917.
XX PA (UYQU ) UNIV QUEENSLAND.
XX PI Peak IRA, Jennings MP;
XX WPI: 2001-488774/53.
XX DR N-PSDB; AAS09161.
XX XX
XX New Nhha surface antigen polypeptides and polynucleotides from
FT Neisseria meningitidis, useful in producing vaccines for treating or
FT preventing broad spectrum of Neisseria meningitidis -
XX PS Claim 9; Fig 1; 91pp; English.
XX CC
XX CC The present invention relates to the isolation of novel Neisseria
CC meningitidis mutant polypeptides of the surface antigen Nhha
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC characterised by deletions of non-conserved amino acids, particularly
CC the deletion of variable regions. The deletion mutants are useful in
CC diagnostics, therapeutic and prophylactic vaccines against a broader
CC spectrum of N. meningitidis, and in designing and/or screening of
CC immunise against a broader spectrum of N. meningitidis strains than
CC would be expected from a corresponding wild-type surface antigen.
CC The present sequence representing the wild type surface antigen Nhha
CC from N. meningitidis strain PMC21 is 1 of 10 Nhha polypeptide sequences
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX SQ Sequence 591 AA;
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Query Match 89.3%; Score 2716.5; DB 22; Length 591;
Best Local Similarity 90.7%; Pred. No. 2.6e-156;
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

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Db 1 mnklyrliwnsalnawvvseltrnhktrasatvktavlatilfatvgasanneegee 60
Qy 58 YLEPVQRTAVVLSPRSDEKGTGEGTGED-SNNAVYFDEKRVLKAGATITLKAGDNLKIQ 116
Db 61 yldpvqrtavlivnsdkegtkekeveensdwavyfnekvgltareitlkagdnllkq 120
Qy 117 NTNENTNENTNDSTFTYSLKDLTDLTSVTEKLSFGANGKNVNITSDTKGLNFAKETAG 176
Db 121 -----ngntftysllkldtldsvgteklfsfngknvnitsdtkglnfaketag 170
Qy 177 TNGDPTVHLNGIGSTLTDLLNTGATTNVTNDVDDDEKKRAASVKDVLNAGWNKIGVKP 236
Db 171 tngdttvhlngigstltdtllntgattenvndndvdddekkraasvkdvlagnwnikgvkp 230
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QY 237 GTTASDNVDFVRTVEPLSADFTKTTVNVESKONGKRTEVKIGAKTSVKEKDGKLV 296  
Db |||||  
QY 231 gttasdnvdfvrtvtefilsadtktttvnveskngkktvkigaktsvkekdglvt 290  
Db |||||  
QY 297 GKGKGENSGSTDEGGLVTAKEVIDAVNKGWRMKTTTTANGOTGOADKFETVTSKTKVTF 356  
Db |||||  
QY 291 gkdkgengsstdegeglvtakevidavnkagwrmkttttangtggadkfetvsgtnvtf 350  
QY 357 ASGNCTTATVSKDDGNITVKYDVNVGDALNVNOLONGWNLDSKAVAGSSGKVISGNVS 416  
Db |||||  
QY 351 asgkgttatvskddgnitvmydvnvgdalnvngdqngwnldskavagssgkvvisgnvs 410  
QY 417 PSKGXMDETVNIAGNNIEITRNGKNIDIATSMTPQFSSVSLGACADAPTLSVDDDEGALN 476  
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QY 411 pskgxmdetvniagnnieitrngknidiatsmtptqfssvslgacadaptilsvdgd-aln 469  
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QY 597 QW 598  
Db ||  
QY 590 qw 591

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Job time: 319 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:37:08 ; Search time 39.66 Seconds  
(without alignments)  
368.293 Million cell updates/sec

Title: US-09-771-382-8  
Perfect score: 3042  
Sequence: 1 MNKISRIIWNLSALNAWVVS.....TASGNSRGHFGTSASVGYQW 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	3042	100.0	598	US-09-377-155-5	Sequence 5, Appli
2	3042	100.0	598	US-09-669-974-5	Sequence 5, Appli
3	3021	99.3	598	US-09-377-155-13	Sequence 13, Appl
4	3021	99.3	598	US-09-669-974-13	Sequence 13, Appl
5	2948	96.9	594	US-09-377-155-7	Sequence 7, Appli
6	2948	96.9	594	US-09-669-974-7	Sequence 7, Appli
7	2852	93.8	594	US-09-377-155-9	Sequence 9, Appli
8	2852	93.8	594	US-09-669-974-9	Sequence 9, Appli
9	2821.5	92.8	599	US-09-377-155-15	Sequence 15, Appl
10	2821.5	92.8	599	US-09-669-974-15	Sequence 15, Appl
11	2716.5	89.3	591	US-09-377-155-21	Sequence 21, Appl
12	2716.5	89.3	591	US-09-669-974-21	Sequence 21, Appl
13	2709	89.1	592	US-09-377-155-2	Sequence 2, Appli
14	2709	89.1	592	US-09-669-974-2	Sequence 2, Appli
15	2705.5	88.9	591	US-09-377-155-11	Sequence 11, Appl
16	2705.5	88.9	591	US-09-669-974-11	Sequence 11, Appl
17	2658	87.4	592	US-09-377-155-17	Sequence 17, Appl
18	2658	87.4	592	US-09-669-974-17	Sequence 17, Appl
19	2616.5	86.0	589	US-09-377-155-19	Sequence 19, Appl
20	2616.5	86.0	589	US-09-669-974-19	Sequence 19, Appl
21	1312.5	43.1	2353	US-09-377-155-33	Sequence 33, Appl
22	1312.5	43.1	2353	US-08-913-942-4	Sequence 4, Appli
23	1312.5	43.1	2353	US-09-669-974-33	Sequence 33, Appl
24	1311.5	43.1	2354	US-09-268-347-47	Sequence 47, Appl
25	1286.5	42.3	2411	US-09-268-347-36	Sequence 36, Appl
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27	1245	40.9	607	US-08-685-467-6	Sequence 6, Appli

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34	1054	34.6	1098	4	US-09-377-155-32	Sequence 32, Appl
35	1054	34.6	1098	4	US-08-913-942-2	Sequence 2, Appli
36	1054	34.6	1098	4	US-09-669-974-32	Sequence 32, Appl
37	1054	34.6	1098	4	US-09-268-347-44	Sequence 44, Appl
38	1040	34.2	658	1	US-08-409-995-5	Sequence 5, Appli
39	1040	34.2	658	3	US-08-685-467-5	Sequence 5, Appli
40	1040	34.2	658	4	US-08-913-942-5	Sequence 5, Appli
41	1004.5	33.0	679	4	US-08-913-942-15	Sequence 15, Appl
42	1004.5	33.0	679	4	US-09-268-347-26	Sequence 26, Appl
43	762	25.0	1002	4	US-09-268-347-24	Sequence 24, Appl
44	753	24.8	1004	4	US-09-268-347-30	Sequence 30, Appl
45	703	23.1	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1  
US-09-377-155-5  
; Sequence 5, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-5

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Best Local Similarity	100.0%;	Pred. No. 4.5e-239;		
Matches 598;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY	121	NTNENTNDSFFYSYLSKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNPAKETAGTNGD	180	
Db	121	NTNENTNDSFFYSYLSKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNPAKETAGTNGD	180	
QY	181	PTVHLNGIGSTLDTLLNTGATTVNTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA	240	
Db	181	PTVHLNGIGSTLDTLLNTGATTVNTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA	240	
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Db	241	SDNVDFRVYDVFVLSADTKTTTVNVESKDNCKRTEVIGAKTSVKEKDGKLVTKGK	300	
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## RESULT 2

US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 100.0%; Score 3042; DB 4; Length 598;  
Best Local Similarity 100.0%; Pred. No. 4.5e-239;  
Matches 598; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 121 NTNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
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Db 421 KMDETVINAGNNIEITRNGKNIDIAISMTPOFSSVSLGAGADAPTLISVDDGALNVGSK 480  
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## RESULT 3

US-09-377-155-13  
; Sequence 13, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-13

Query Match 99.3%; Score 3021; DB 4; Length 598;  
Best Local Similarity 99.3%; Pred. No. 2.3e-237;  
Matches 594; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
QY 1 MNKISRIIWSALNAWVVSSELTRNHTKRASATVATAVLATLTLFATVQANATDDDDLYLE 60  
Db 1 MNKISRIIWSALNAWVVSSELTRNHTKRASATVATAVLATLTLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLRKAGAITLKGADNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLRKAGAITLKGADNLKIKQNTNE 120  
QY 121 NTNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 121 NTNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
QY 181 PTVHLNGIGSTLTDLTLLTGATTVNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240  
Db 181 PTVHLNGIGSTLTDLTLLTGATTVNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 240  
QY 241 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVKEKDGKLVTCGKG 300  
Db 241 SDNVDFVRTYDVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVKEKDGKLVTCGKG 300  
QY 301 GENGSSDEGEGLTAKEVIDAVNKAQWRMKTTTTANGOTGOADKFETVTSCTKVTFFASGN 360  
Db 301 GENGSSDEGEGLTAKEVIDAVNKAQWRMKTTTTANGOTGOADKFETVTSCTKVTFFASGN 360  
QY 361 GTTATVSKDDOGNITVKYDVNVGDALNVNQLNSGNWLDKSAVAGSSGKVISGNVSPSKG 420

Db	361	GTATATVSKDDQGNITVKYIVNVGDALNVQLQNSGNWNLDSKAVAGSSGKVVISGNVSPSGK	420
Qy	421	KMDETVINAGNNIEITRNCKNIDIAATSMTPQFSSVSLGAGADAPITLSVDDDEGALNVGSK	480
Db	421	KMDETVINAGNNIEITRNCKNIDIAATSMTPQFSSVSLGAGADAPITLSVDDDEGALNVGSK	480
Qy	481	DANKPVRITNVAPGVKEGDVTNVAQLKGVQAQNLNRRIDNVDGNARAGIAQAIAATAGLAQA	540
Db	481	DANKPVRITNVAPGVKEGDVTNVAQLKGVQAQNLNRRIDNVDGNARAGIAQAIAATAGLAQA	540
Qy	541	YLPCKSMWATGGGTYRGEAGYATGYSSISDITGNWVITKGTASGNSRGHFGTASGVQW	598
Db	541	YLPCKSMWATGGGTYRGEAGYATGYSSISDITGNWVITKGTASGNSRGHFGTASGVQW	598

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RESULT      5
US-09-377-155-7
; Sequence 7, Application US/09377155
; Patent No. 6197312
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/377,155
; CURRENT FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 7
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-377-155-7

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Query Match	96.9%	Score 2948;	DB 4;	Length 594;
Best Local Similarity	97.3%;	Pred. No. 2e-231;		
Matches 582; Conservative	2;	Mismatches 10;	Indels 4;	Gaps
Qy	1	MNKSRIWNSALNANWVVVSELTRNHTKRASATVAVATLTLFATVQANATDDDLYLE	60	
Db	1	MNKYRIWNSALNANWVVVSELTRNHTKRASATVAVATLTLFATVQANATDDDLYLE	60	
Qy	61	PVQRTAVVLFSRDKETGKEGTEDSNWAVYFDEKRVLKAGAITLTKAGDNLKIKONTNE	120	
Db	61	PVQRTAVVLFSRDKETGKEGTEDSNWAVYFDEKRVLKAGAITLTKAGDNLKIKO----	116	
Qy	121	NTNENTNDSFTYSLLKDDLTLDSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD	180	
Db	117	NTNENTNDSFTYSLLKDDLTLDSVETEKLSFGANGKNVNITSDTKGLNFAKETAGTNGD	176	
Qy	181	PTVHLNGIGSTLDTLLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNKIGVKPGTTA	240	
Db	177	PTVHLNGIGSTLDTLLNTGATTNVTNDVNTDDEKKRAASVKDVLNAGWNKIGVKPGTTA	236	
Qy	241	SDNDVDFVRTDYTFEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSV1KEKDGKLVTKGK	300	
Db	237	SDNDVDFVRTDYTFEFLSADTKTTTVNVESKDNCKRTEVKIGAKTSV1KEKDGKLVTKGK	296	
Qy	301	GENGSSTDECEGLVTAKEVIDAVNKAGWRMKTTFANGQTGOADKFEFVTSGTVTFASGN	360	
Db	297	DENGSSSTDECEGLVTAKEVIDAVNKAGWRMKTTFANGQTGOADKFEFVTSGTNVTFASGK	356	
Qy	361	GTTATFVKDDOGNITVKYDVNVGDALNVQLONSGNWLDKSAVAGSSGKVISGNVSPSKG	420	
Db	357	GTTATFVKDDOGNITVKYDVNVGDALNVQLONSGNWLDKSAVAGSSGKVISGNVSPSKG	416	
Qy	421	KMDETVINAGNNIE1TRNGKNID1AT5MTPOFSSSVLSGAGADPTLSVDDEGALNVGSK	480	

Db 417 KMDFTVINAGNNIEITRNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476  
QY 481 DANKPVRITNVAPGVKEGDTVNVAAQLKGVAQNLRINDVNGNARAGTAQAIAIATAGLAQA 540  
Db 477 DTNKPVRITNVAPGVKEGDTVNVAAQLKGVAQNLRINDVNGNARAGTAQAIAIATAGLVQA 536  
QY 541 YLPCKSMAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGTSASVGYOW 598  
Db 537 YLPCKSMAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGTSASVGYOW 594

RESULT 6  
US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 96.98; Score 2948; DB 4; Length 594;  
Best Local Similarity 97.38; Pred. No. 2e-231;  
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;  
QY 1 MNKISRIIWSALNANVWVSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNANVWVSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDEKGEKGTEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDEKGEKGTEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 116  
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176  
QY 181 PTVHLNGIGSLTDLTLNTGATTNVDNVTDDDEKRAASVKDVLNAGNWKVKGPGTTA 240  
Db 177 PTVHLNGIGSLTDLTLNTGATTNVDNVTDDDEKRAASVKDVLNAGNWKVKGPGTTA 236  
QY 241 SDNVDFVRTYDVFELSDATKTTTVNVYESKONGKRTVEVIGAKTSVKEKDKGLVTGK 300  
Db 237 SDNVDFVRTYDVFELSDATKTTTVNVYESKONGKRTVEVIGAKTSVKEKDKGLVTGK 296  
QY 301 GENSSSTDEGBGLVTAKEVIDAVNKAGWRMKTITTTANGOTGOADKFEVTSCTKVTFASGN 360  
Db 297 DENGSSTDEGBGLVTAKEVIDAVNKAGWRMKTITTTANGOTGOADKFEVTSCTKVTFASGN 356  
QY 361 GTTATVSKDDQGNITVYDYNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKG 420  
Db 357 GTTATVSKDDQGNITVYDYNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKG 416  
QY 421 KMDFTVINAGNNIEITRNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 480  
Db 417 KMDFTVINAGNNIEITRNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476

Db 417 KMDFTVINAGNNIEITRNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476  
QY 481 DANKPVRITNVAPGVKEGDTVNVAAQLKGVAQNLRINDVNGNARAGTAQAIAIATAGLAQA 540  
Db 477 DTNKPVRITNVAPGVKEGDTVNVAAQLKGVAQNLRINDVNGNARAGTAQAIAIATAGLVQA 536  
QY 541 YLPCKSMAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGTSASVGYOW 598  
Db 537 YLPCKSMAIGGGTYRGEAGYAIGYSSISDGTGNVVIKGTASGNSRGHFGTSASVGYOW 594

RESULT 7  
US-09-377-155-9  
; Sequence 9, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-9

Query Match 93.8%; Score 2852; DB 4; Length 594;  
Best Local Similarity 94.6%; Pred. No. 1.2e-223;  
Matches 566; Conservative 5; Mismatches 23; Indels 4; Gaps 1;  
QY 1 MNKISRIIWSALNANVWVSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNANVWVSELTRNHTKRASATVATVATLFLFATVQASTDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDEKGEKGTEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDEKGEKGTEDSNWAVYFDEKRVLKAGAITLKGADNLKIKQNTNE 120  
QY 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
Db 121 NTNA----SSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176  
QY 181 PTVHLNGIGSLTDLTLNTGATTNVDNVTDDDEKRAASVKDVLNAGNWKVKGPGTTA 240  
Db 177 PTVHLNGIGSLTDLTLNTGATTNVDNVTDDDEKRAASVKDVLNAGNWKVKGPGTTA 236  
QY 241 SDNVDFVRTYDVFELSDATKTTTVNVYESKONGKRTVEVIGAKTSVKEKDKGLVTGK 300  
Db 237 SDNVDFVRTYDVFELSDATKTTTVNVYESKONGKRTVEVIGAKTSVKEKDKGLVTGK 296  
QY 301 GENSSSTDEGBGLVTAKEVIDAVNKAGWRMKTITTTANGOTGOADKFEVTSCTKVTFASGN 360  
Db 297 DENGSSTDEGBGLVTAKEVIDAVNKAGWRMKTITTTANGOTGOADKFEVTSCTKVTFASGN 356  
QY 361 GTTATVSKDDQGNITVYDYNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKG 420  
Db 357 GTTATVSKDDQGNITVYDYNVGDALNVQNLQNSGNWLDKAVAGSSGKVISGNVSPSKG 416  
QY 421 KMDFTVINAGNNIEITRNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 480  
Db 417 KMDFTVINAGNNIEITRNGKNIDIAISMAPPQFSSVSLGAGADAPTLSVDDDEGALNVGSK 476  
QY 481 DANKPVRITNVAPGVKEGDTVNVAAQLKGVAQNLRINDVNGNARAGTAQAIAIATAGLAQA 540



Db	477	DANKPVRITNVAFCVKEGDVTNTAQLKGVAAQNLNHNIDVNGNARAGIAQAATATAGLVQA	536
Qy	541	YLPKSMNAITGGGTGYRCEAGYATGYSSISDTGNWVILKGTASGNSRGHFTSASGVQW	598
Db	537	YLPKSMNAITGGGTGYRCEAGYATGYSSISDGNWVILKGTASGNSRGHFGASASGVQW	594

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RESULT      8
US-09-669-974-9
; Sequence 9, Application US/09669974
; Patent No. 633173
; GENERAL INFORMATION:
; APPLICANT: PEAK, Ian Richard Anselm
; APPLICANT: JENNINGS, Michael Paul
; APPLICANT: MOXON, E. Richard
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
; FILE REFERENCE: 065064/0128
; CURRENT APPLICATION NUMBER: US/09/669,974
; CURRENT FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US 09/377,155
; PRIOR FILING DATE: 1999-08-19
; APPLICATION NUMBER: PCT/AU98/01031
; PRIOR FILING DATE: 1998-12-14
; PRIOR APPLICATION NUMBER: GB 9726398.2
; PRIOR FILING DATE: 1997-12-12
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 9
; LENGTH: 594
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-669-974-9

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Query Match	93.8%	Score	2852;	DB	4;	Length	594;
Best Local Similarity	94.6%;	pred.	No. 1.2e-223;				
Matches	566;	Conservative	5;	Mismatches	23;	Indels	4;
Gaps	1;						
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Db	1	MNKIYRIIWN	SALNAWVASELT	RNHTKRASATVAT	LATLLEFATVQAST	DDDDDLYLE	60
Qy	61	PVQRTAVVL	SPRSDEGEGEGED	SNWVYFDEKRVYL	KAGATILTKAGDNLK	IKONTNE	120
Db	61	PVQRTAVVL	SPRSDEGEGEGE	VEDSNWGYFDEKGLT	AGTITLTKAGDNLK	IKONTNE	120
Qy	121	NTNENTND	SSFTYSLKKDLDTL	TSVETEKLSFGANGK	NVNITSDPTKGLNFAK	ETAGTNGD	180
Db	121	NTNA----	SSFTYSLKKDLDTL	TSVGTREKLSFSAN	KVNITSDTKGLNFAK	KTAEETNGD	176
Qy	181	PTVHLNGIG	STLDTLTLNTGATT	NVTNDNVNDD	DEKKRAASVDVLNAG	WNITKGVKPGTTA	240
Db	177	TTVHLNGIG	STLDTLTLNTGATT	NVTNDNVNDD	DEKKRAASVDVLNAG	WNITKGVKPGTTA	236
Qy	241	SDNVDFVRY	TDTVEFLSADT	TKTTTVNVESKONG	RTEVKIGAKTSVIREK	DGKLVGTGKG	300
Db	237	SDNVDFVRY	TDTVEFLSADT	TKTTTVNVESKONG	RTEVKIGAKTSVIREK	DGKLVGTGKD	296
Qy	301	GENGSSTDE	GGLVTAKEVIDA	VNKACWRMTTANG	OTGQADKEETVTSGT	KVTFASGN	360
Db	297	GENSSSTD	GKGLVTAKEVIDA	VNKACWRMTTANG	OTGQADKEETVTS	GTNTVTFASGK	356
Qy	361	GTTATVSKD	DGNTITVKYDVW	VGDALNVQLONG	WNLDSKAVAGSSCKV	LTSGNVSPSKG	420
Db	357	GTTATVSKD	DGNTITVMYDVW	VGDALNVQLONG	WNLDSKAVAGSSCKV	LTSGNVSPSKG	416
Qy	421	KMDETVIN	INAGNNIEITRNG	NIDATSWTPQFSSV	LSGAGADAPTL	SVDDGALNVGSK	480
Db	417	KMDETVIN	INAGNNIEITRNG	NIDATSWTPQFSSV	LSGAGADAPT	LSVDDGALNVGSK	476
Qy	481	DANKPVRIT	NVAPGVKEGDV	TNVAQLKGVQNL	NNRIDNVDCN	RAGIAQAATAG	LAQA 540

[illegible]

Query Match	92.8%;	Score	2821.5;	DB	4;	Length	599;
Best Local Similarity	92.7%;	Pred. No.	3.8e-221;				
Matches	555;	Conservative	13;	Mismatches	30;	Indels	1;
Qy	1	MNKISRIIWN	SALNAWVVS	ELTNH	TKRASAT	VATATV	ATLLFATVOANATD-DDDL
Db	1	MNKIYRIIWN	SALNAWVVS	ELTNH	TKRASAT	VKTAVT	ATLLFATVOANATDEEBEL
Qy	60	EPVORTAVV	LSFRSDKEGT	EGEKTE	DSNMAVY	FDEKRV	LKAGAITLKAGDNLKIKQNTN
Db	61	EPVVSALV	QLQFMIDK	EGENGES	TGNIGWSI	YIDYNNH	TLHGATVTLKAGDNLKIKQNTN
Qy	120	ENTNENTN	DSFFTYS	LKKDLT	DLTSVETE	KLSPFANG	KNVNITSDTKGLNFAKETAGTNG
Db	121	KNTNENTN	DSFFTYS	LKKDLT	DLTSVETE	KLSPFANG	KNVNITSDTKGLNFAKETAGTNG
Qy	180	DPTVHLNG	IGSTLTD	TLTNTG	ATTVNT	NDNVT	DDKKRAASVKDVLNAGNWKVKPGQTT
Db	181	DTTVHLNG	IGSTLTD	TLTNTG	ATTVNT	NDNVT	DDKKRAASVKDVLNAGNWKVKPGQTT
Qy	240	ASDNVDF	VRTYDTVEF	LSADP	TKTTTVN	VESKDN	GKRTVEKTSVTEKDKGLVTGKG
Db	241	ASDNVDF	VHTYDTVEF	LSADT	KTITTVN	VESKDN	GKRTVEKIGAKTSVTEKDKGLVTGKG
Qy	300	KGENGS	STDEGE	GLVTAKE	VIDA	VNKAGWR	KMTTITANGQOTQADKFETVTSGETVKTFTASG
Db	301	KGENGS	STDEGE	GLVTAKE	VIDA	VNKAGWR	KMTTITANGQOTQADKFETVTSGETVKTFTASG
Qy	360	NGTTATV	YSKDDQ	GNITVKY	DVNVG	DALNV	NQLONSGNWNLDSKAVAGSGKVIYSGNVSPSK
Db	361	KGTTATV	YSKDDQ	GNITVKY	DVNVG	DALNV	NQLONSGNWNLDSKAVAGSGKVIYSGNVSPSK
Qy	420	GKMDETV	NINAGN	NIET	TRNGK	NI	DIATSMTPQFSSVSLGAGADAPTL
Db	421	GKMDETV	NINAGN	NIET	TRNGK	NI	DIATSMTPQFSSVSLGAGADAPTL
Qy	480	KDANKP	VEITNV	APCV	KEGDTN	VAOLK	GVAGNLLNRRIDNV
Db	481	KDANKP	VEITNV	APCV	KEGDTN	VAOLK	GVAGNLLNRRIDNV
Qy	540	AYLP	GKSMMA	ICGGTY	RGEAGYA	IC	YSSISDSTGNWIKGTSAGNSRHHGFTSASVQYOW
Db	540	AYLP	GKSMMA	ICGGTY	RGEAGYA	IC	YSSISDSTGNWIKGTSAGNSRHHGFTSASVQYOW

Db 541 AYLPGKSMMAIGGTYRGEAGYAIYSSISDGGNWIILKTASGNSRGRHFGASASVGQW 599  
|||||

RESULT 10  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 92.8%; Score 2821.5; DB 4; Length 599;  
Best Local Similarity 92.7%; Pred. No. 3.8e-221;  
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;  
Qy 1 MNKISRIIWNALNNAWVVSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLXL 59  
Db 1 MNKIRIWNALNNAWVVSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL 60  
Qy 60 EPVORTAVLSFRSDKEGTGEGTEGSDNNAVYFDEKRVLKAGAITLKAGNLKIKONTN 119  
Db 61 EPVRSALVLQFMIDKEGGENESTGNIWISYDNIINTLHAGTVTLKAGNLKIKONTN 120  
Qy 120 ENTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 179  
Db 121 KNTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180  
Qy 180 DPTVHLNGIGSTLTDLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNKGVKPGTT 239  
Db 181 DTTVHLNGIGSTLTDLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNKGVKPGTT 240  
Qy 240 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDNKRTVEVKIGAKTSVKEKDGKLVTKG 299  
Db 241 ASDNVDFVRTYDVEFLSADTKTTTVNVESKDNKRTVEVKIGAKTSVKEKDGKLVTKG 300  
Qy 300 KGEGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFVTSIGTNTVTFASG 359  
Db 301 KGEGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFVTSIGTNTVTFASG 360  
Qy 360 NGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 419  
Db 361 KGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420  
Qy 420 GKMDETVINAGNNEITRNGKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALNVS 479  
Db 421 GKMDETVINAGNNEITRNGKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALNVS 480  
Qy 480 KDANKPVRITNVAPGVKEGDTVNAQLKGAQNLLNNDVNDGNARAGIAQAATAGLAQ 539  
Db 481 KDANKPVRITNVAPGVKEGDTVNAQLKGAQNLLNNDVNDGNARAGIAQAATAGLVQ 540  
Qy 540 AYLPGKSMMAIGGTYRGEAGYAIYSSISDGGNWIILKTASGNSRGRHFGASASVGQW 598  
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Db 541 AYLPGKSMMAIGGTYRGEAGYAIYSSISDGGNWIILKTASGNSRGRHFGASASVGQW 599  
RESULT 11  
US-09-377-155-21  
; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 89.3%; Score 2716.5; DB 4; Length 591;  
Best Local Similarity 90.7%; Pred. No. 1.3e-212;  
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;  
Qy 1 MNKISRIIWNALNNAWVVSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
Db 1 MNKIRIWNALNNAWVVSELTRNHTKRASATVATVATLTLFATVQASANNQEEDL 60  
Qy 58 YLEPVQRTAVVLFSRSDKEGTGEGTEGSDNNAVYFDEKRVLKAGAITLKAGNLKIKQ 116  
Db 61 YLDPVQRTAVVLVNSDKGTGEGTEGSDNNAVYFDEKRVLKAGNLKIKQ 120  
Qy 117 NTNENTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 176  
Db 121 -----NGTNFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAG 170  
Qy 177 TNGDPTVHLNGIGSTLTDLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNKGVK 236  
Db 171 TNGDPTVHLNGIGSTLTDLLNTGATTNVNDVTDDEKKRAASVKDVLNAGWNKGVK 230  
Qy 237 GTTASDNVDFVRTYDVEFLSADTKTTTVNVESKDNKRTVEVKIGAKTSVKEKDGKLV 296  
Db 231 GTTASDNVDFVRTYDVEFLSADTKTTTVNVESKDNKRTVEVKIGAKTSVKEKDGKLV 290  
Qy 297 GKKGEGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFVTSIGTNTV 356  
Db 291 GKKGEGSSTDEGGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFVTSIGTNTV 350  
Qy 357 ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 416  
Db 351 ASGNGTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410  
Qy 417 PSKGKMDETVINAGNNEITRNGKNIDATSMTPQSSVSLGAGADAPTLSDVDEGALN 476  
Db 411 PSKGKMDETVINAGNNEITRNGKNIDATSMTPQSSVSLGAGADAPTLSDVDEG-ALN 469  
Qy 477 VGSKDANKPVRITNVAPGVKEGDTVNAQLKGAQNLLNNDVNDGNARAGIAQAATAG 536  
Db 470 VGSKDANKPVRITNVAPGVKEGDTVNAQLKGAQNLLNNDVNDGNARAGIAQAATAG 529  
Qy 537 LAQAYLPCKSMMAIGGTYRGEAGYAIYSSISDGGNWIILKTASGNSRGRHFGASASVG 596  
Db 530 LVQAYLPCKSMMAIGGTYRGEAGYAIYSSISDGGNWIILKTASGNSRGRHFGASASVG 589  
Qy 597 QW 598

Qy	1	MNKLSRIIWSALN	AVVVVSELTRN	NHTRKASATV	ATVATL	LLFATV	QANATDD	----	DD	56										
Db	1	MNKLYRIIWSALN	AVVVVSELTRN	NHTRKASATV	KVAVL	TATL	LLFATV	QASANNERPKKD	60											
Qy	57	LYLEPVORTAV	LSFRSDKEGT	GEKTEGD	-SNWAVY	VFDEKRV	LKAGATT	LKAGDN	LKTK	115										
Db	61	LYLEPVORTAV	LLVNSDKEGT	GEKEKVBES	OWAVYFN	EKGVLTR	AREITL	LKAGDN	LKTK	120										
Qy	116	QNTNENTNENT	NDSSFTYSL	KKDLTDLTSV	ETEKLSPF	GANGKNV	NTSDTK	GLNF	AKETA	175										
Db	121	Q-----	NGTNFTYSL	KKDLTDLTSV	TEKLSPF	SANGKNV	NTSDTK	GLNF	AKETA	170										
Qy	176	GTNGDPVHL	NGIGSTLTD	FLNTGATT	NVTNDV	DEKKRA	ASVKDVL	NAGWNT	KGKV	235										
Db	171	GTNGDTHVHL	NGIGSTLTD	LLNTGATT	NVTNDV	DEKKRA	ASVKDVL	NAGWNT	KGKV	230										
Qy	236	PGTTASNDV	PRYDVEFL	SADTKTTT	VNVE	SKDNGK	RTEVK	ICAKT	SVIKE	DGKLV	295									
Db	231	PGTTASNDV	PRYDVEFL	SADTKTTT	VNVE	SKDNGK	KTEVK	IGVKT	SVIKE	DGKLV	290									
Qy	296	TGKGKGEN	SSTDEGE	GLVTAKE	VIDAVN	KAGWRM	TKTTTANG	QTGQAD	KFEV	TSTGTVT	355									
Db	291	TGKDKGEN	SSTDEGE	GLVTAKE	VIDAVN	KAGWRM	TKTTTANG	QTGQAD	KFEV	TSTGTVT	350									
Qy	356	FASNGT	TATVSK	DDQGNIT	VKYDV	VNVGD	ALNVQ	LQNS	GNWLN	DSKAVAG	SSGKV	415								
Db	351	FASGKGT	TATVSK	DDQGNIT	VMYDV	VNVGD	ALNVQ	LQNS	GNWLN	DSKAVAG	SSGKV	410								
Qy	416	SPSKGK	WDET	VNINAG	NNIEITR	NGKNID	IATSWT	POFSSV	SLGACAD	APT	LSVDD	EGAL	475							
Db	411	SPSKGK	WDET	VNINAG	NNIEITR	NGKNID	IATSWT	POFSSV	SLGACAD	APT	LSVDD	-AL	469							
Qy	476	NVGSKD	ANKP	VRITN	VP	APVY	KGVD	VTNVA	Q	LKV	GAO	NLNNR	IND	VGN	RAG	TAQ	AIATA	535		
Db	470	NVGSK	KNK	PRITN	VP	APVY	KGVD	VTNVA	Q	LKV	GAO	NLNNR	IND	VGN	RAG	TAQ	AIATA	529		
Qy	536	GLAQAY	LPGK	SMMA	I	GCGT	YVR	GEAGYA	I	GY	SSIS	SDT	CN	WYIK	GTAS	GN	RG	HFGT	SASV	595

Db 530 GLVQAVLPGRSMNAIGGTYRGEAGYAIGYSSISDGGNMIIKGTASGNSRGRHFGASAYG 589  
QY 596 YQW 598  
Db 590 YQW 592

Query Match	89.1%	Score	2709;	DB	4;	Length	592;
Best Local Similarity	90.4%;	Pred.	No. 5.le-212;				
Matches	545;	Conservative	12;	Mismatches	30;	Indels	16;
Gaps							
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Db	1	MNKIYRIIWSALNAWVVVSELTRNHTKRASATVKVATATLALLPATVQASANNERPRKKD	60				
Qy	57	LYLEPVORTAVVLFSRDSKEGTGSKEGTED--SNWAVFDERRVLKAGAITLUKAGDNLKIK	115				
Db	61	LYLDPVORTAVVLVNSDKBGTGKEKEVENSNDWAVFNEKGVLTARTITLUKAGDNLKIK	120				
Qy	116	QNTNENTNENTNDSSFYSLKKDLDTLTSVTEKLSFGANGKNYNITSDTKGLNFAKETA	175				
Db	121	Q-----NGTNFYSLKKDLDTLSVTEKLSFGANGKNYNITSDTKGLNFAKETA	170				
Qy	176	GTNGDPTVHLNGIGSTLDTLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGWNKGVK	235				
Db	171	GTNGDPTVHLNGIGSTLDTLLNTGATTNTVNDNVTDDEKKRAASVKDVLNAGWNKGVK	230				
Qy	236	PGTTASDNVDFVRYDYVEFLSADTKTTTVNVESKDNGKRTVEVIGAKTSVYIKEKDGLV	295				
Db	231	PGTTASDNVDFVRYDYVEFLSADTKTTTVNVESKDNGKRTVEVIGAKTSVYIKEKDGLV	290				
Qy	296	TGKGKGNGSGSTDEBEGGLVTAKEVIDAVNKGWRMKTITANGQTQOADKFEVTVSGTKVT	355				
Db	291	TGRDKGNGSGSTDEBEGGLVTAKEVIDAVNKGWRMKTITANGQTQOADKFEVTVSGTNVT	350				
Qy	356	FASNGGTATTAVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNV	415				
Db	351	FASGKGTTATTAVSKDDQGNITVYDVNVGDALNVNQLNSGWNLDKSAVAGSSGKVISGNV	410				
Qy	416	SPSKGKDETVNINAGNNIETRNKNIDTATSMTPOPSSVSLGAGADAPTLSDVDEGAL	475				
Db	411	SPSKGKDETVNINAGNNIETRNKNIDTATSMTPOPSSVSLGAGADAPTLSDVGDG-AL	469				
Qy	476	NVGSKDANKPVRIITNVPFVGEGDVTNVAQLKGVAQNLNNRIDNVGNARAGIAQAIATA	535				

Db	470	NVCSKKDKPVRITNVAPGVKGDVTVNVAQLKCGVAQNLRINDVQGNARAGTAQAIAATA	523
Qy	536	GLAQAYLPKSMMAIGGGTYRGGAYGAIGYSSISDTCGNVVIKCTASGNSRGHFGTASVGC	595
Db	530	GLQVAYLPKSMMAIGGGTYRGGAYGAIGYSSISDTCGNVVIKCTASGNSRGHFGASVGC	589
Qy	596	YOW 598	
Db	590	YOW 592	

Query Match	88.9%	Score	2705.5	DB	4	Length	591
Best Local Similarity	90.4%	Pred. No.	9.9e-212				
Matches	544	Conservative	14	Mismatches	29	Indels	15
Gaps	4						
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DB	1	MNEILRIIWN	SNALNAWVVVSEL	TNRH	TKRASATVKTAV	LATLL	FATVOASANNEQEEDL 60
QY	58	YLPBPQV	TAVVLSPR	DKETG	EGKEGTED-SN	WAVYDF	DEKRVLRKAGAITLKAGDNLKIKQ 116
DB	61	YLPVLT	AVLIVNS	DKETG	EGKEKYEENS	DWAVYFNEK	GVLTAREITLKAGDNLKIKQ 120
QY	117	NTNENT	NTNDS	SFTYSL	KKDLTDL	TSVET	EKLSFGANGKNVITSDTKGLNFAKETAG 176
DB	121	-----	NGTNFTY	SLKKDLTDL	TSVGT	EKLSFGANGKNVITSDTKGLNFAKETAG 170	
QY	177	TNGDP	PTVHL	NGICST	LTD	TLT	GATTNTVNTNDNTVTDDEKKRAASVKDVLNAGWNIKGVPK 236
DB	171	TNGD	TTVHL	NGICST	LTD	TLT	GATTNTVNTNDNTVTDDEKKRAASVKDVLNAGWNIKGVPK 230
QY	237	GTTASD	NVDFRV	YDVTVE	FLSADPTK	TTVNV	YESKDNCGRTEVKIGAKTSVKEKDGKLVTT 296
DB	231	GTTASD	NVDFRV	YDVTVE	FLSADPTK	TTVNV	YESKDNCGRTEVKIGAKTSVKEKDGKLVTT 290
QY	297	GKKG	GENG	SS	TDEG	GLVTAKE	VIDAVNKAGWRMKTITTTANGQTQADKFETVTSCTKVT 356
DB	291	GKDG	GENG	SS	TDEG	GLVTAKE	VIDAVNKAGWRMKTITTTANGQTQADKFETVTSCTNVT 350
QY	357	ASNG	GT	TATV	VSKDQ	GNITV	KYVDVNVGDALNVNQLQNSGWNLDKAVAGSGKVIISGNVS 416
DB	351	ASGK	GT	TATV	VSKDQ	GNITV	KYVDVNVGDALNVNQLQNSGWNLDKAVAGSGKVIISGNVS 410
QY	417	PSGK	KMD	ETV	NI	NAGN	NIETIRNCKNIDTATSMTPQFSSVSLGAGADAPTLVSVDDEGALN 476
DB	411	PSGK	KMD	ETV	NI	NAGN	NIETIRNCKNIDTATSMTPQFSSVSLGAGADAPTLVSVDGD- ALN 469
QY	477	VGSK	DANK	PV	RI	NTV	APGVKEGDVTNTVAQLKGVAQNLLNRRIDNVDGNARAGTAAQAIATAG 536

Db 470 VGSKKDNKPVRTTNVAPGVKEGDTNVAQLKGAQNLRIDNVDGNARAGIAQAIATAG 529  
QY 537 LAQAYLPKSMMAIGGGTYRGEAGYAIGYSSISDTGNWVIKGTASGNSRGHFGTSASVGY 596  
Db 530 LVOAYLPKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIIRKGTASGNSRGHFGASVGY 589  
QY 597 QW 598  
Db 590 QW 591

Search completed: July 3, 2002, 08:37:10  
Job time: 336 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:38:17 ; Search time 58.79 seconds  
(without alignments)  
977.401 Million cell updates/sec

Title: US-09-771-382-8  
Perfect score: 3042  
Sequence: 1 MNKISRIIWNLSALNAWVVS.....TASGSRGHFGTSASVGYQW 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71.\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	2716.5	89.3	591	2	G81133	adhesin NMB0992 [i
2	2521	82.9	592	2	A81888	probable surface f
3	622	20.4	298	2	I64138	adhesin homolog HI
4	403	13.2	2059	2	D82671	surface protein XF
5	390	12.8	1107	2	AC0976	probable autotrans
6	383.5	12.6	1190	2	A82615	surface protein XF
7	365	12.0	1588	2	A86036	probable adhesin Z
8	365	12.0	1588	2	H31188	probable adhesin E
9	342	11.2	658	2	AH0110	probable surface p
10	241	7.9	1004	2	C82672	surface-exposed ou
11	223	7.3	1091	2	G4964	hypothetical prote
12	220	7.2	1910	2	AF0394	probable adhesin h
13	217	7.1	1536	2	A43855	high-molecular-wei
14	216	7.1	3705	2	AB0123	probable autotrans
15	214	7.0	4919	2	T31105	hypothetical prote
16	213	7.0	949	2	D98083	Aida-I adhesin-lik
17	213	7.0	1005	2	H85611	probable adhesin z
18	213	7.0	1018	2	H83135	probable adhesin p
19	211	6.9	1608	2	A28182	hemolysin A - Serr
20	210	6.9	1361	2	T03415	S-layer protein -
21	209	6.9	1286	2	S28634	adhesin AIDA-I pre
22	208.5	6.9	1109	2	A56143	surface-array prot
23	206.5	6.8	961	2	A05048	putative autotransp
24	203.5	6.7	1325	2	A64905	ydek protein - Esc
25	203	6.7	2551	2	B98047	hypothetical prote
26	202	6.6	5188	2	B85547	probable RTX famil
27	202	6.6	5291	2	F90696	hypothetical prote
28	201	6.6	585	2	F85809	hypothetical prote
29	200	6.6	1635	2	A10452	hemolysin [importe

30 199 6.5 585 2 F90961 flagellin [importe  
31 199 6.5 2249 2 A41477 190K surface anti  
32 199 6.5 4936 2 AH2515 hypothetical prote  
33 198.5 6.5 1417 2 A83080 hypothetical prote  
34 198 6.5 3013 2 AB0480 probable invasin Y  
35 197 6.5 1275 2 T33369 hypothetical prote  
36 195 6.4 1577 2 A35140 hemolysin A precu  
37 195 6.4 3029 2 S76109 hypothetical prote  
38 192.5 6.3 1430 2 AF0351 probable autotrans  
39 192.5 6.3 1487 2 AG2560 hypothetical prote  
40 192 6.3 2468 2 A83412 hypothetical prote  
41 191.5 6.3 936 2 I40711 sapB protein - Cam  
42 191.5 6.3 1651 2 JC1340 outer membrane pro  
43 191 6.3 1477 2 B43855 high-molecular-wei  
44 190.5 6.3 1327 2 B90674 Aida-I adhesin-lik  
45 190.5 6.3 1349 2 E85524 probable beta-barr

RESULT 1  
G81133  
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)  
C:Species: Neisseria meningitidis  
C:Date: 31-Mar-2000.#sequence\_revision 31-Mar-2000 #text\_change 19-Jan-2001  
C:Accession: G81133  
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B. ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Pizza, M. Science 287, 1809-1815, 2000  
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A:Reference number: A81000; MUID:20175755  
A:Accession: G81133  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-591 <TE>  
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g722 A:Experimental source: serogroup B, strain MC58  
C:Genetics:  
A:Gene: NMB0992

Query Match 89.3%; Score 2716.5; DB 2; Length 591;  
Best Local Similarity 90.7%; Pred. No. 3.8e-131;  
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

QY 1 MNKISRIIWNLSALNAWVVSSELTRNHTKRASATVATAVLATLILFATVQANATD---DDDL 57  
DB 1 MNKIYRIIWNLSALNAWVVSSELTRNHTKRASATVATAVLATLILFATVQASANNEEQEEDL 60  
QY 58 YLEPQVQRTAVVLVSFRSDKEGTEKEGED- SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116  
DB 61 YLDPQVQRTAVVLIVANSKDEGTEKEKEKEVEENSDWAVYFNEKGVLTAREITLKAGDNLKIKQ 120  
QY 117 NTNENTNTNDSSSTYSLLKDLTLDTLSVETEKLSFGANGKNVNITSDTKGLNFAKETAG 176  
DB 121 -----NGTNFTYSLUKDLTLDTLSVETEKLSFGANGKNVNITSDTKGLNFAKETAG 170  
QY 177 TNGDPTVHLNGISLTDLTFLNTGATTNTVNDVTDDEKKRAASVKVDVNLNAGWNKGVKP 236  
DB 171 TNGDPTVHLNGISLTDLTFLNTGATTNTVNDVTDDEKKRAASVKVDVNLNAGWNKGVKP 230  
QY 237 GTTASDNVDVFRYTDVTEFLSADTKTTTNNVESKONGKRTVEKIGAKTSVIREKDGKLVTF 296  
DB 231 GTTASDNVDVFRYTDVTEFLSADTKTTTNNVESKONGKRTVEKIGAKTSVIREKDGKLVTF 290  
QY 297 GKGKGENSGSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGQTGQADKFETVTSGTKVTF 356  
DB 291 GKGKGENSGSTDEGEGLVTAKEVIDAVNKGWRMKTITTTANGQTGQADKFETVTSGTKVTF 350  
QY 357 ASNGTGTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGNLDSKAVAGSSGKVISGNYS 416

ALIGNMENTS

Db 351 ASKGGTATVSKDDQGNITVYDVNVGDALNVQLNSGNLDSKAVAGSGKVISGNVS 410  
QY 417 PSKGMDETNIINAGNIEITRNKKNIDDIATSMTPQFSSVSLGAGADAPTLSDVDEGALN 476  
Db 411 PSKGMDETNIINAGNIEITRNKKNIDDIATSMTPQFSSVSLGAGADAPTLSDVGD-ALN 469  
QY 477 VSGDKANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLRNIDNDVGNARAGIAQAATAG 536  
Db 470 VSGDKANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLRNIDNDVGNARAGIAQAATAG 529  
QY 537 LAQAYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRHHGFTSASVGY 596  
Db 530 LVQAYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRHHGFTSASVGY 589  
QY 597 QW 598  
Db 590 QW 591

RESULT 2  
A:1888  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.  
A:Reference number: A81775; MUID:2022556  
A:Accession: A81888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1200

Query Match 82.9%; Score 2521; DB 2; Length 592;  
Best Local Similarity 85.5%; Pred. No. 3.4e-121;  
Matches 520; Conservative 16; Mismatches 46; Indels 26; Gaps 8;  
QY 1 MNKISRIIWNALNNAVWVSELTRNHTKRASATVATAVLATLLFATVQANATD-DDDLYL 59  
Db 1 MNKISRIIWNALNNAVWVSELTRNHTKRASATVATAVLATLLFATVQANATDEDEEEL 60  
QY 60 EPVORTAVLSFRSDKECTGKEG-----TEDSNWAV--YFDEKRVLKAGAITLKAGDNL 112  
Db 61 ESQVR-SVSGIOASMEGSELETISLWNTDSKEFVDPYI-----VVLKAGDNL 110  
QY 113 KIKONTNENTNDSFTYSLKLDLTLSVETEKLSFGANGKNVITSDTKGLNFAK 172  
Db 111 KIKONTNENTNA-----SSFTYSLKLDLTGLINVETEKLSFGANGKNVITSDTKGLNFAK 166  
QY 173 ETAGTNGDPTVHLNGIGSTLTDLTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNNIK 232  
Db 167 ETAGTNGDPTVHLNGIGSTLTDLTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNNIK 224  
QY 233 GVKPGTTA--SDNVDFVRYTDFEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEK 290  
Db 225 GVKPGTGGSENVDFRYTDFEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEK 284  
QY 291 DGKLVTKGKGGSSDDEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEVTS 350  
Db 285 DGKLVTKGKGGSSDDEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEVTS 344  
QY 351 GTRKTVFASGNGTTATVSKDDQGNITVYDVNVGDALNVQLNSGNLDSKAVAGSGKV 410  
Db 345 GTNVTFASGKGTATVSKDDQGNITVYDVNVGDALNVQLNSGNLDSKAVAGSGKV 404

QY 411 ISGNVSPSKGMDETNIINAGNIEITRNKKNIDDIATSMTPQFSSVSLGAGADAPTLSDV 470  
Db 405 ISGNVSPSKGMDETNIINAGNIEITRNKKNIDDIATSMAPQFSSVSLGAGADAPTLSDV 464  
QY 471 DEGALNVGSKDANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLRNIDNDVGNARAGIAQ 530  
Db 465 DEGALNVGSKDANKPVRITNVAPGVKEGDTNVVAQLKGVAQNLRNIDNDVGNARAGIAQ 524  
QY 531 AIATAGLAQAYLPKSMMAIGGTYRGEAGYAGYSSISDGTGNWVTKGTASGNSRHHGFT 590  
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Db 585 SASVGYQW 592

RESULT 3  
I64138  
adhesin homolog H11732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: I64138  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Vente  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: I64138  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:H11732

Query Match 20.4%; Score 622; DB 2; Length 298;  
Best Local Similarity 46.2%; Pred. No. 6.6e-25;  
Matches 150; Conservative 39; Mismatches 90; Indels 46; Gaps 9;  
QY 1 MNKISRIIWNALNNAVWVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
Db 1 MNKIFKIVNVTQTVWVSELTRAHTKRTSATVATAVLATVLSATVQA----- 49  
QY 61 PVORTAVLSFRSDKECTGKEGCTEDSNWAVYFDEKRVLKAG-AITLKAGDNLKIKONTN 119  
Db 50 -INDAGTFVKVQSTEDDIEDSAATKDDN-----KNOALKAGDTLLTKAGNKLAKL--- 99  
QY 120 ENTNENTNDSFTYSLKLDLTLSVETEKLSFGAN-----GNKVNITSDTKGLNFAK 172  
Db 100 -----DOGGKSVTFALAKDLVKAKVSDTLTGGTTPAAGGATPKVSIITSDGLKAK 154  
QY 173 ETAGTNGDPTVHLNGIGSTLTDLTLLNTGATNTVNDVTDDEKRAASVKDVLNAGNNIK 232  
Db 155 ---GTNGDTAVHLNGLASTLPDVTNTGASTSVT-FSPSDIEKTRAATIKDVLNAGNNIK 210  
QY 233 GVKPGTTASDNVDFRYTDFEFLSADTKTTTVNVEKDNCKRTEVKIGAKTSVKEKDG 292  
Db 211 GAKVAGGNTENVLDVAGYDNVEFTIGDKNTLDVVLTAKEGKTEVKTPTKTSVKNNG 270  
QY 293 KLVTKG-----GKGNGS-STDE 309  
Db 271 KLVTKGKDKDANTGATNATEDTDE 295

RESULT 4  
D82671  
surface protein xF1529 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq





Db 814 NVAAGSADTDAVNAGVQLKVTDAQVSRNTQSIITNLNTQVSNLDRVTNIENIGDIIVTGS 873  
QY 451 PQF-----SSVSLGAGADAP-----TSLVDDE-GALNVGSKDANKPV 486  
Db 874 TKYFKNTDGCADANAQADSVAGSGSIAAENSVALGNTNSVADEANTVSGSSTQOR-- 931  
QY 487 RITNVPKVGKGVDTNVAQLK----- 507  
Db 932 RITNVAAGVNTDAVNVAQLKASEAGSVRYETNADGSVNYSVNLNLDGSGGTTTIGNVSA 991  
QY 508 -----GVAQ-----NLNRRIDNVGNARAGTAAQTATAGLAQAYL 542  
Db 992 AVNDTDAVNTAQLKRSVEEANTYTDQKMGEMNSKIKIENKSGGTSASAMAGLPOAYA 1051  
QY 543 PGKSMIAIGGTVRGEAGYAGYSSISDTGNWVTKGTASNSRGHFTCSASVGYOW 598  
Db 1052 PGANMTSIAGGTNGESAIVAIGSVMSSESGWYKLGQTSQGDYSAATGAGFOW 1107  
RESULT 6  
A82615  
surface protein XF1981 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C>Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequencing  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: A82615  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1190 <SIM>  
A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF8783.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A  
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Canaro, L.E.A.; Carraro, D.M.; Carreir, H  
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krueger, J.E.; Kuramae, E.B.; Laig  
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, H  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
M.; Tshuhako, M.H.; Vallada, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
A:Reference number: A59328  
A:Reference: annotation  
C:Genetics:  
A:Gene: XF1981

Query Match 12.6%; Score 383.5; DB 2; Length 1190;  
Best Local Similarity 24.6%; Pred. No. 5.5e-12;  
Matches 169; Conservative 89; Mismatches 226; Indels 203; Gaps 30;  
QY 47 VOANATDDLLYLPVORTAVVLSFRSDKKGTEGKETEDSNNAVYPDEKRVLKAGAITL 106  
Db 572 VAAGTADTDAVNFSQLQ-----AVSSTASKGNWLLASGANSN-----VVPGESVDL 618  
QY 107 KAGD-NLKIKONTNENTNENTNDSSFTY--SLKKD--LTDLTSVETEKLSFGAN----- 155  
Db 619 KNSDGNLLTKTT-----DSNOVTFMLATALKVDSLTGNTAMTDDGVTGVSNTLGST 672  
QY 156 -----GNK--VNI-----TSDTKGLNFA----- 171  
Db 673 GLVITDGPSTSSGISAGNQKIITNVAAGTADTDAVNFSQLQAVSSSTASKGNWLLASGANS 732  
QY 172 -----KETAGT-----NGDPTVHLNGIGS-----TLTDLPLNLTGAT--NV 205  
Db 733 SNVAPGESVDLKNTDGNIVISKESSGNDVLFNLSLSLKLDKLTGDTVMTNGVTGSGV 792

QY 206 TNDN-----VTDEKKRAASVKDVLNAG--WNKIGVKPQTTASD-----N 243  
Db 793 TLGSMGLVITDGPVSISGGI-----NAGSQKITNVAAGTADTDAVNLSQLNTAMAGS GAKS 848  
QY 244 VDVRYDYVFEVLSADTKTTTNNVESKDNKRTKTEVIGAKTSVIKEKDKLVTKGKGEN 303  
Db 849 VHYSTYD-----GGTGGNYNGDGTGTRSTIAGVGTGLASA-----EGATAVSGSAAAS 898  
QY 304 G-SSTDEGEGLVTAKEVIDAVNKAGRPMKTTTANGQTQADKPEETVTSCTKVTFASNGT 362  
Db 899 GKGSTAIGRNVASADGSVALGD--GAKDARGAESEYTGKYGQNNNTVGTGVSVDASKGE 957  
QY 363 TATVSKDDQGNITVKVDVNVGDALNVNQL-----QNSGNWLDKSAVAGSSGKIVSGNVSPS 418  
Db 958 TRVVS-----NVADAKEAT--DAVNLQDLRVAODANRYVDNKIESLSESGTF----- 1003  
QY 419 GKMDETVINAGNNTIEITRNGKNIDIATISMTPOFSSVSLGAGADA-----PTL 467  
Db 1004 -----VKVNSLNN-----SATPIAAGVDATAIGVGTASGADSIAMGNKASA 1045  
QY 468 SVDEGAL-----NVGSKDANKPVRTITNVAPGVKEGDTVNTVAQLKGAQNLLNN 515  
Db 1046 SADNVAIGNHVSADRVANTVSVGSAGSER--QVTNVAAGTADTDAVNVSQLNOGLITAKQ 1103  
QY 516 RIDNVDCNAR-----AGTAAQAIATAGLAQAYLPGKSMMAIGGGTYRGEAGYAGYSSISDT 571  
Db 1104 YTCGVVGSRLRDTDGGVAAAIATANLPQAVIPGRGTSVGVSSYRGOSATAVGVSSVSES 1163  
QY 572 GNVVIKGTASGNSRGHFTGSASVGYOW 598  
Db 1164 GRWVFKSGSANRSQVIGAGVGYOW 1190  
RESULT 7  
A86036  
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C:Species: Escherichia coli  
C>Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: A86036  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
iller, L.; Grothbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A86036  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1598 <STO>  
A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5029  
Query Match 12.0%; Score 365; DB 2; Length 1588;  
Best Local Similarity 25.0%; Pred. No. 6.9e-11;  
Matches 144; Conservative 81; Mismatches 252; Indels 98; Gaps 19;  
QY 111 NLKIKONTNENTNENTNDSSFTYSLKKDLTDLTSVET--EKLSE-----GANGNKVNIT 162  
Db 1025 NMIEQNT-QIINQAGNTDATY-IQENGAGINVYRTNDDGLAFNDASAQGVGATAIGN 1082  
QY 163 SDTKGLNFAKETAGTCDPTVHLNGIGSTLTDLLNTGA--TTNVTNDNV-----TDEK 215  
Db 1083 SVARGDSVAIGOGSDVDVTGIALGSSVSSRVIAKGRDTSITENGVIQVDTTDEL 1142  
QY 216 KRAASVKD-----VLNAGWNKIGVKPQTTASQNVNDVRYTDTVEFLSADTKTTTVNVES 269  
Db 1143 LGALSIGDDCKYRQIIN-----VADGSEAHDAVT--VRLONAIGAVATPTTKYFHANS 1194  
QY 270 KDNK-----RTEVKIGAKTSVIKEK-----DGKLVTKGKGE----- 302

Db 1195 TEEDSLAVGDTSLAMGAKTIVNGDKIGIGYAYVDANALNGIAIGSAQVHVNSIAIG 1254  
QY 303 NGSSDTDEGELVTAKEVIDAVNKAHRMKTITTTANGO- -----TGQADKEFTVTSCKT 355  
Db 1255 NGSTTRGAQNTAYNMADPQNSVGEFSVGSADGQRQITNVAAGSADTDVNVGOLKVT 1314  
QY 356 FASGNGTTATVSKDDQ- ----GNITVKYDVNVGDAL- -----NVNQLQNSGWNLDS 400  
Db 1315 DAQVQSQNTSITNLDNRVTNLDNRVTNIENGIGDIVTTGTSKYFKTNTDGVDAQAQKDS 1374  
QY 401 KAVAGSSGKVISGNVSPSKGM---DETNNINAGNIEITRN---GKNIDIATSWTPQPS 454  
Db 1375 VAIGSGSIAAANDNSVALGTSGVATEENTISVGSSTNORRITNVAAGKNATDAYNVVAQLKS 1434  
QY 455 SVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEDVTNVAOLKGVQV--- 511  
Db 1435 SEAGGVRYDTKADGSDIDYDNITLGGNGG--TTRISNVSAVNNNDVVNVAQLKQSVQETK 1493  
QY 512 -----NLNNRIDNVGDNARAGIAQAIATAGLAQAYLPKGSMAIIGGTTYRGEAGYAI 563  
Db 1494 QYTDQRMVEMDNKLSKTESKLSGSIASAMAMTGLPOAYTPGASMASIGGTYNGESAVAL 1553  
QY 564 GYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQW 598  
Db 1554 GVSMSVANGRWYKLOGSTNSQGEYSAAALGAGIQW 1588

RESULT 8  
H91188 probable adhesin Ecs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD)  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.-G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: H91188  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA037903.1; PID:g13363955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: Ecs4480

Query Match 12.0%; Score 365; DB 2; Length 1588;  
Best Local Similarity 25.0%; Pred. No. 6.9e-11;  
Matches 144; Conservative .81; Mismatches 252; Indels 98; Gaps 19;  
QY 111 NLKIKONTNENTNDSFTYSLKOLTDLTSVET--EKLSE-----GANGNKVNIT 162  
Db 1025 NMIEQNT-QIINQLAGNTDATY-IGENGAGINVRVTDNDGLAFNDASAGVGATAGYN 1082  
QY 163 SDTKGLNFAKETAGTNGDPTVHLNGISLTDLTLNAGA-TTNTVNDV-----TDDEK 215  
Db 1083 SVAKGSSVAIGOGYSVDVDTGTALGSSSVSRVIAKGRSDTSITGVVIGYDITDDEL 1142  
QY 216 KRAASVKD-----VLNAGNKGKVPKGTASDNVDFVRYDTVEFLSADTKTTNVNES 269  
Db 1143 LGALSTGDDGKYQIIN-----VADGSEAHDAVT-VRLQNAIGAVATTPKYFHANS 1194  
QY 270 KNGK-----RTEVKIGAKTSVIEK-----DGKLVTKGKGE----- 302  
Db 1195 TEEDSLAVGDTSLAMGAKTIVNGDKIGIGYAYVDANALNGIAIGSAQVHVNSIAIG 1254  
QY 303 NGSSDTDEGELVTAKEVIDAVNKAHRMKTITTTANGO- -----TGQADKEFTVTSCKT 355  
Db 1255 NGSTTRGAQNTAYNMADPQNSVGEFSVGSADGQRQITNVAAGSADTDVNVGOLKVT 1314  
QY 356 FASGNGTTATVSKDDQ- ----GNITVKYDVNVGDAL- -----NVNQLQNSGWNLDS 400

Db 1315 DAQVQSQNTSITNLDNRVTNLDNRVTNIENGIGDIVTTGTSKYFKTNTDGVDAQAQKDS 1374  
QY 401 KAVAGSSGKVISGNVSPSKGM---DETNNINAGNIEITRN---GKNIDIATSWTPQPS 454  
Db 1375 VAIGSGSIAAANDNSVALGTSGVATEENTISVGSSTNORRITNVAAGKNATDAYNVVAQLKS 1434  
QY 455 SVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEDVTNVAOLKGVQV--- 511  
Db 1435 SEAGGVRYDTKADGSDIDYDNITLGGNGG--TTRISNVSAVNNNDVVNVAQLKQSVQETK 1493  
QY 512 -----NLNNRIDNVGDNARAGIAQAIATAGLAQAYLPKGSMAIIGGTTYRGEAGYAI 563  
Db 1494 QYTDQRMVEMDNKLSKTESKLSGSIASAMAMTGLPOAYTPGASMASIGGTYNGESAVAL 1553  
QY 564 GYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQW 598  
Db 1554 GVSMSVANGRWYKLOGSTNSQGEYSAAALGAGIQW 1588

RESULT 9  
AH0110 probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain C092)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0110  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0902

Query Match 11.2%; Score 342; DB 2; Length 658;  
Best Local Similarity 22.5%; Pred. No. 3.3e-10;  
Matches 144; Conservative 87; Mismatches 254; Indels 156; Gaps 19;  
QY 27 TKRASATVAT-----AVLATLLFPATVQ-----ANATDDDDLLPEVQRTAVVLSFRSDK 75  
Db 105 TNLAPATISTSTDAVVGSQLYNLVQDGTTRYFHANSVNPPTDSLASGLETIAV----- 156  
QY 76 EGTGEKEGTSDSNWAVYFDEKRVLKAGAITLKAGDNLKIKONTNENTNDSFTYSL 135  
Db 157 -----GPATVVSQDNGVIGINTALVGAATGGIAIGFGT 190  
QY 136 KDLTDLTSVET-----EKLSEFGANGKNVITSDTKGLNFAKETAGTNG----- 179  
Db 191 QVTAAGATAIGSAQAQAQAGSALGAGA-----VTSQANSIALGAASINTVGAOSSYSAYA 246  
QY 180 -----DPTVHLNGISLTDLTLNAGTATVNTDNVT-----DDEKRAASVKDVNLA 227  
Db 247 LTAPOASVGBELGCTALGNRKITGVAAGSASSDAVNVAQLTAVGDQVQQTANTITSLGGR 306  
QY 228 GWNKGVKPCCTTASDNVDFVRYDT-VEFLSADTKTTTNNVESKDNCKRT-----EVKI 280  
Db 307 VTTIEGSMASIANGGVKYFHANSQPDPSVASGTSNVSAIGPASLASGASNAALASAGAVAI 366  
QY 281 GAKTSVIEKDKGLVTKGKGENGSSTDEGEGLVTAKEVIDAVNKAHRMKTITTTANGOTG 340  
Db 367 G--DGAASADGSAIGQSGSDNGRGE-----NYIG 396  
QY 341 QADKFEFTVTSCKTIVTASGNGTATVTSKDDQGNITVKYDVNVGDALNVNQLQNSGWNLDS 400  
Db 397 KYSNASNTSSGTVSVGNTATGETRTVSNVADG-----LQATDAVNLRQLDQ----- 442







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Qy 415 -----VSPSKGKMDETVN---INAGNNIEITRNGK--NIDIATSMTPQFSSVSLGAGAD 463
Db 876 SNSLLDISVAEGK--KTFNNGTIESGKNLNTNTGAFNLVDNATIR-----SFGVLNI 926
Qy 464 APTLSVDDEGALNVGSK-DANKPVRITNVAPG-----VKEGDVTN-----V 503
Db 927 TSTGNVSNNGTLISNERLNTSAANFTNESNCTVMSNGLLNIIAKQGNITNKNLIASROQ 986
Qy 504 AOLKGAONLNNRIDNVDCNARAGIAQAIAATAGLA-----QAYLPG----- 544
Db 987 LNLTAADNITN-----DSNTSNKIATVLSLGNISLNSKQOQVYNLGEIYAGNNISVKAHQ 1041
Qy 545 -----KSMMAIGGTYRGEAGYAIGYSSISDGTGNWVKGTCAGNGRNGHFGTSASVGY 596
Db 1042 LKNDVKLMGDITTKKEGOASYKLYQAS-----NGGHFGNDGSSGY 1082

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Search completed: July 3, 2002, 08:38:24  
Job time: 295 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:48:50 ; Search time 29.79 Seconds  
(without alignments)  
777.250 Million cell updates/sec

Title: US-09-771-382-8  
Perfect score: 3042  
Sequence: 1 MNKISRIIWSALNAWVVS.....TASGNSRGHFTSASVGYQW 598

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	223	7.3	1039	1 AG43_ECOLI	P3180 escherichia
2	211	6.9	1608	1 HLYA_SERMA	P15320 serratia ma
3	209	6.9	1286	1 AIDA_ECOLI	Q03155 escherichia
4	203.5	6.7	1325	1 YDEK_ECOLI	P32051 escherichia
5	199	6.5	2249	1 OMPA_RICRI	P15921 rickettsia
6	195	6.4	1577	1 HLYA_PROMI	P16466 proteus mir
7	190.5	6.3	2003	1 YDBA_ECOLI	P33666 escherichia
8	189	6.2	2021	1 OMPA_RICCN	Q52657 rickettsia
9	185.5	6.1	1654	1 OMPB_RICRI	Q53047 r outer mem
10	185	6.1	1300	1 120K_RICRI	P14914 rickettsia
11	185	6.1	1953	1 BIGA_SALTY	P25927 salmonella
12	184.5	6.1	1655	1 OMPB_RICCN	Q9Kka3 r outer mem
13	182	6.0	1567	1 ICEN_XANCT	P18127 xanthomonas
14	181	6.0	918	1 YMJB_CAEEL	P34487 caenorhabdi
15	181	6.0	1645	1 OMPB_RICTY	P69689 r outer mem
16	180.5	5.9	2334	1 WAPA_BACSU	Q07833 bacillus su
17	180	5.9	1569	1 YPJA_ECOLI	P52143 escherichia
18	178.5	5.9	1656	1 OMPB_RICJA	Q06653 r outer mem
19	177.5	5.8	933	1 SLAP_CAMFE	P35827 campylobact
20	171	5.6	671	1 ALYS_ENTFA	P37710 enterococcu
21	169	5.6	1228	1 SLAP_BACST	P35825 bacillus st
22	168	5.5	825	1 GUN3_BACSA	P19570 bacillus sp
23	168	5.5	1643	1 OMPB_RICPR	Q53020 r outer mem
24	167.5	5.5	2329	1 YS89_CAEEL	Q09624 caenorhabdi
25	166	5.5	1007	1 Y741_CHLMU	Q9Pjt6 chlamydia m
26	165	5.4	1694	1 IGA0_HAEIN	P44969 haemophilus
27	165	5.4	1702	1 IGA2_HAEIN	P45384 haemophilus
28	164.5	5.4	1861	1 APU_THETU	P38536 t amylolull
29	164	5.4	550	1 FLIC_SHIFL	Q08860 shigella fl
30	164	5.4	1025	1 SLAP_CAUCR	P35828 caulobacter
31	163.5	5.4	928	1 HXA2_HAEIN	P45354 haemophilus
32	161	5.3	504	1 FLIC_SALNA	Q52959 salmonella
33	161	5.3	504	1 FLIC_SALRO	Q06982 salmonella

34	160.5	5.3	788	1 SPL_RAT	Q01714 rattus norv
35	160.5	5.3	917	1 HXA3_HAEIN	P45355 haemophilus
36	160.5	5.3	928	1 PM10_CHLPN	Q9rb65 chlamydia p
37	160	5.3	497	1 FLIC_ECOLI	P04949 escherichia
38	160	5.3	504	1 FLIC_SALSE	Q06983 salmonella
39	159.5	5.2	1322	1 ICEA_PANAN	P20469 pantoea ana
40	159	5.2	504	1 FLIC_SALBU	Q06969 salmonella
41	159	5.2	504	1 FLIC_SALDU	Q06971 salmonella
42	158.5	5.2	1200	1 ICEN_PSESY	P06620 pseudomonas
43	158	5.2	948	1 HP11_DEIRA	P56867 deinococcus
44	158	5.2	1310	1 VAC3_HELPY	Q48253 helicobacte
45	158	5.2	1637	1 MRSP_STAAU	P80544 staphylococ

ALIGNMENTS

```
RESULT 1
AG43_ECOLI
ID AG43_ECOLI STANDARD; PRT; 1039 AA.
AC P3180; P76360; P75614; P97241; Q46771;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen 43 precursor (AG43) (Fluffing protein).
GN FLU OR B2000.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBITaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=97251358; PubMed=9097040;
RA Itoh T., Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K.,
RA Kasai H., Kimura S., Kitakawa M., Kitagawa M., Makino K., Miki T.,
RA Mizobuchi K., Mori H., Mori T., Motomura K., Nakade S., Nakamura Y.,
RA Nashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y.,
RA Sivasubram S., Tagami H., Takeda J., Takemoto K., Wada C.,
RA Yamamoto Y., Horluchi T.;
RT "A 460-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 40.1-50.0 min region on the linkage map.";
RL DNA Res. 3:379-392(1996).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=ML 308-225;
RA Henderson I.R., Owen P.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP PRELIMINARY SEQUENCE OF 53-78.
RC STRAIN=ML 308-225;
RX MEDLINE=89291704; PubMed=2661530;
RA Caffrey P., Owen P.;
RT "Purification and N-terminal sequence of the alpha subunit of antigen
43, a unique protein complex associated with the outer membrane of
Escherichia coli.";
RL J. Bacteriol. 171:3634-3640(1989).
RN [5]
RP SEQUENCE OF 53-63.
RC STRAIN=K12 / EMG2;
RX MEDLINE=97443975; PubMed=9298646;
RA Link A.J., Robison K., Church G.M.;
RT "Comparing the predicted and observed properties of proteins encoded
```





```
Db 466 SAAKPEAEVYSGKQTVYLRGIWYSNFLTAVMSFPCTASGANVNLGRLNAFAGNVV 525
QY 351 GT-----KVTFAAGNGTTATVSKDDGNTTVKYDVNVGDALNVNOLQ--NSGNLDSKA 402
Db 526 GTILNQEGROYVYSGATATVGVNNEGREVLSGGITDGVVLSGGLOAVSSGGKASATV 585
QY 403 VAGSSGKVI--SGNVSPSKGMDVTNINAGN---NIEITRNKNIDIAATSMT-PQFSSV 456
Db 586 INEGGAQFVYDGGQVGTCTNIKNKGTIRVDSGASALNALS-SGNLFTSGATLPETLTM 644
QY 457 -----SLGAGAD-----APTLSDVDEGALN----- 476
Db 645 AALSVSQNHASNIIVLENGLLRVTSGGTATDTTIVNSAGRLRIDDGFTINGTTINADGIV 704
QY 477 VGSKDANKPVRIINVA-----PGVKEGDTVNVAAQLKGV---AQLNNRIDNVGD 522
Db 705 AGNIQNDGNFNLINLAENYDFETELSGSLVVKDNTGIMTYAGTLTAQAGVNVK----- 758
QY 523 NARAGTAAQAIATAGLA---QAYLPKGSMAIGGTYRGEAGYAGYSSISDYG-----NW 574
Db 759 NGGIIFDSAVVNADMAVQNAYINISDOATING-----SVNNGSIVINNS 804
QY 575 VIRKTASGNSRGHGFTS 591
Db 805 IINGNITNDADLSFGTA 821
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## RESULT 4

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YDEK_ECOLI
ID YDEK_ECOLI STANDARD; PRT; 1325 AA.
AC P32051; P76140; P77168;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical lipoprotein ydek precursor (ORF1).
GN YDEK OR ORF1 OR B1510.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed=9097039;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Itoh T.,
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,
RA Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,
RA Sempel G., Seki Y., Sivasaundaram S., Tagami H., Takeda J.,
RA Takenoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 28.0-40.1 min region on the linkage map."
RL DNA Res. 3:363-377(1996).
RN [3]
RP SEQUENCE OF 595-1325 FROM N.A.
RX MEDLINE=94100243; PubMed=8274505;
RA Cartwright P.J., Timms M.W., Lithgow T., Hoej P.B., Hoogenraad N.J.;
RT "An Escherichia coli gene showing a potential ancestral relationship
to the genes for the mitochondrial import site proteins ISP42 and
RT MOM38."
RL Biochim. Biophys. Acta 1153:345-347(1993).
CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
```

```
CC (Potential).
CC -!- SIMILARITY: TO E.COLI YFAL.
CC -!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS
CC ISP42 AND MOM38.
CC -!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
CC FRAMESHIFT IN POSITION 653.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: A5000248; AAC74583.1; -
CC EMBL: D90793; BAA15190.1; ALT_INIT.
CC EMBL: D90794; BAA15197.1; ALT_INIT.
CC EMBL: X73295; CAA51730.1; ALT_FRAME.
CC PIR: S34315; S34315.
CC EcoGene: EG11780; ydek.
CC PROSITE: PS00013; PROKAR_LIPOPROTEIN; 1.
CC Hypothetical protein; Membrane; Lipoprotein; Signal;
CC Complete proteome.
CC FT SIGNAL 1 18 POTENTIAL.
CC FT CHAIN 19 1325 HYPOTHETICAL LIPOPROTEIN YDEK.
CC FT LIPID 19 19 N-ACYL DIGLYCERIDE (POTENTIAL).
CC FT CONFLICT 884 884 N -> K (IN REF. 3).
CC FT CONFLICT 1317 1317 M -> S (IN REF. 3).
CC SQ SEQUENCE 1325 AA; 136514 MW; 26A3A066FA19AD7D CRC64;
Query Match 6.7%; Score 203.5; DB 1; Length 1325;
Best Local Similarity 22.6%; Pred. No. 0.0057;
Matches 149; Conservative 72; Mismatches 274; Indels 163; Gaps 29;
QY 1 MKKISRIIWNALNAVWVSELTRNHRKTRASATVATATLTLFATVVOANATDDDDLYLE 60
Db 1 MNRIRVWNCTLQVFOACSELRRACKSTVNLKSSGLTTRKFSRL----- 47
QY 61 PVQRTAVVLSFRSDKEGTG---EKEGTEDSNWAVYDFEKR--LKAGAITLKAGDNLKIK 115
Db 48 ---TLGVLLALSGSASGASLEVDNDQITNIDTDVAYDAYLVGWYGTGLNLAGGNASLT 104
QY 116 QNT-----NENTNENTNDSSFYSLKDLTDLTSLVETKLSFGANGKNVNI-TSDTFKGL 168
Db 105 TIITSVIGANEDSEGVNVVLCGTWRL-----YDSGNARPLNVGSGTGL 150
QY 169 N-----FAKETAGTNGDPTVHLNGIGSTLTDLTLLNTGATTTVNDNDVDEKKRA 218
Db 151 NIKQKHVDGGLRLGSGTGGTVNVVEGDSVLTTELFEG-SYGTGSLNITD----- 203
QY 219 ASVKDVLNAGWNKGVKPGTTASDNVDVFTYDTVEFLSADTKTTTVNVESKNGKRETV 278
Db 204 -----KG-----YVTSSIVA-----ILGYQAGSNGQVVE 228
QY 279 KIGAKTSVIEKDGKLVTKGKCGKSGSSTDEGEGELTAKEVIDAVNKGARMKMTTANGQ 338
Db 229 KGG--EWLKNNDSSIEFQIGNOGTGEATIREGLVTAENTIIGGNATG-----IGTLNVQ 282
QY 339 TGOADRFETVTSKTKVTFASGNGTTATVSKDDGNGITVK-YD-VNVGDALN--VNLQNS 394
Db 283 ----DQDSVITVRLRYNGYFENG---TVNISNGLNINNKVSLVGVQDGHGVNVVTDKG 335
QY 395 GWNL-----DSKAVAGSSKGVISGNVSPSKGMDVTNINAGN----- 432
Db 336 HWFLGTGEAFRIYITGDAGDGLNVSSEKGVDSGIITAG---MKET---GTGNITVYKDK 389
QY 433 NIEITRNKNIDIAATSMTPQFSSVSLCAGADAPTLSDVDEGALN-----GSKDANKPVR 487
Db 390 NSVITNLGTLNGLDGHCENMISNOGLVSVNGSSLSGVTGTVGNVSIITGGMVEVKNVY 449
QY 488 ITNVAPGVKEGDTVNVAAQLKGVAAQNLNNRIDNVGNARAGIAQAI---TAGLAQAYLPG 544
```

```

Db 450 TTIGVAGVGNLISDGG--KFVSQNTITLGLDKASGIGTGLNLMDATSSDETVCINVGNE-G 506
Qy 545 KSMMAIGGGTYRGEAGYAI-----GYSSISDGTGNVVIKGTASGNSR-----GHFGT 590
Db 507 SGIVNVNGATLNSTGYGFIGNASKGIVNISTDSLMLK-TSSTNAQLQGVGLGT 563

RESULT 5
OMPA_RICRI
ID OMPA_RICRI STANDARD: PRT: 2249 AA.
AC P15921;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface
  antigen) (rOmpA) (rOmp A).
GN OMPA.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=90354033; PubMed=2117568;
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;
RT "A protective protein antigen of Rickettsia rickettsii has tandemly
  repeated, near-identical sequences.";
RL Infect. Immun. 58:2760-2769(1990).
CC -!- FUNCTION: ELICITS PROTECTIVE IMMUNITY.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
  S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- PTM: GLYCOSYLATED (PROBABLE).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC -----
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  between the Swiss Institute of Bioinformatics and the EMBL outstation -
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M31227; AAA26380.1; -
DR PIR; A41477; A41477.
DR InterPro; IPR003858; rOmpA_rOmpB; 1.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; Repeat; Signal; Cell wall; s-layer; Glycoprotein.
FT SIGNAL 1 28
FT CHAIN 29 2249
FT DOMAIN 212 1180
FT REPEAT 212 286 A (TYPE I).
FT REPEAT 287 358 B (TYPE II).
FT REPEAT 359 430 C (TYPE II).
FT REPEAT 431 505 D (TYPE I).
FT REPEAT 506 577 E (TYPE II).
FT REPEAT 578 652 F (TYPE I).
FT REPEAT 653 724 G (TYPE II).
FT REPEAT 725 799 H (TYPE I).
FT REPEAT 800 874 I (TYPE I).
FT REPEAT 875 949 J (TYPE I).
FT REPEAT 950 1021 K (TYPE II).
FT REPEAT 1022 1093 L (TYPE II).
FT REPEAT 1094 1165 M (TYPE II).
FT REPEAT 1166 1180 TYPE I (INCOMPLETE).
SQ SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;

Query Match 6.5%; Score 199; DB 1; Length 2249;
Best Local Similarity 22.3%; Pred. NO. 0.018;
Matches 143; Conservative 71; Mismatches 261; Indels 166; Gaps 29;
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Qy 34 VATAVLATLLFATVQANATDDDDLYLEPVQRTAVVLSFRSDEKGTGEGTSDSNVAVF 93
Db 39 VATGVIAATNNAFAFNNVNNN--WNEITAAGV-----ANGTPAGGQNNWAFY 86
Qy 94 D-----EKRVUKA-----GAI-----TLKAGDNLKIKQ 116
Db 87 GGDYTVTADAADRIIKAINVAGTTPVGLNITQNTVVGSIITKGNLLPVTNAGKSLTLNG 146
Qy 117 NTNENTNENTNDSFTYSLKDLTDLTSVETEKLSFGANG-----NKVNIYS--DT 165
Db 147 NNAVANHGFDAPADNY-----TGLNIALG-----GANAALIISOAPSKITLAGNDG 196
Qy 166 KGLNEFAKETAGTNGDPTVHLNGIGSTLTDLTLLTGATNTVNTDNV---TDDEKKRAASYK 222
Db 197 GGIITVTKDAALNGT-----IGNNALATVNVGAGTATLGGAVIKATTTKLITNAASVL 249
Qy 223 DVLNAGNWKIGVKPGTASDNVDFVRYTYDVEFLSADTKYT---TVNVESKD---NG-- 273
Db 250 TLTNANAVLTGAIDNTTGGDNVGLNLGALSQVTDIGNTNSLATISVGAGTATLGGAV 309
Qy 274 -KRTEVKIGAKTSVIEKDKLVGT---KGKGENCSSTDEGEGLVTA---EVIDAVN 324
Db 310 IKATTTKLTDAAASAVKFTNPVVVVTGAIDNTGNANNGIVTFTGNTVGVNATLATVN 369
Qy 325 KAGWRMKTTTANGQTQADKFETVSGTKVTFASNGTGTATVSKDDQGNIT---VKYDYN 381
Db 370 VCAGLLQ---VOGGVVKANTINLTDNASAVTFT--NPVVVTGAIDNTGNANNGIVTFTGN 424
Qy 382 ---VGDALNVNLQNSGWNLDKAVAGSGKVISGNSPSKMKDETVNINA--GNNIEI 436
Db 425 SVTVDIGNTNALATVNVGAGTATLGGAVIKATTTKLITNAASVLTLT--NANAVALTGAIDN 483
Qy 437 TENGKNIDIAT-----SMTQPSSVSLGAGADAPTLSDVDEGALNVGSKDANK 484
Db 484 FTGGDNVGLNLGALSQVTDIGNTNSLATISVGAG--TATLGGAVIKATTTKLTDAAAS 541
Qy 485 PVRTINVPVKGEGDVNTVNAQLKGVAQNLNNRINDVNGNARA---GIAQAIATAGLAQA 540
Db 542 AVKFTN--PVVVVTGAIDNTG-----NANNGIVTFTGNTVTDIGNTNSLAT----- 586
Qy 541 YLPKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVIKGPAS 581
Db 587 -----ISVGAGT-----ATLGGAVIKATTT 606

RESULT 6
HLIA_PROMI
ID HLIA_PROMI STANDARD: PRT: 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN=ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT "Nucleotide sequencing of the Proteus mirabilis calcium-independent
  hemolysin genes (hpmA and hpmB) reveals sequence similarity with the
  Serratia marcescens hemolysin genes (shlA and shlB).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD
  CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY
  DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM
  ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA
  REQUIRES HPMB FUNCTION.
CC
```

CC -1- SUBCELLULAR LOCATION: Outer membrane.  
CC -1- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA  
CC MAY BE RESPONSIBLE FOR PORE FORMATION.  
CC -1- SIMILARITY: TO S. MARCESCENS HEMOLYSIN (SHLA).  
CC -----  
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CC -----  
DR EMBL; M30186; AAA25657.1; .  
DR PIR; A35140; A35140.  
KW Hemolysis; Toxin; Outer membrane; Signal.  
FT SIGNAL 1 29  
FT CHAIN 30 1577 HEMOLYSIN.  
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;  
  
Query Match 6.4%; Score 195; DB 1; Length 1577;  
Best Local Similarity 20.5%; Pred. No. 0.018;  
Matches 152; Conservative 110; Mismatches 233; Indels 246; Gaps 39;  
  
QY 23 TRNTRKRASATVATA-----VLATLLFATVQANATDDDDLLYLEPQRTAVVLSF 71  
DB 619 TNKQTSSELISDAQLTVYGVNDVNVIGSLIKSADKLGIHSLGIDNVKSAQQVTKIDDE 678  
QY 72 RSKQEGTGEKGTEDSNWAVYFEKRVLKAGATLTKAGDNLKTONTNENTNTNDSSF 131  
DB 679 KTSIAITGHAKEVDKQYSAGF-----HITHTKNTSTETEQAQS 719  
QY 132 TYS-----LKKDLT-----DL-----TSVETEKLSFGANGKVNITSDTKGLNFAKET 174  
DB 720 TISGANVDLQANKDVTAGSGLTKTAGNASITGDNVAFVSTENK-----KQT 766  
QY 175 AGTNGDPTVH-----LNGIGS-----TLTDTLLNTGATTVTND-NVTDDEK 215  
DB 767 -DNTDPTTISGFSYTGKGVKSKADFOYDKQHTQTEVTKNRGSQTEVAGDLTITAN-- 822  
QY 216 KRAASVKDLNAGNKKVPGTASDNDV--FVRTYDVEFL-----SADTKTTTVNV-- 267  
DB 823 -----KDLLHEG-----ASHVEGRYQESGENTQHLAVNDSETSKTDSLNVGI 865  
QY 268 -----ESKDKGRTEVKIGAKTSVKE--KD-----G 292  
DB 866 DVGVDLYSGVTVPVKAIEDGVNT--TKPGNNTDLTKKVTARDAIANLANLSLETPTNVG 924  
QY 293 KLVTGKKGKSGSSTDG--GEGLVTAKEVIDAVNK---AGWRMKT-----TANGQTG 340  
DB 925 VEVGKGGGSGQSDTSQAVSTSNACKIDIDSNNKLHDQGHYQSQEGISLTANTHTS 984  
QY 341 QA--DKPETVTSGTK-----VTFASNGTATTATVSKDDGNTITVKYDVNVGALNVQLQNS 394  
DB 985 EATLDKHQTHFTHTGQGGQGVSTKTSQDITVAIKGSGQTT-----DNALMETRAKGS 1037  
QY 395 GW--NLDSKAVAGSGKVISGNSPSKGMDETWINAGNNIETR-----NG 440  
DB 1038 QFTSNGDISINVGNAIHYGAQDAQKGG--TV-INAGGDLTAAQATDTHSESQSNNVG 1093  
QY 441 K-NIDITATSTPQFSSVSLAGADAPTL--SVDDDEGALNVGSKDANKPVRTNTPAVPYKEG 498  
DB 1094 SANLKVGT--TPE--SKDYGGGFGNAGTTHHSKEQTAKVCTIGTSQGIELNAGHNLTLQ 1149  
QY 499 DVTNVAOLKGVQANLNRIID-----NVDGNARAGIAQ-----AIATAGLAQA 540  
DB 1150 --THLSQEDIALNATNKVDLQSSASEHTEKGNLNSGGVQAGFGKMKMTDDASSVNGL--- 1204  
QY 541 YLPCKSMWAIG-----GGTYRGEAGYAGYSSI-----SDTCGNWV 575  
DB 1205 ---GSAQFAIGKODEKSVSREGGTINNSGNLTINGNSVHLQGAQVNSKDTQLTQSQSGDIE 1261

QY 576 IKGTASGNSRGHFGTASVGY 596  
DB 1262 ITSQAQSTDYKNNNGT--DIGF 1280  
  
RESULT 7  
ID YDBA\_ECOLI STANDARD; PRT; 2003 AA.  
AC P33666; P76087; P76088; P76856; P76857; P76859;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein ydba.  
GN YDBA OR B1401/B1405.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_TaxID=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=K12 / MG1655;  
RC MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=K12;  
RC MEDLINE=97251357; PubMed=9097039;  
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sempel G., Seki Y., Sivasubraman S., Tagami H., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
RT corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 464-2003 FROM N.A.  
RX STRAIN=K12;  
RC MEDLINE=92190338; PubMed=1665988;  
RA Moszer I., Glaser P., Danchin A.;  
RT "Multiple IS insertion sequences near the replication terminus in  
RT Escherichia coli K-12.";  
RL Biochimie 73:1361-1374(1991).  
CC -1- SIMILARITY: TO S.TYPHIMURIUM ORF NEAR CYS8 (AC P25928).  
CC -1- CAUTION: THIS IS A CONCEPTUAL TRANSLATION: THE GENE CODING FOR  
CC THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT  
CC BETWEEN AMINO ACIDS 839 AND 840.  
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CC -----  
DR EMBL; AF000237; AAC74483.1; ALT\_SEQ.  
DR EMBL; AF000237; AAC74487.1; ALT\_SEQ.  
DR EMBL; D90778; BAA15009.1; ALT\_SEQ.  
DR EMBL; D90778; BAA18880.1; ALT\_SEQ.  
DR EMBL; D90779; BAA18881.1; ALT\_SEQ.  
DR EMBL; X62680; ; NOT\_ANNOTATED\_CDS.  
DR EcoGene; EG11307; ydba.  
KW Hypothetical protein; Complete proteome.  
FT CONFLICT 489 489 I -> V (IN REF. 2).  
FT CONFLICT 495 495 I -> V (IN REF. 2).  
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;





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FT CONFLICT 92 126 I -> V (IN REF. 1).
FT CONFLICT 126 137 V -> I (IN REF. 1).
FT CONFLICT 137 157 T -> N (IN REF. 1).
FT CONFLICT 157 169 G -> D (IN REF. 1).
FT CONFLICT 169 368 IS -> VN (IN REF. 1).
FT CONFLICT 368 374 KATLGGAIIKATTTK -> LLQVQGVVKRANTIN (IN REF. 1).
FT CONFLICT 640 669 N -> D (IN REF. 1).
FT CONFLICT 669 793 V -> I (IN REF. 1).
FT CONFLICT 793 804 N -> D (IN REF. 1).
FT CONFLICT 804 823 VN -> IS (IN REF. 1).
FT CONFLICT 823 898 LLRVQGVVKSNTIN -> KATLGGAIIKATTTK (IN REF. 1).
FT CONFLICT 898 908 D -> Y (IN REF. 1).
FT CONFLICT 908 985 P -> N (IN REF. 1).
FT CONFLICT 985 1009 N -> K (IN REF. 1).
FT CONFLICT 1009 1013 L -> S (IN REF. 1).
FT CONFLICT 1013 1182 Y -> S (IN REF. 1).
FT CONFLICT 1182 1314 K -> Q (IN REF. 1).
FT CONFLICT 1314 1451 N -> Y (IN REF. 4).
FT CONFLICT 1451 1624 H -> N (IN REF. 1).
FT CONFLICT 1624 1628 G -> D (IN REF. 1).
FT CONFLICT 1628 1872 E -> G (IN REF. 1).
FT CONFLICT 1872 1875 A -> V (IN REF. 1).
FT CONFLICT 1875 1879 T -> P (IN REF. 1).
FT CONFLICT 1879 1936 MS -> LP (IN REF. 1).
FT CONFLICT 1936 1965 E -> A (IN REF. 1).
FT CONFLICT 1965 1997 MTAPLP -> ITPPLS (IN REF. 1).
FT CONFLICT 1997 2021 G -> R (IN REF. 1).
FT SEQUENCE 2021 AA; 203328 MW; 327FC42D/CB34668 CRC64;

Query Match 6.2%; Score 189; DB 1: Length 2021;
Best Local Similarity 21.6%; Pred. No. 0.048;
Matches 176; Conservative 86; Mismatches 287; Indels 264; Gaps 40;

QY 10 NSALNAAVVVSELTNR-HTKRASATVAT-AVLATLLFATVQANATDDDD-----LYLEPV 62
DB 415 NNGIVFTGDSVTGNTGNATLISVGAGKATLGGAIIKATTTKLTDNASAVTFNPV 474
QY 63 QRTAV-----VLSFRSDEGEGEGETEDSNWAVFDEKRVLKAGAI-----TLKA 108
DB 475 VVTGAIDNTGNANNGIVFTGDSVTG-TNIGTNALATISVGAGKATLGGAIIKATTTK 533
QY 109 GDNLIKQNTN-----ENT-NEN-----TDSFTYSL-KKDLTDLTSVETEKLSF 152
DB 534 TDNASAVTFNPVVVGAIDNTGNANNGIVFTGDSVTGNTGNATLISVGAGKATL 593
QY 153 GA-----NGKNVITSDTKGLNFAKETAGTN-----GDPTVHLNGIGSTLT 193
DB 594 GGAIKATTTKLTDNASAVTFNPVVVGTGAIDNTGNANNGIVFTGNTSTVTGN-IGNTNA 652
QY 194 DTLNLTGA-----TNNVNDVNTDDEKRAASVKDVLNAGNIKGVKPGTTA 240
DB 653 LATNVVAGIATLEGAVIKATTTKLTN-----AASVLTNTNVNAVLTGAIDNTTG 702
QY 241 SDNVDFVRYTDFEFLSADTKT-----TVNV-----ESKONG-----KRTVEKIGAKTSVLEK 290
DB 703 VDNVGVNLNCAISQVFTGNTGNATLISVGAGKATLGGAIIKATTTKLTDNASAVTF 762
QY 291 DGLVLTG-----KKGEGSSSTDEGEGLVTAK-----EVIDAVNKA-----GWRMKTTTA 335
DB 763 NPVVVGTGAIDNTGNANNGIATFGDSVTGNTGNATLISVGAGLRRVGGGVKRSNTI 822
QY 336 N-----GOTQADK-FEIVTSGTKVTFASGN-GTTATVS-----367
DB 823 NLTDNASAVTFNPVVVGTGAIDNTGNANNGIVFTGDSVTGNTGNATLISVGAGKA 882
QY 368 -----KDDQGNITVKYDVNVGDALNVQNLQNSGNLDSKAVAGSGKVISG 413
DB 883 TLGGAIIKATTTKLTDNASAVTFNPVVVGTGAID-----NIG-NANNGIVFTGDSVTG 936
QY 414 NVSPSKGMDETVINAGNNIEI--TRNGKNIDIATSMTPQFSSVSLGADAP-----T 466
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DB 937 NIGNTNAL--ATNVVGAGVTLQAGGSLDANNIDFGARSTLEFNGLDGGCNAIPYFKGA 994
QY 467 LSVDDGECALNVGSK-----DANK-PVRI TN-----490
DB 995 IANGNAILNVNTKLLTAYHLTTGTVAEINIGAGNLFAIDASAGDVTLLNAQDIHFRALD 1054
QY 491 -----VAPGVKEGDV-----TNVAQLKGVAQNLNLR 516
DB 1055 SALVLSNLGTGVNNILLADLVAPGVDEGTVVFDGGVGNLIGSNVA---GAARN---1107
QY 517 IDNVGNA-----RAGIAQAIATAGLAQAYLPK-----SMAIGGGTYR-GEAGYAI 563
DB 1108 IGDVGNGKFTLLIYNAVTTTDDVNLEGIQNLVNNADFTSTTAFNAGTIQINDATYTI 1167
QY 564 -----GYSSISDTGNWVWIKGTASGNSR 585
DB 1168 DANNGLNIPAGNIKFAHAQAQLILQNSSGNDR 1200

RESULT 9
OMP_B_RICRI STANDARD; PRT; 1654 AA.
ID OMP_B_RICRI
AC Q53047;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=R;
RX MEDLINE=92167802; PubMed=1724278;
RA Gilmore R.D. Jr., Cieplak W. Jr., Policastro P.F., Hackstadt T.;
RT "The 120 kilodalton outer membrane protein (rOmp B) of Rickettsia rickettsii is encoded by an unusually long open reading frame: evidence for protein processing from a large precursor.";
RL Mol. Microbiol. 5:2361-2370(1991).
RN [2]
RP SEQUENCE OF 279-1654 FROM N.A.
RC STRAIN=R;
RX MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
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CC EMBL; X16353; CAA34403.1;
DR InterPro; IPR003858; rOmpA_rOmpB.
DR Pfam; PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
```



FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.  
FT DOMAIN 1181 1188 POLY-THR.  
SQ SEQUENCE 1654 AA; 166184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.1%; Score 185.5; DB 1; Length 1654;  
Best Local Similarity 22.8%; Pred. No. 0.056;  
Matches 158; Conservative 81; Mismatches 272; Indels 181; Gaps 37;

QY 15 ANVVSELTNRHTKRA-----SATVATAVLATL-----LFAVQA-NATDDD 55  
DB 181 ASTLVFNLANPTOKAPLILGDNVANGVNTLNVNGFIQVSNKSPATVRAINADQ 240  
QY 56 DYLEPVPQRTAVLSFRSKDEGTGKEGTEDSNWAIVFDEKRVLRKAGAITLKAGDNLK-- 113  
DB 241 GIIFNTDANNANLNLOAGGT-TINFCTGDTGRVLVLLSKHAAATNFNIGSLGNLKV 299  
QY 114 IKQNT-----NENTWENTND-----SSFTYSLKDLTDLTSVETEKLSFGANG 156  
DB 300 IEFNTVAVDQGLTANAGAAANAVIGTNNGAGRAAGFVVSVD-----NG 341  
QY 157 NKVNITSDTKGNFKAETAGTNGDPTV-HLNGIGSLPLTDLTLLNTGATTNVTNDN--VTD 213  
DB 342 KVATIDGQVYAKDMVYQSANATQVNRHIVDVGADGTAFKTAASKVTITQDSNFGNTD 401  
QY 214 EKKRAASVK--DVLNAGWNIG--VKPGTTASDNVDVFTYD---TVEFLSADTKTTTVN 266  
DB 402 FGNLAAQIKVPNAITLTGNTGDASNPGNTAG-----VITFDANGTLESASADANVAVTN 456  
QY 267 ----VESKDNG-----KRTEVKIGAKTSVKEKDGKLVTKG-----GKGNGSST 307  
DB 457 NITAASGAGVGVVQLSGTHAAELRLGNAGSIFKLADGTGVINGKVNOTALVGGALAAAGTIT 516  
QY 308 DEGEGLTAKEVIDAVNAGKWRMTTANGOTGQADKPFETVTSCTKVTASNGT----- 362  
DB 517 LQGSATITGD--IGNAGGAAALQRIITLAN-----DAKKTLLTGGANIIGAGGGTIDLQA 568  
QY 363 -----TATVSKDQGNITTVYDV-----NVGDALNVNQLNSGWN-----LDSK 401  
DB 569 NGGTIKLTST-----QNNIVDFDLAIAITDQTCVVDASSLTNAQTITNGKIGTIGANKK 623  
QY 402 AVA-----GSGGKVIS--GNVSPKGMDETVNINAG-----NNIETR-----NGKNI- 443  
DB 624 TLGQFNIGSSKTVLSNGVA-----INELVIGNDGAVQFAHDTYLITRTTNAAGQKIIF 678  
QY 444 -DIATSMTPQFSSVSLGAGADAPTLSVDDEGALNVGSKDANKPVRITNVAPGVKGDVTN 502  
DB 679 NPVNNGTTLAAGTNLGS-----ATNPLAEINFGSKGVNVDV--VLNVGEGVNL-YATN 729  
QY 503 VAQLKGVAQNLNRRIDNVDG--NARAGIAQAIATAGLAQ-----AYLPKSKMMAIGGGT 554  
DB 730 IITTDA--NVGSFVFNAGTNIIVSG-----TVGQOQGNKFNVALENGTIVKFLGNAT 780  
QY 555 YRGEAGYATGYSSISDSTGNWIKTRASGNSRG 586  
DB 781 FNGNTTIAAN-STLQIGGNTADCVASADGTG 811

RESULT 10

ID 120K\_RICRI STANDARD; PRT; 1300 AA.  
AC P14914;

DT 01-APR-1990 (Rel. 14, Created)

DT 01-FEB-1996 (Rel. 33, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE 120 kDa surface-exposed protein.

GN P120.

OS Rickettsia rickettsii.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiidae; Rickettsia.

OX NCBI\_Taxid=783;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=R;  
RX MEDLINE=90136087; PubMed=25154118;  
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;  
RT "Cloning, expression and sequence analysis of the gene encoding the  
RL 120 kDa surface-exposed protein of Rickettsia rickettsii";  
RL Mol. Microbiol. 3:1579-1586(1989).  
CC -!- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS  
CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -!- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES  
CC CONFERRING ANTIGENICITY TO THE PROTEIN.  
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.

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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
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EMBL; X16353; CA334402.1; -;  
DR PIR; S07575; S07575.  
DR InterPro; IPR003858; OmpA\_rOmpB.  
DR Pfam; PF02708; rOmpA\_rOmpB; 1.  
KW Antigen; Glycoprotein; Cell wall; S-layer.  
FT CARBOHYD 7 7  
FT CARBOHYD 66 66 N-LINKED (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (POTENTIAL).  
FT CARBOHYD 103 103 N-LINKED (POTENTIAL).  
FT CARBOHYD 147 147 N-LINKED (POTENTIAL).  
FT CARBOHYD 268 268 N-LINKED (POTENTIAL).  
FT CARBOHYD 330 330 N-LINKED (POTENTIAL).  
FT CARBOHYD 375 375 N-LINKED (POTENTIAL).  
FT CARBOHYD 415 415 N-LINKED (POTENTIAL).  
FT CARBOHYD 424 424 N-LINKED (POTENTIAL).  
FT CARBOHYD 430 430 N-LINKED (POTENTIAL).  
FT CARBOHYD 436 436 N-LINKED (POTENTIAL).  
FT CARBOHYD 444 444 N-LINKED (POTENTIAL).  
FT CARBOHYD 515 515 N-LINKED (POTENTIAL).  
FT CARBOHYD 547 547 N-LINKED (POTENTIAL).  
FT CARBOHYD 593 593 N-LINKED (POTENTIAL).  
FT CARBOHYD 655 655 N-LINKED (POTENTIAL).  
FT CARBOHYD 698 698 N-LINKED (POTENTIAL).  
FT CARBOHYD 710 710 N-LINKED (POTENTIAL).  
FT CARBOHYD 799 799 N-LINKED (POTENTIAL).  
FT CARBOHYD 800 800 N-LINKED (POTENTIAL).  
FT CARBOHYD 826 826 N-LINKED (POTENTIAL).  
FT CARBOHYD 844 844 N-LINKED (POTENTIAL).  
FT CARBOHYD 861 861 N-LINKED (POTENTIAL).  
FT CARBOHYD 879 879 N-LINKED (POTENTIAL).  
FT CARBOHYD 920 920 N-LINKED (POTENTIAL).  
FT CARBOHYD 926 926 N-LINKED (POTENTIAL).  
FT CARBOHYD 1116 1116 N-LINKED (POTENTIAL).  
FT CARBOHYD 1128 1128 N-LINKED (POTENTIAL).  
FT CARBOHYD 1140 1140 N-LINKED (POTENTIAL).  
FT CARBOHYD 1146 1146 N-LINKED (POTENTIAL).  
FT CARBOHYD 1211 1211 N-LINKED (POTENTIAL).  
SQ SEQUENCE 1300 AA; 132801 MW; E09E52C3F647243D CRC64;

Query Match 6.1%; Score 185; DB 1; Length 1300;  
Best Local Similarity 21.9%; Pred. No. 0.045;  
Matches 162; Conservative 91; Mismatches 269; Indels 218; Gaps 38;

QY 30 ASATVATAVLATLLFATVOAN--ATDDDDLYLEPVPQRTAVVL--SFRSDKEGTEGEGTE 85  
DB 22 ADGTTAFKTAASKVTITQDSNFGNTDFGNLAAQIKVPNAITLTGNTGDSNFGNTAG-- 79  
QY 86 DSNWAYVFDEKRVLRKAGAITLKAGDNLKIKQNTN--ENTNENTNDSFTVSLKDLTDLT 143  
DB 80 ----VITFDANGTLESAS----ADANVAVTNNTTATEASGAGVQLSGTHAAELRLGNAG 131

```

144 SVTEKLSFCA--NGKVNITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTLLNTGA 201
132 SI--FKLADSTVING-KVNOTA-----LVGGALAAAGTITLDG-SATITGDIGNAGG 178
202 TTNVTVNDVTDDEKKRAASVKOVNLNAGNWKIGVKPGT-----TASDN---VDF 246
179 AAALQRITTLANDAK-----KTLTGLGANILGAGGTTIDQANGGRTIKLTSTQNNIWDV 232
247 ---VRYDRT-----VEFLSADTKT-----TTNVVESKDNKRTVE 277
233 DLAIATDQGVGDVSDSLTNAQTITNGKTIICANNKTLGQFNIGSKTKVLSNGVAIN 292
278 VKIGAKTSVKEKDGKLV-----GKKG-----GEN-GSSTD----- 308
293 LVIGNDGAQVFAHDTYLIITTTNAAQGGKIIFNPVNVNGTTLAAGTNLGSATNPLAEINF 352
309 --EGEGLVTAKEVIDAVNKAQWRMKTTTAN-----GQTG--QADKFETVT 349
353 GSKGVNVDVTLNVGEGVNLATNITTTDANVGSFVNAGTNIVSGTVGGQCGKNTVA 412
350 --SGTKVTF--ASGNCTTATVSKDD---QGNITVKYDVNVGDAALNVNQLNSG---WNL 398
413 LENGTTVKFLGNATFNNTTIAANSTLQIGGNTADC-VASADGTGIVEPVNTGPITVTL 471
399 DSKA-----VAGSSGKVIS--GNVSPSKGMDVETNI----- 428
472 NKQAPVNAKQITVSPGNVINEIGNAGNHGAVTDTTAFENSSILGAVVFLPRGIPFN 531
429 NAGNIEIT-----RNGKNIDIAISM-----PQFSSVSLGAGAD----- 463
532 DAGMTPLTKSTVGNTAKGFVPSVVLGVDSVIADGOVIGDQNNIVGLGLGSONGII 591
464 --APTLVS-----DDEGALNVGSKDANKPVRITNVNAPGVKEGDTVNAQKGAQNINN 515
592 VNATTLVAGISTLNNQGTVTLSSGVPNTGTYVGLGTGIGASKFKQVT---FTTDYNN 647
516 RIDVDCNARAGIATAATAGLAQAVLPKGSMAIGGTYRGEAGYAGYSSISDTCNNV 575
648 LGNIATNATINDGVTVTTGGIAGIFDGR--ITLGSVNGNGNVPADGILSNSTS---- 701
576 IKGTASGNSRGHFTGSASVG 595
702 MIGTTRANN---GTVTYLG 717

RESULT 11
BIGA_SALTY
ID BIGA_SALTY STANDARD; PRT: 1953 AA.
AC P25927; P25928; Q9XCQ3;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Putative surface-exposed virulence protein bigA precursor.
GN BIGA OR STM3478.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=14028;
RA Stojiljkovic I., Valentine P., Heffron F.;
RT "Salmonella typhimurium rhs homolog.";
RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX MEDLINE=21534948; PubMed=11677609;
RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
Waterston R., Wilson R.K.;
"Complete genome sequence of Salmonella enterica serovar Typhimurium
LT2.";
RL Nature 413:852-856(2001).
[3]
RP SEQUENCE OF 1-765 FROM N.A.
RC STRAIN=LT2;
RX MEDLINE=911100301; PubMed=1987123;
RA Wu J.Y., Siegel L.M., Kredich N.M.;
RT "High-level expression of Escherichia coli NADPH-sulfite reductase:
RT requirement for a cloned cysG plasmid to overcome limiting siroheme
RT cofactor.";
RL J. Bacteriol. 173:325-333(1991).
CC -!- CAUTION: Ref.3 sequence differs from that shown due to frameshifts
CC in positions 414 and 732.
CC
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CC
CC EMBL; AF133696; AAD39458.1; -
CC EMBL; AE008859; AAL22340.1; -
CC EMBL; M64606; AAA27042.1; ALT_FRAME.
CC EMBL; M64606; AAA27043.1; ALT_FRAME.
CC PIR; C39200; C39200.
CC PIR; D39200; D39200.
CC StyGene; SG10437; bigA.
CC Virulence; Repeat; Signal; Complete proteome.
CC SIGNAL 1 27
CC CHAIN 28 1953
CC
CC PUTATIVE SURFACE-EXPOSED VIRULENCE
CC PROTEIN BIGA
CC 15 X 11 AA TANDEM REPEATS.
CC 1 (INCOMPLETE).
CC 2 (INCOMPLETE).
CC 3 (INCOMPLETE).
CC 4.
CC 5.
CC 6.
CC 7.
CC 8.
CC 9.
CC 10.
CC 11.
CC 12.
CC 13.
CC 14.
CC 15 (INCOMPLETE).
CC D -> DRGDDVTPDD (IN REF. 1).
CC A -> R (IN REF. 3).
CC D -> N (IN REF. 1).
CC QYLE -> ITLQ (IN REF. 1).
CC SA -> T (IN REF. 1).
CC SEQUENCE 1953 AA; 200150 MW; 611B3F1C954D91AE CRC64;

Query Match 6.1%; Score 185; DB 1; Length 1953;
Best Local Similarity 20.6%; Pred. No. 0.072;
Matches 143; Conservative 91; Mismatches 275; Indels 184; Gaps 28;

QY 8 INNSAL--NAWVVVSELTNRNHTKRASAT---VATAVLATLILFATVQANATDDDLYLEPV 62
DB 286 VWNVSEODNHW---QLTTADGKTLNVGTWDTDANAIVI-----EGTQENGLYWKYD 334
QY 63 QRTAVLVLSFRSDKEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEG 122
DB 335 SRGYLIIA-----DDNTTVISGDDQAHNSDRGMDISGQDRTGVIIISGRTV 380
QY 123 NENTNDSSTFYSLKKDLT---DLTSVETEKLFSFGANGKVNITSDTKGLNFAKETAGTNGD 180
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Db 381 NTLGDSSTVDGATGMVIGSGDGTNTTISGSHSTVDNATGALISGNGTTTTFAGDIAVSGG 440  
 QY 181 PTVHLNGIGSTLTDR-----LLNTGATTNTNDVTDDEKKAASVKDVLNAGNNIKGVKP 236  
 Db 441 TAILIDGNDAIKNTGSDISAGSGTVIDGNARVNNDGDMTITD-----GGTG 491  
 QY 237 GTTASNDNVFRTYDVEFLSADTKTTTNNVESKNGKREYKIGAKTSVIREKDGKLVY 296  
 Db 492 GHITGDNVVI-----DNAGSTTVSGADATYALIEGDNALVI 527  
 QY 297 GKG-----KGNGSSTDEGEGLVT--A 316  
 Db 528 NEGNOTISGAVGTRIDGDDAHTTNTGDIADVAGSAAVINGDNGSLTQAGDLLVTDGA 587  
 QY 317 KEVI--DAVNKAGWRKMTTANGOTQADKFETVTSKTKVF-----ASNGGTATVS 367  
 Db 588 MGIIYGTGNEA-----KNTGNATVRDADSVGFVAGEKNTFNKGDIDVSLNGTGALVS 642  
 QY 368 KDOGNITVKYDVNVGDALNNQLNSGNWLDKAVAGSGRV--ISGNVSPS-----418  
 Db 643 -GDMSQVTLDDGINV--VSVDSEGVFSATGVSVDGSDNAVDITGNVNISADYQDDDL 698  
 QY 419 -GKKWDETNNIAGNNIETRNK-NI-----DIATSMTPQFSSVSLGAGADATPLSVDDRG 473  
 Db 699 AAGAPPLTGVVVGNGTNTVTLNGLNIDNDLSATGGQYLDVVGLSVTGGDNDVEID--G 756  
 QY 474 ALNVGSKDANKPRTITNVPAGVKEGDVNTVAQLKGAQNNLRIDNVDGNARAGIAQATA 533  
 Db 757 GINI--THSEDLPGTS-----ADITGISVSGNSTVTLNGH-STIDTNTVVGGHVILA 806  
 QY 534 -----TAGLAQAYLP-----GKSMIAIGGTYRGEAG-----YAI---563  
 Db 807 RVNNGSLLIGDSDVVVDNVNVIPTGYTYNNALLMADGEGSTENKNGDITSHGVYSVIRA 866  
 QY 564 -GYSSISDTGNVVIKGTASGNSRGHGTSAVSG 595  
 Db 867 DNGSEVNSGDIIVATSSNSSEDRAAITRASG 899  
 RESULT 12  
 ID OMPB\_RICCN STANDARD; ID OMPB\_RICCN PRT; 1655 AA.  
 AC Q9KKA3; Q9KKA3; Q9KKA3;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
 DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)  
 DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein  
 antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].  
 GN OMPB OR RC1085  
 OS Rickettsia conorii.  
 OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
 OC Rickettsiaceae; Rickettsiae; Rickettsia.  
 OX NCBI\_TaxID=781;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-Malish 7;  
 RX MEDLINE=21442074; PubMed=11557893;  
 RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,  
 RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,  
 RA Raoult D.;  
 RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii";  
 RL Science 293:2093-2098(2001).  
 RN [2]  
 RP SEQUENCE OF 33-1649 FROM N.A.  
 RC STRAIN=Indian tick typhus, and Malish 7;  
 RX MEDLINE=20393643; PubMed=10939649;  
 RA Roux V., Raoult D.;  
 RT "Phylogenetic analysis of members of the genus Rickettsia using the  
 RT gene coding the outer-membrane protein ompB (ompB).";  
 RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).  
 RN [3]

RP SEQUENCE OF 353-1655 FROM N.A.  
 RC STRAIN-Malish 7;  
 RA Stenos J., Walker D.;  
 RT "The rickettsial outer membrane protein A and B genes of Rickettsia  
 RL australis, the most divergent rickettsia of the spotted fever group.";  
 RL submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.  
 CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR  
 CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL  
 CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY  
 CC SIMILARITY).  
 CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR  
 CC (BY SIMILARITY).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
 CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).  
 CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.  
 CC  
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 CC or send an email to license@isb-sib.ch).  
 CC  
 CC EMBL; AE008659; AAL03623.1; -  
 CC EMBL; AF123721; AAF34124.1; -  
 CC EMBL; AF123726; AAF34129.1; -  
 CC EMBL; AF149110; RAD39533.1; -  
 CC InterPro; IPR003858; rOmpA\_rOmpB.  
 CC Pfam; PF02708; rOmpA\_rOmpB; 1.  
 CC Antigen; S-layer; Cell wall; Complete proteome.  
 CC CHAIN 1 1334  
 CC CHAIN 1335 1655  
 CC VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).  
 CC VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).  
 CC CONFLICT 353 354 KD -> GH (IN REF. 3).  
 CC CONFLICT 776 776 F -> S (IN REF. 3).  
 CC CONFLICT 1159 1159 E -> D (IN REF. 3).  
 CC CONFLICT 1177 1177 G -> S (IN REF. 3).  
 CC CONFLICT 1492 1492 H -> R (IN REF. 3).  
 CC SEQUENCE 1655 AA; 168342 MW; 549E19377D9FCE37 CRC64;  
 SQ  
 Query Match 6.1%; Score 184.5; DB 1; Length 1655;  
 Best Local Similarity 22.1%; Pred No. 0.063;  
 Matches 147; Conservative 76; Mismatches 292; Indels 149; Gaps 30;  
 QY 10 NSALNAAVVVVSELTRNHTKRASATVATVATLTLFATVQANATDDDDLLYLEPVQRTAVVL 69  
 Db 211 NGTLN-----VTNGFIKVSSEFATVNVINIGDGGIMFTDADNVNTLNLAQAGATI 263  
 QY 70 SPFSKDEGTEGEGTESNVAVFDEKRVLKAGAILKAGDNLK-----IKQ 116  
 Db 264 TF-----NGTDGTGRLLSKNAAATDFNVTSGLGSLNGKIEFTNVAVNGOLKA 313  
 QY 117 NTNEN-----TNTENTNDSS-FYSLKAKDLTDLTSVETEKLSFGANGKNVNITSDTKGLNF 170  
 Db 314 NAGANAAVITGNNGAGRAAGVVSVD-----NKGATIDQGVYAKDM 355  
 QY 171 AKETAGTNGDPT-----VHLNGIGSTLTDTLLNTGATTNTVNTDNDVTDDEKRAASVKD--- 223  
 Db 356 VIQSANAVGOVNERHIVDVCTDGTGTTAFKAASKVAITQNSNFCGTTDFGNLAAQIIVPNTM 415  
 QY 224 VLNAGNNIKGVKPGTTASNDNVDFRTYD---TVEFLSADTKTTTVN-----VESKNG--- 273  
 Db 416 TLNGNFTGDSNPGNTAG-----VITFDANGTLASASADANAVAVTNNITAISAGAGVVQ 470

```
QY 274 ----KRTEVIGAKTSVIKEDGKLVTK-----GKGENSGSTDEGLVTAKEVID 321
Db 471 LSGTHAAELRIGNAGSVFKLADGTVINKVQNTALVGLAAGTITLDGSATFG-----D 526
QY 322 AVNKAGWRMTTNTANGTGQADKPEYTV-----SGTKVTFASNGTTFATVSKDDQG 372
Db 527 IGNAGG----AAALQGITLANDATKTLTLGGANIGANGGTINFQANGGTIKLTS---TQN 580
QY 373 NITVKYDV-----NYGDALNVNQLNSGNWLDKSKAVAGSSGKVISGNVSPSKGM-DE 424
Db 581 NIVVDFDLAIATDGTGVVDASSLTNAQTLTINGKIGTVGANNKTLGQFNIGSSKTVLSDG 640
QY 425 TVNIN--AGNN--IEITRNGKNIDIASTMPQ-----FSSV-----SILGACADAPTLSDV 470
Db 641 DVAINELVIGNGAVQFAHNTYLTIRTNAGOGKLIIFNPVNNNTTLAGTNLGS-ATN 699
QY 471 DEGALNVGSKDANKPVRITNVAPGVKGGDVNTVNAOLKGVQNLNLRIDNVG-NARAGIA 529
Db 700 PLABINFGSKGAANVDVNLVNGKGNL-YATNITTTDA---NVGSFIFNAGGTNIVSG-- 753
QY 530 QAIATAGLAO-----AYLPGSKMAIGGTYRGEAGYALGYSSISDGTGNWIKGTASG 582
Db 754 ----TVGQGGQGNKFTVALONGTIVKFLGNATFNNGNTTIAAN-STLOIGGNYTADFVASA 808
QY 583 NSRG 586
Db 809 DGTG 812
```

## RESULT 13

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ICEN_XANCT STANDARD; PRT; 1567 AA.
AC P18127;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ice nucleation protein.
GN INAX.
OS Xanthomonas campestris (pv. translucens).
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;
OC Xanthomonas.
OX NCBI_TaxID=343;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=X56S;
RX MEDLINE=91080859; PubMed=22593339;
RA Zhao J., Orser C.S.;
RT "Conserved repetition in the ice nucleation gene inax from
RL Xanthomonas campestris pv. translucens.";
RL Mol. Gen. Genet. 223:163-166(1990).
CC -1- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE
CC CRYSTALLIZATION IN SUPERCOOLED WATER.
CC -1- SUBCELLULAR LOCATION: Outer membrane (By similarity).
CC -1- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS
CC OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A
CC REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.
CC -1- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE
CC NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.
CC -1- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN
CC FAMILY.
```

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-----  
EMBL: X52970; CAA37140.1; -  
PIR: S11672; S11672.  
HSSP: P06620; IINA.  
DR InterPro: IPR000258; Ice\_nucleatn.

```
DR Pfam; PF00818; Ice_nucleation; 81.
DR PRINTS; PR00327; ICENUCLEATN.
DR PROSITE; PS00314; ICE_NUCLEATION; 57.
KW Ice nucleation; Repeat; Outer membrane.
SQ SEQUENCE 1567 AA; 152548 MW; CBB451D959ECAD63 CRC64;
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Query Match 6.0% Score 182; DB 1; Length 1567;  
Best Local Similarity 20.2%; Pred. No. 0.079;  
Matches 115; Conservative 83; Mismatches 274; Indels 98; Gaps 19;

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QY 77 GTGKEGTEGDSNVAAYFDEKRVLRKAGAITLKAGDNLKIKONTN-----ENTNENTNDSF 131
Db 735 GSTQSGSDSLTAGYGSTQTARKGSDVTAGYGSTGTAGADSTLIAGYGSTQTSKSSSL 794
QY 132 TYSUKKDLT-----DLTSVETEKLSFGA-----NGKNVITSTKGLNFAKE 173
Db 795 TAGYGSTQTARKGSDITAGYGSTGTAGADSTLIAGYGSTQTSKSSSLTAGYGSTQTARE 854
QY 174 -----TAGTNGDPTVHLNGIGSTLT---DTLLNTGATTNVTNDVTDKKAASV 221
Db 855 GSDVTAGYGSTGTAGADSTLIAGYGSTQTAGSDSLTAGYGSTQTARKGSD----- 905
QY 222 KDVLNAGWNINKGVKPGTASDNVDVFTYDTVEFLSADTKTTTNNVESKDKGRTEVKIG 281
Db 906 ---VTAGYGSTG-----TAGADSTLIAGYGSTQTSKSSSLTAGYGSTQTARKGSDMTAG 957
QY 282 AKTSVIREKDGKLVTKGKGENSGSTDEGELVTAKEVIDAVNKAGWRMTTNTANGTQ 341
Db 958 YGSTGTAGADSTLIAGYGSTQTSKSSSLTAGYGSTQTSKSSSLTAGYGSTQTSKSSSL 1003
QY 342 ADKFTVTSKTKVTFASNGTTFATVSKDDQGNITVKYDVNVGDALNVNQLNSGNWLDK 401
Db 1004 AGYGSTGTAGADSTLIAGYGSTQTAGSD---SSLTAGY-----GSTQTAGSDVTAGYGST 1057
QY 402 AVAGSSGKVISGNVSPSKMDKDETNNINAGNNIEITRNGKNIDIASTMPQTSVSSVLGAG 461
Db 1058 GTAGADSTLIAGYGSTQTAGSDSLTAGYGST-QTAGQSGDI-----TAGYGSTGT-AG 1109
QY 462 ADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKGGDVNTVNAOLKGVQNLNLRIDNV 521
Db 1110 ADSSLIA--GYGSTQTAGYDSNLTAGYGSTQTAGSDSLTAGYGSTTAGHDSLIAGY 1167
QY 522 GNARAGIAQAATA-GLAQAYLPCKSMMAIGGTYRGEAGY-----AIGYSSISDTG--NW 574
Db 1168 STQTAGYNSLITTCYGSTQTAGQESSSLTAGYGST--STAGYDSTLTAGYGSTQTAGYKST 1225
QY 575 VIKGTASGNSRGH-----FGTSASVGYQ 597
Db 1226 LTAGYGSNSTAGHSSSLIAGYGSTQIAGYE 1255
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## RESULT 14

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YMJUB_CAEEL STANDARD; PRT; 918 AA.
ID YMJUB_CAEEL
AC P34487;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Hypothetical 96.6 kDa protein F59B2.12 in chromosome III.
DE F59B2.12.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BRISTOL N2;
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
RA Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
```

RA	Johnston L., Jones M., Kershaw J., Kirsten J., Laister N.,
RA	Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
RA	Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
RA	Sims M., Smaldon J., Smith A., Smith M., Sonhammer E., Staden R.,
RA	Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
RA	Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
RA	Wohlman P.;
RT	"2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT	elegans.;"
RL	Nature 368:32-38(1994).
CC	-----
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CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC	entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/">http://www.isb-sib.ch/announce/</a>
CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; Z11505; CAA77581.1; -
DR	PIR; S31132; S31132
DR	WormPep; F5982.12; CE01024.
KW	Hypochemical protein.
SQ	SEQUENCE 918 AA; 965660 MW; E464FD86B14945DE CRC64;

Query Match	6.0%	Score 181;	DB 1;	Length 918;
Best Local Similarity	21.8%;	Pred. No. 0.047;		
Matches 129;	Conservative	89;	Mismatches 216;	Indels 158;
				Gaps 29;

[illegible]

RESULT 15  
OMPB\_RICTY

OMP<sub>B</sub>-RICTY STANDARD; PRT; 1645 AA.

P96989;  
15-JUL-1998 (Rel. 36, Created)  
16-JUL-1998 (Rel. 36, Last sequence update)  
16-OCT-2001 (Rel. 40, Last annotation update)

Outer membrane protein B precursor (168 kDa surface-layer protein) (Surface protein antigen) (Cell surface antigen 5) (ScA5) (rOmpB) (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide]. OMP<sub>B</sub> OR SLP.  
Rickettsia typhi.  
Bacteria; Proteobacteria; alpha subdivision; Rickettsiales; Rickettsiaceae; Rickettsiae; Rickettsia.  
NCBI\_TaxID=785;

[1]  
SEQUENCE FROM N.A.  
STRAIN=WILMINGTON;  
MEDLINE=94040787; PubMed=8224886;  
Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;  
"Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi.";  
Gene 133:129-133(1993).  
[2]

PARTIAL SEQUENCE.  
STRAIN=WILMINGTON;  
MEDLINE=921114896; PubMed=1370573;  
Ching W.N., Carl M., Dasch G.A.;  
"Mapping of monoclonal antibody binding sites on CNBr fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";  
Mol. Immunol. 29:95-105(1992).  
[3]

IDENTIFICATION OF CLEAVAGE SITE.  
MEDLINE=92104668; PubMed=1729180;  
Hackstadt T., Messer R., Cieplak W., Peacock M.G.;  
"Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: identification of an avirulent mutant deficient in processing";  
Infect. Immun. 60:159-165(1992).

-1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.  
-1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.  
-1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.  
-1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP<sub>B</sub> FAMILY.

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EMBL: L04661; AAB48987.1; -  
InterPro: IPR003858; rOmpA\_rOmpB.  
DR Pfam: PF02708; rOmpA\_rOmpB; 1.  
Antigen: S-layer; Transmembrane; Cell wall.  
FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.  
FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.  
FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).  
FT CONFLICT 657 657 H -> N (IN REF. 2).  
FT CONFLICT 842 842 V -> I (IN REF. 2).  
FT CONFLICT 1071 1071 G -> A (IN REF. 2).  
FT CONFLICT 1306 1306 G -> S (IN REF. 2).  
SQ SEQUENCE 1645 AA; 169698 MW; QCB5641C7EB185EE CRC64;

Query Match 6.0%; Score 181; DB 1; Length 1645;  
Best Local Similarity 20.6%; Pred. NO. 0.093;  
Matches 156; Conservative 91; Mismatches 271; Indels 238; Gaps 38;

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QY 28 KRASATVATAVLATLLEA-----TVQANATDDDDLYLE-----PVRT 65
Db 10 KIISAGLVATASTATIVAGFSGVAMGVQYQNRRTTNAATTVDGAGFDQTGAGVNLPVATN 69
QY 66 AVVLSFRSDKEGTEKEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTN-----119
Db 70 SVI-----TANSNNAITFTPNPNG-NLNSLFDTANTLAVTINENTTLGFV 113
QY 120 ENTNENTNDSFTYSKKDLT---DUTSVETEKLSFGAN-GNKVNI-----TSDTKGLN 169
Db 114 TNVTKQGNFNFTIGACKSLITIGHGITAQAAATTKSAQNVVSKVNAGAAINDNLSGVG 173
QY 170 FAKETAGTNGDPTVHLNGIGSTLTDTLNLTGATNVNTD-----NVTDDKKRAASYKDV 224
Db 174 SIDFTAAPS---VLEFNLIPTTQEAPLTLGDNAKIVNGANGILNITNGFVK-----VSDK 226
QY 225 LNAWNKIKGVKPGTTASDNVDVFTYTFVEELSADTKTTVVNESKD-----NGK 274
Db 227 TFAG--IKTINIGD--NOGLMFNTTPDAANALNLQGGGNTINFNRDGTGKLVLSKNGN 282
QY 275 RTEVKI---GAKTSVIKED---CKLVTGKKG-----ENGs-----STDEG- 310
Db 283 ATEFNVTGSLGGLKGVIEFDTTAAAGKLIANGAANAVIGTDNGAGRAAGFIVSDVNGN 342
QY 311 ----EGLVTAKEVIDAVNAKAGWRKTTTANGOT-----QOADKFETVTSCTKVT 356
Db 343 AATISGOVYAKDIV-----IQSANAGQVTFEHLVDVGLGKTNFKTADSKVIITE 393
QY 357 ASGNGTATVSKDQGNITVKYDVN-----VGDAIYNVQLONGWNLDSKAVAGSS 407
Db 394 NASFGST-----DFGNLAVQIVVPNNKILTNFNGFIDG-----KNG-NTAGVITFNAN 440
QY 408 GKVISGNVSPS-----KGMDETUNI-----NAGNNLEITRNGKNIDIAT 447
Db 441 GTLVSGWTDPNIVVTNKAIEVEGAGIVQLSGIHGAELRLGNAGSIFKLA-DGTVINGPV 499
QY 448 SMTQFSSVSLGAGA---DAPTLSDVD--EGALNVGSKD---ANKPVRTINVAP---GV 495
Db 500 NONPLVNNALAGSIQLDGSIIITGDIGNGAVNAALQDITLANDASKILTSGANIIGA 559
QY 496 KEG-----DVTNVAQLKGAON-----LNNRIDNV 520
Db 560 NAGGAIHQANGGTIQLTSTONNILDVDFDVTDDTQGVVDASSLTNNQTLTINGSIGTI 619
QY 521 DGNAR-----AGIAQAIATAG---LAQAYLPKGSMAIGGTY-----RGEAGYAIG 564
Db 620 GANTKTILGRENVSSTILNAGDVAINELVWENDGSVHLTHNTYLYITKTINAANQGGKIIV 679
QY 565 YSSISDTGNWVIKGTASGNSRG-----HFGTSASVG 595
Db 680 AADPINTDTALADCTNLGSAESPLSNTHFATKAANG 715
```

Search completed: July 3, 2002, 08:48:58  
Job time: 704 sec







QY 1 MNKISRIIWSALNAWVYSELTRNHTKRASATVAVLATLIFATVQANATDDDDLYLE 60  
 DB 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVAVLATLIFATVQANATDDDDLYLE 60  
 QY 61 PQVTAIVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120  
 DB 61 PQVTAIVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120  
 QY 121 NTNENTNDSFFYSLKDKLDTLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
 DB 121 NTNENTNDSFFYSLKDKLDTLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
 QY 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKRAASVKDVLNAGNVIKVKPGTTA 240  
 DB 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKRAASVKDVLNAGNVIKVKPGTTA 240  
 QY 241 SONVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIKEKDKGLVTGK 300  
 DB 241 SONVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIKEKDKGLVTGK 300  
 QY 301 GENGSTDEGEGLVTAKEVIDAVNKAAGWRMKTNTANGQTQADKPTVTSGTKVTFASGN 360  
 DB 301 GENGSTDEGEGLVTAKEVIDAVNKAAGWRMKTNTANGQTQADKPTVTSGTKVTFASGN 360  
 QY 361 GTTATVSKDDOQGNITVKYDVNVDGALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
 DB 361 GTTATVSKDDOQGNITVKYDVNVDGALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
 QY 421 KMDETVNIAGNNIETIRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
 DB 421 KMDETVNIAGNNIETIRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
 QY 481 DANKPVRITNAPGVKEGDTVNVQALKGVAQNLRNIDNVGNARAGIAQAATAGLAQA 540  
 DB 481 DANKPVRITNAPGVKEGDTVNVQALKGVAQNLRNIDNVGNARAGIAQAATAGLAQA 540  
 QY 541 YLPKGSMAIAGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRHFSTASVGYOW 598  
 DB 541 YLPKGSMAIAGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRHFSTASVGYOW 598

RESULT 4

QJ9PR9 ID QJ9PR9 PRELIMINARY; PRT: 598 AA.  
 AC QJ9PR9;  
 DT 01-OCT-2000 (TremBLrel. 15, Created)  
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
 DE OUTER MEMBRANE PROTEIN GNA992.  
 GN GNA992.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NGH36;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226382; AAF42531.1.  
 SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 98.0%; Score 2982; DB 2; Length 598;  
 Best Local Similarity 98.0%; Pred. No. 6.1e-116;

Matches 586; Conservative 2; Mismatches 10; Indels 0; Gaps 0;  
 QY 1 MNKISRIIWSALNAWVYSELTRNHTKRASATVAVLATLIFATVQANATDDDDLYLE 60  
 DB 1 MNKIYRIIWSALNAWVYSELTRNHTKRASATVAVLATLIFATVQANATDDDDLYLE 60  
 QY 61 PQVTAIVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120  
 DB 61 PQVTAIVLSFRSDKEGTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKONTNE 120  
 QY 121 NTNENTNDSFFYSLKDKLDTLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
 DB 121 NTNENTNDSFFYSLKDKLDTLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
 QY 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKRAASVKDVLNAGNVIKVKPGTTA 240  
 DB 181 PTVHLNGIGSTLTDLLNTGATTNTNDVTDDEKRAASVKDVLNAGNVIKVKPGTTA 240  
 QY 241 SONVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIKEKDKGLVTGK 300  
 DB 241 SONVDFVRTYDVEFLSADTKTTTVNVEKDKNGKRTVEKIGAKTSVIKEKDKGLVTGK 300  
 QY 301 GENGSTDEGEGLVTAKEVIDAVNKAAGWRMKTNTANGQTQADKPTVTSGTKVTFASGN 360  
 DB 301 GENGSTDEGEGLVTAKEVIDAVNKAAGWRMKTNTANGQTQADKPTVTSGTKVTFASGN 360  
 QY 361 GTTATVSKDDOQGNITVKYDVNVDGALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
 DB 361 GTTATVSKDDOQGNITVKYDVNVDGALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
 QY 421 KMDETVNIAGNNIETIRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
 DB 421 KMDETVNIAGNNIETIRNGKNIDATSMTPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
 QY 481 DANKPVRITNAPGVKEGDTVNVQALKGVAQNLRNIDNVGNARAGIAQAATAGLAQA 540  
 DB 481 DANKPVRITNAPGVKEGDTVNVQALKGVAQNLRNIDNVGNARAGIAQAATAGLAQA 540  
 QY 541 YLPKGSMAIAGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRHFSTASVGYOW 598  
 DB 541 YLPKGSMAIAGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRHFSTASVGYOW 598  
 RESULT 5  
 QJ9PH7 ID QJ9PH7 PRELIMINARY; PRT: 594 AA.  
 AC QJ9PH7;  
 DT 01-OCT-2000 (TremBLrel. 15, Created)  
 DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)  
 DT 01-DEC-2001 (TremBLrel. 19, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
 GN GNA992 OR NHHA.  
 OS Neisseria meningitidis.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BZ198, AND 297-0;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizza M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing."  
 RL Science 287:1816-1820(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BZ198;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;

RT "Identification and characterization of a gene encoding a novel outer  
membrane protein of *Neisseria meningitidis*.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226368; AAF42517.1; -;  
DR EMBL: AF226358; AAF42507.1; -;  
DR EMBL: AF157604; AAK68865.1; -;  
SQ SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;

Query Match 96.9%; Score 2948; DB 2; Length 594;  
Best Local Similarity 97.3%; Pred. No. 1.5e-114;  
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

QY 1 MNKISRIIWSALNANWVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
DB 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120  
DB 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 116  
QY 121 NTNENTNDSFTYSLKXDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
DB 121 NTNENTNDSFTYSLKXDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176  
QY 181 PTVHLNGIGSTLTDLTLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVPCTTA 240  
DB 177 PTVHLNGIGSTLTDLTLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVPCTTA 236  
QY 241 SDNVDFVRTYDVTVEFLSADTKTTTNNVYESKDNKRTTEVKIGAKTSVKEKDKGLVTGKG 300  
DB 237 SDNVDFVRTYDVTVEFLSADTKTTTNNVYESKDNKRTTEVKIGAKTSVKEKDKGLVTGKG 296  
QY 301 GENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFVTSCTKVTFAAGN 360  
DB 297 GENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFVTSCTKVTFAAGN 356  
QY 361 GTTATVSKDQGNITVYKVDYVNGDALVNLQNSGNWLDKAVAGSSGKVISGNVSPSKG 420  
DB 357 GTTATVSKDQGNITVYKVDYVNGDALVNLQNSGNWLDKAVAGSSGKVISGNVSPSKG 416  
QY 421 KMDETVINAGNIEITRNKGNIDIAISMTPOFSSVSLGAGADAPTLVSVDDEGALNVGSK 480  
DB 417 KMDETVINAGNIEITRNKGNIDIAISMTPOFSSVSLGAGADAPTLVSVDDEGALNVGSK 476  
QY 481 DANKPVRITVAPGVKGGDVTNVAQLKGVQNLNRRIDNVDGNARAGIAIAIATAGLAQA 540  
DB 477 DANKPVRITVAPGVKGGDVTNVAQLKGVQNLNRRIDNVDGNARAGIAIAIATAGLAQA 536  
QY 541 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVVKGTASGNSRGHFGTSASVGYOW 598  
DB 537 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVVKGTASGNSRGHFGTSASVGYOW 594

RESULT 6  
Q9JPS2 ID Q9JPS2 PRELIMINARY; PRT; 594 AA.  
AC Q9JPS2;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE31;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,  
R Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
*Meningococcus* by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226379; AAF42528.1; -;  
SQ SEQUENCE 594 AA; 62114 MW; 1E2A63A78F53D256 CRC64;

Query Match 94.7%; Score 2882; DB 2; Length 594;  
Best Local Similarity 95.3%; Pred. No. 8.1e-112;  
Matches 570; Conservative 6; Mismatches 18; Indels 4; Gaps 1;

QY 1 MNKISRIIWSALNANWVSELTRNHTKRASATVATAVLATLLFATVQANATDDDDLYLE 60  
DB 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVATAVLATLLFATVQASTDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120  
DB 61 PVQRTAVVLSFRSDEKTEGTEGSDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120  
QY 121 NTNENTNDSFTYSLKXDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180  
DB 121 NTNA-----SSFTYSLKXDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176  
QY 181 PTVHLNGIGSTLTDLTLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVPCTTA 240  
DB 177 PTVHLNGIGSTLTDLTLLTNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIKGVPCTTA 236  
QY 241 SDNVDFVRTYDVTVEFLSADTKTTTNNVYESKDNKRTTEVKIGAKTSVKEKDKGLVTGKG 300  
DB 237 SDNVDFVRTYDVTVEFLSADTKTTTNNVYESKDNKRTTEVKIGAKTSVKEKDKGLVTGKG 296  
QY 301 GENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFVTSCTKVTFAAGN 360  
DB 297 GENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFEFVTSCTKVTFAAGN 356  
QY 361 GTTATVSKDQGNITVYKVDYVNGDALVNLQNSGNWLDKAVAGSSGKVISGNVSPSKG 420  
DB 357 GTTATVSKDQGNITVYKVDYVNGDALVNLQNSGNWLDKAVAGSSGKVISGNVSPSKG 416  
QY 421 KMDETVINAGNIEITRNKGNIDIAISMTPOFSSVSLGAGADAPTLVSVDDEGALNVGSK 480  
DB 417 KMDETVINAGNIEITRNKGNIDIAISMTPOFSSVSLGAGADAPTLVSVDDEGALNVGSK 476  
QY 481 DANKPVRITVAPGVKGGDVTNVAQLKGVQNLNRRIDNVDGNARAGIAIAIATAGLAQA 540  
DB 477 DANKPVRITVAPGVKGGDVTNVAQLKGVQNLNRRIDNVDGNARAGIAIAIATAGLAQA 536  
QY 541 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVVKGTASGNSRGHFGTSASVGYOW 598  
DB 537 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGTGNWVVKGTASGNSRGHFGTSASVGYOW 594

RESULT 7  
Q9JPI3 ID Q9JPI3 PRELIMINARY; PRT; 594 AA.  
AC Q9JPI3;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS *Neisseria meningitidis*.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; *Neisseria*.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NG3/88, AND BZ232;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scariato V., Masignani V., Giuliani M.M., Arico' B.,



RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Huddt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN  
RP SEQUENCE FROM N.A.  
RC  
RX STRAIN=H38;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226383; AAF42532.1; -;  
DR EMBL: AF157608; AAK68869.1; -;  
SQ SEQUENCE 599 AA; 62844 MW; BBA16BEF53C1970C CRC64;

Query Match 92.8%; Score 2821.5; DB 2; Length 599;  
Best Local Similarity 92.7%; Pred. No. 2.5e-109;  
Matches 555; Conservative 13; Mismatches 30; Indels 1; Gaps 1;

QY 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATD-DDDLYL 59  
Db 1 MNKTYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDEDEEL 60  
QY 60 EPVORTAVLSFRSDKEGTEKEDTSNNAVYFDEKRVLKAGAITLKAGDNLKIKONTN 119  
Db 61 EPVRSALVLOFMIDKKGENSESTGWSIYDNNHTLHGATVTLKAGDNLKIKONTN 120  
QY 120 ENTNENTNDSFTYSLKKDLTSLVTEKLSFGANGKNYNTSDTKGLNFAKETAGTNG 179  
Db 121 KNTNENTNDSFTYSLKKDLTSLVTEKLSFGANGKNYNTSDTKGLNFAKETAGTNG 180  
QY 180 DPTVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIRKVPKPTT 239  
Db 181 DTTVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIRKVPKPTT 240  
QY 240 ASDNVDPVRYDTVEFLSADTKTTTVNVEKDKNGKREVKIGAKTSVKEKDKGLVTGK 299  
Db 241 ASDNVDPVRYDTVEFLSADTKTTTVNVEKDKNGKREVKIGAKTSVKEKDKGLVTGK 300  
QY 300 KGENSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFEVTSVSGTVPASG 359  
Db 301 KGENSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFEVTSVSGTVPASG 360  
QY 360 NGTTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 419  
Db 361 KGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420  
QY 420 GKMDETVINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGS 479  
Db 421 GKMDETVINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDDGALNVGS 480  
QY 480 KDANKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNRINDVNDGNARAGIAQATAGLAQ 539  
Db 481 KDANKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNRINDVNDGNARAGIAQATAGLVO 540  
QY 540 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGRHFTSASVGYQW 598  
Db 541 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGRHFTSASVGYQW 599

RESULT 10

Q9JPS6

ID Q9JPS6 PRELIMINARY; PRT: 600 AA.

AC Q9JPS6;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)

DE OUTER MEMBRANE PROTEIN GNA992.

GN GNA992.

OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E26;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Huddt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226371; AAF42520.1; -;  
SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;

Query Match 91.1%; Score 2772; DB 2; Length 600;  
Best Local Similarity 91.4%; Pred. No. 2.8e-107;  
Matches 553; Conservative 15; Mismatches 25; Indels 12; Gaps 3;

QY 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFAT-----VOANATD 53  
Db 1 MNKTYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOASADNVQASADN 60  
QY 54 DDDLYLPVORTAVLSFRSDKEGTEKEDTSNNAVYFDEKRVLKAGAITLKAGDNLK 113  
Db 61 EEEYLEPVVTVAPVLSFYSDAEDTGEKEVTENTNMGIYFDKNGVTKAGITITLKAGDNLK 120  
QY 114 IKONTNENTNDSFTYSLKKDLTSLVTEKLSFGANGKNYNTSDTKGLNFAKE 173  
Db 121 IKONTNENTNA----SFTYSLKKELTDLTSVTEKLSFGANGKNYNTSDTKGLNFAKE 176  
QY 174 TACTNGDPTVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIRK 233  
Db 177 TACTNGDPTVHLNGIGSTLTDLLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIRK 236  
QY 234 VKPGTTASDNVDPRYDTVEFLSADTKTTTVNVEKDKNGKREVKIGAKTSVKEKDKG 293  
Db 237 VKPGTTASDNVDPRYDTVEFLSADTKTTTVNVEKDKNGKREVKIGAKTSVKEKDKG 296  
QY 294 LVTKGKGENSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFEVTSVSGTK 353  
Db 297 LVTKGKGENSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTQADKFEVTSVSGTN 356  
QY 354 VTFASNGTGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISG 413  
Db 357 VTFASNGTGTATVSKDDQGNITVKYDYNVGDALNVNQLNSGWNLDKAVAGSSGKVISG 416  
QY 414 NVSPSKGMDETVINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVDEG 473  
Db 417 NVSPSKGMDETVINAGNNIETTRNGKNIDTATSMTPQFSSVSLGAGADAPTLSDVGD- 475  
QY 474 ALNVGSKDANKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNRINDVNDGNARAGIAQIA 533  
Db 476 ALNVGSKDANKPVRIITNAPGVKEGDTNVAQLKGVAQNLNNRINDVNDGNARAGIAQIA 535  
QY 534 TAGLAQAYLPKSMMAITGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGRHFTSAS 593  
Db 536 TAGLQAYLPKSMMAIGGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGRHFTSAS 595  
QY 594 VGYQW 598  
Db 596 VGYQW 600

RESULT 11

Q9JPS3

ID Q9JPS3 PRELIMINARY; PRT: 590 AA.

Q9JPS3;  
01-OCT-2000 (TREMBlrel. 15, Created)  
01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
OUTER MEMBRANE PROTEIN GNA992.  
GNA992.  
Neisseria meningitidis.  
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
NCBI\_TaxID=487;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=NGE28;  
MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,  
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappuoli R.;  
RT \*Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226378; AAF42527.1; -.  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 91.0%; Score 2769; DB 2; Length 590;

Best Local Similarity 92.3%; Pred. No. 3.7e-107;

Matches 554; Conservative 9; Mismatches 25; Indels 12; Gaps 3;

QY 1 MKKISRIIWNLSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATDDDL-L 59  
DB 1 MKKIYRIIWNLSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATDEEDL 60  
QY 60 EPVQRTAVVLSRDSKDEGTEGEGED-SNWAYFDEKRVLKAGAITLKAGDNLIKQNT 118  
DB 61 DPVQRTAVVLSRDSKDEGTEGEGEDSNWAYFDEKRVLKAGAITLKAGDNLIKQ-- 118  
QY 119 NENTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 178  
DB 119 -----NGTFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTN 170  
QY 179 GDTVHLNGIGSTLTDLLTGATNTVNDVTDDEKRAASVKDVLNAGWNIKGVKPGT 238  
DB 171 GDTVHLNGIGSTLTDLLTGATNTVNDVTDDEKRAASVKDVLNAGWNIKGVKPGT 230  
QY 239 TASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVKEKDGKLVTC 298  
DB 231 TASDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVKEKDGKLVTC 290  
QY 299 KGKGENSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQOAKDFETVTSKTVPFA 358  
DB 291 KGKGENSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQOAKDFETVTSKTVPFA 350  
QY 359 NGCTTATVSKDDQGNITVYKVDVNVGDALNVNOLQNSGNWLDKAVAGSSGKVISGNVSP 418  
DB 351 NGCTTATVSKDDQGNITVYKVDVNVGDALNVNOLQNSGNWLDKAVAGSSGKVISGNVSP 410  
QY 419 KGKMDETVINAGNNIEITRNKNIDIAISMTPPQFSSVSLGAGADAPTLVSDDGALNVG 478  
DB 411 KGKMDETVINAGNNIEITRNKNIDIAISMTPPQFSSVSLGAGADAPTLVSDDGALNVG 470  
QY 479 SKDANKPVRIITVAPGVKEGDVTNVQALKGVAQNLRIDNVGDNARAGIAQAIATAGLA 538  
DB 471 SKDANKPVRIITVAPGVKEGDVTNVQALKGVAQNLRIDNVGDNARAGIAQAIATAGLV 530  
QY 539 QAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQW 598  
DB 531 QAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQW 590

RESULT 12

Q9JPS8  
ID Q9JPS8 PRELIMINARY; PRT; 599 AA.  
AC Q9JPS8;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
OUTER MEMBRANE PROTEIN GNA992.  
GNA992.  
Neisseria meningitidis.  
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
NCBI\_TaxID=487;  
[1]  
SEQUENCE FROM N.A.  
RC STRAIN=A22;  
MEDLINE=20175756; PubMed=10710308;  
RA Pizzia M., Scarlato V., Massignani V., Giuliani M.M., Arico' B.,  
Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
Brocker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
Moxon E.R., Grandi G., Rappuoli R.;  
RT \*Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.\*;  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226364; AAF42513.1; -.  
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

Query Match 90.5%; Score 2752.5; DB 2; Length 599;

Best Local Similarity 91.7%; Pred. No. 1.8e-106;

Matches 551; Conservative 14; Mismatches 31; Indels 5; Gaps 3;

QY 1 MKKISRIIWNLSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLYL 59  
DB 1 MKKIYRIIWNLSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATDDEEYL 60  
QY 60 EPVQRTAVVLSRDSKDEGTEGEGEDSNWAYFDEKRVLKAGAITLKAGDNLIKQNTN 119  
DB 61 EPVQRTAVVLSRDSKDEGTEGEGEDSNWAYFDEKRVLKAGAITLKAGDNLIKQNTD 120  
QY 120 ENTNENTNDSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 179  
DB 121 ENTNENTNASSFTYSLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180  
QY 180 DPTVHLNGIGSTLTDLLTGATNTVNDVTDDEKRAASVKDVLNAGWNIKGVKPGTT 239  
DB 181 DPTVHLNGIGSTLTDLLTGATNTVNDVTDDEKRAASVKDVLNAGWNIKGVKPGTT 238  
QY 240 A--SDNVDFVRYTDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVKEKDGKLVTC 297  
DB 239 TQSGENVDFVRYTDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVKEKDGKLVTC 298  
QY 298 KGKGENSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQOAKDFETVTSKTVPFA 357  
DB 299 KGKGENSSSTDEGEGLVTAKEVIDAVNKAGWRMKTTTANGOTQOAKDFETVTSKTVPFA 358  
QY 358 SNGTGTATVSKDDQGNITVYKVDVNVGDALNVNOLQNSGNWLDKAVAGSSGKVISGNVSP 417  
DB 359 SNGTGTATVSKDDQGNITVYKVDVNVGDALNVNOLQNSGNWLDKAVAGSSGKVISGNVSP 418  
QY 418 SKGMDETVINAGNNIEITRNKNIDIAISMTPPQFSSVSLGAGADAPTLVSDDGALNV 477  
DB 419 SKGMDETVINAGNNIEITRNKNIDIAISMTPPQFSSVSLGAGADAPTLVSDDGALNV 478  
QY 478 GSKDANKPVRIITVAPGVKEGDVTNVQALKGVAQNLRIDNVGDNARAGIAQAIATAGL 537  
DB 479 GSKDANKPVRIITVAPGVKEGDVTNVQALKGVAQNLRIDNVGDNARAGIAQAIATAGL 538  
QY 538 QAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQ 597  
DB 539 QAYLPCKSMMAIGGGTYRGEAGYAGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQ 598

```
Qy 598 W 598
Db 599 W 599

RESULT 13
Q9JPR7
ID Q9JPR7 PRELIMINARY; PRT; 598 AA.
AC Q9JPR7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SW107;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Meningococcus by Whole-Genome Sequencing.;
RL Science 287:1816-1820(2000).
DR EMBL: AF226385; AAF42534.1; -.
SQ SEQUENCE 598 AA; 62431 MW; 0881CC094F33B4D4 CRC64;

Query Match 89.8%; Score 2733; DB 2; Length 598;
Best Local Similarity 90.8%; Pred. No. 1.1e-105;
Matches 545; Conservative 15; Mismatches 36; Indels 4; Gaps 2;

Qy 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60
Db 1 MNKIRIISALNANWVVSSELTRNHTKRASATVATVATLTLFATVOASATDDDDLYLE 60
Qy 61 PVQRTAVVLSFRSDKEGTEGSDSNWAVYFDEKRVKAGAITLKAGDNLIKQNTNE 120
Db 61 PVQRTAVVLSFRSDKEGTEGSDSNWAVYFDEKRVKAGAITLKAGDNLIKQNTNE 120
Qy 121 NTNENTNDSFTYSLKLDLTLSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Db 121 NTNENTNDSFTYSLKLDLTLSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 180
Qy 181 PTVHLNGISGTLTDLTLLNTGATTNVTNDVTDDEKRAASVKQVNLNAGWIKGVKPCQTA 240
Db 181 TTVHLNGISGTLTDLTLAGSASHVDAGNQST--HYTRAASIKQVNLNAGWIKGVKQSTT 238
Qy 241 --SDNVDFVRTYDVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVIREKDGKLVTKG 298
Db 239 GQSENVDFVRTYDVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVIREKDGKLVTKG 298
Qy 299 KGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFEFVTSKGVTFAS 358
Db 299 KGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFEFVTSKGVTFAS 358
Qy 359 GNGTATVSDDDQGNITVKYDVNVGDALNVNOLNSGNLDSKAVAGSSKGVISGNVSPS 418
Db 359 GNGTATVSDDDQGNITVKYDVNVGDALNVNOLNSGNLDSKAVAGSSKGVISGNVSPS 418
Qy 419 KGKMDETVNIAGNNIEITRNCKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVG 478
Db 419 KGKMDETVNIAGNNIEITRNCKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALNVG 478
Qy 479 SKDANKPVRITNVAPGVKGDVTNVAQLKGVAQNLRNDRIDNVGDNARAGIAQAATAGLV 538
Db 479 SKDANKPVRITNVAPGVKGDVTNVAQLKGVAQNLRNDRIDNVGDNARAGIAQAATAGLV 538

RESULT 14
Q9JPS7
ID Q9JPS7 PRELIMINARY; PRT; 591 AA.
AC Q9JPS7;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DE 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BZ147;
RX MEDLINE=20175756; PubMed=10710308;
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT Meningococcus by Whole-Genome Sequencing.;
RL Science 287:1816-1820(2000).
DR EMBL: AF226366; AAF42515.1; -.
SQ SEQUENCE 591 AA; 62113 MW; 533453CAE5A91E1F CRC64;

Query Match 89.3%; Score 2716.5; DB 2; Length 591;
Best Local Similarity 90.7%; Pred. No. 5.4e-105;
Matches 546; Conservative 13; Mismatches 28; Indels 15; Gaps 4;

Qy 1 MNKISRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATD---DDDL 57
Db 1 MNKIRIISALNANWVVSSELTRNHTKRASATVATVATLTLFATVOASANNEDEEDL 60
Qy 58 YLEPVQRTAVVLSFRSDKEGTEGSDSNWAVYFDEKRVKAGAITLKAGDNLIKQ 116
Db 61 YLPVQRTAVVLSFRSDKEGTEGSDSNWAVYFDEKRVKAGAITLKAGDNLIKQ 120
Qy 117 NTNENTNDSFTYSLKLDLTLSVETEKLSFGANGKNVITSDTKGLNFAKETAG 176
Db 121 -----NGNFTYSLKLDLTLSVETEKLSFGANGKNVITSDTKGLNFAKETAG 170
Qy 177 TNGDPTVHLNGISGTLTDLTLLNTGATTNVTNDVTDDEKRAASVKQVNLNAGWIKGVK 236
Db 171 TNGDPTVHLNGISGTLTDLTLLNTGATTNVTNDVTDDEKRAASVKQVNLNAGWIKGVK 230
Qy 237 GTTASDNVDFVRTYDVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVIREKDGKLV 296
Db 231 GTTASDNVDFVRTYDVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVIREKDGKLV 290
Qy 297 KGKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFEFVTSKGVTF 356
Db 291 GKDKNGSSTDEGEGLVTAKEVIDAVNKGWRMKTNTTANGOTGQADKFEFVTSKGVTF 350
Qy 357 ASNGTATVSKDDQGNITVKYDVNVGDALNVNOLNSGNLDSKAVAGSSKGVISGNVS 416
Db 351 ASGKGTATVSKDDQGNITVKYDVNVGDALNVNOLNSGNLDSKAVAGSSKGVISGNVS 410
Qy 417 PSKGMDETNIAGNNIEITRNCKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALN 476
Db 411 PSKGMDETNIAGNNIEITRNCKNIDIAATSMTPQFSSVSLGAGADAPTLSDVDEGALN 469
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:36:23 ; Search time 104.77 Seconds  
(without alignments)  
629.740 Million cell updates/sec

Title: US-09-771-382-9

Perfect score: 3023

Sequence: 1 MNRIYRIWNSALNAWVVS.....TASGNSRHCFASASVCYQW 594

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 11073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_032802:\*

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2: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1981.DAT:\*

3: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA1982.DAT:\*

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22: /SIDSI/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3023	100.0	594	20	AA1980
2	3023	100.0	594	22	AA1981
3	2971	98.3	598	20	AA1982
4	2971	98.3	598	22	AA1983
5	2948	97.5	598	20	AA1984
6	2948	97.5	598	22	AA1985
7	2874	95.1	594	20	AA1986
8	2874	95.1	594	22	AA1987
9	2874	95.1	594	20	AA1988
10	2802.5	92.7	599	20	AA1989
11	2802.5	92.7	599	22	AA1990

12	2750.5	91.0	591	21	AA1991
13	2740.5	90.7	591	20	AA1992
14	2740.5	90.7	591	20	AA1993
15	2740.5	90.7	591	22	AA1994
16	2733.5	90.4	592	20	AA1995
17	2721.5	90.0	591	20	AA1996
18	2721.5	90.0	591	22	AA1997
19	2664	88.1	592	20	AA1998
20	2664	88.1	592	22	AA1999
21	2573.5	85.1	589	20	AA2000
22	2573.5	85.1	589	22	AA2001
23	2552	84.4	592	22	AA2002
24	2516	83.2	592	20	AA2003
25	2448.5	81.0	513	22	AA2004
26	2442	80.8	512	22	AA2005
27	2359	78.0	502	22	AA2006
28	2223	73.5	604	22	AA2007
29	2025.5	67.0	433	22	AA2008
30	1879.5	62.2	407	22	AA2009
31	1330.5	44.0	2353	17	AA2010
32	1295.5	42.9	2411	21	AA2011
33	1079	35.7	1094	21	AA2012
34	1050	34.7	1098	17	AA2013
35	1043	34.5	245	20	AA2014
36	1011.5	33.5	679	17	AA2015
37	1011.5	33.5	679	21	AA2016
38	757	25.0	1002	21	AA2017
39	756	25.0	1004	21	AA2018
40	709	23.5	1104	21	AA2019
41	709	23.5	1104	21	AA2020
42	593	19.6	116	21	AA2021
43	396.5	13.1	2314	22	AA2022
44	385.5	12.8	2123	22	AA2023
45	383.5	12.7	1992	17	AA2024

#### ALIGNMENTS

RESULT 1

AA1980  
ID AA1980 standard; Protein; 594 AA.

AC AA1980

DT 08-SEP-1999 (first entry)

DE A surface protein of Neisseria meningitidis.

KW Surface protein; surface glycoprotein; infection; vaccine;

XX immunoreactive peptide.

OS Neisseria meningitidis.

PN WO9931132-A1.

PD 24-JUN-1999.

PF 14-DEC-1998; 98WO-AU01031.

PR 12-DEC-1997; 97GB-0026398.

PA (ISIS-) ISIS INNOVATION LTD.

PA (UYOU) UNIV QUEENSLAND.

PI Jennings MP, Moxon ER, Peak IRA;

XX WPI: 1999-418754/35.

DR N-PSDB; AA1980.

XX Neisseria meningitidis surface proteins useful for treating N.

PT meningitidis infections

XX

```
PS Claim 1; Page 95-97; 132pp; English.
XX The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX Sequence 594 AA;

Query Match 100.0%; Score 3023; DB 20; Length 594;
Best Local Similarity 100.0%; Pred. No. 4.3e-175;
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIWNSALNAMYVVSSELTNRHTRKASATVATAVLATLLFATVQANATDDDDLYLE 60
DB 1 mnkiyriiwnsalnawvvsseltnrhtrkrasatvatavlatllfatvqanatdddlyle 60

QY 61 PVQRTAVVLSFRSDKEGTGEGTSDENWAVYFDEKRVLRKAGAITLRKAGNLIKIKQNTNE 120
DB 61 pvgtrtavvlsfrsdkegtgegtednwavfyfdekrvllrkagaitlrkagdnlikikgtne 120

QY 121 NTNDSSTFYSIKKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180
DB 121 ntndsstfysikkdldtldtsveteklsfgangkvnitstdtkglnfaketagtngdpvh 180

QY 181 LINGIGSLTDLTLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNKIGVKPGTTASDNV 240
DB 181 lingigsltdltnltgattntvndvtddekraasvkdvlnagwnkigvkpgttasdnv 240

QY 241 DFVRTYTVFELSADTKTTTVNVSCKNGKKEVKGIGAKTSVKEKDKGLVTKGKDGKENG 300
DB 241 dfvrtvtfelsadtktttvnvsckngkkevkgigaktsvikekdgklvtgkdgkeng 300

QY 301 SSTDEGEGLVTAKEVIDAVNKAGWRMKTWTANGOTGQADKFETVTSCTNVTFAFGKGTGA 360
DB 301 sstdegeglvtakevidavnkagwrmtktwtangotgqadkfetvtsctnvtfaskgtga 360

QY 361 TVSKDDGNTIVKYDYVNVGDALNVNQLQNSGWNLDKRAVAGSSGKVISGNVSPSKGKXDE 420
DB 361 tvskddgntivkydyvngdalnvnqlqnsqwnldskravagssgkvisgnvspskgxde 420

QY 421 TVNINAGNIEITRNGKNIDIAISMATQFSSVSLGAGADAPTLSVDDEGALNVGSKDTNK 480
DB 421 tvninagnieitrngknidiatsmapqfssvslgagadaptilsvddegalnvsgskdtnk 480

QY 481 PVRTTNVAPGVKEGDTNVAQLKGVAONLNNRIDNVDSNARAGTAQATATAGLVQAYLPG 540
DB 481 pvrtnnvapgvkegdtnvaqlkgvaonlnnrindvdsnaragtaqataglvqaylpg 540

QY 541 KSMMAIGDGYRGEAGYAIGYSSISDGGNNIIKGTASGNSRGHFGASASGYQW 594
DB 541 ksmmaigdyrgeagyaigyssisdggnwiikgtasgnsrghfgasasyqgw 594

RESULT 2
AAU06179
ID AAU06179 standard; Protein; 594 AA.
XX
AC AAU06179;
XX
XX 24-OCT-2001 (first entry)
XX
DE N. meningitidis B2198 surface antigen NhhA polypeptide sequence.
XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX Neisseria meningitidis strain B2198.
QS
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XX FH Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region
FT 51..104
FT /label= V1
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FT /note= "Variable region 2"
FT Region
FT 127..190
FT /label= C3
FT /note= "Conserved region 3"
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FT 191..212
FT /label= V3
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FT Region
FT 232..238
FT /label= V4
FT /note= "Variable region 4"
FT Region
FT 239..594
FT /label= C5
FT /note= "Conserved region 5"
XX
XX WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU000069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09169.
XX
XX New NhhA surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen NhhA
XX (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen NhhA
XX from N. meningitidis strain B2198 is 1 of 10 NhhA polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX Sequence 594 AA;
XX SQ
```

Query Match 100.0%; Score 3023; DB 22; Length 594;  
Best Local Similarity 100.0%; Pred. No. 4.3e-175;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATDDDDLYLE 60  
DB 1 mnkiyriiwnlsalnawvvvseltnrhtrkrasatvatvatltilfatvqanaddddlyle 60

QY 61 PVQRTAVVLSFRSDKEGTEGEGEDSNWAVYFDEKRVLKAGAILKAGDNLIKQNTNE 120  
DB 61 pvrtravvlsfrsdkegtegedsnwavyfdekrvllkagailkagdnlikqntne 120

QY 121 NTNDSFYSYSLKDLTDLTSVETELSGANGKNYITSDTKGLNFAKETAGTNGDPTVH 180  
DB 121 ntndsfysylkdltdltsvetelsfgangknynitsdtkglnfaketagcngdptvh 180

QY 181 LNCIGSTLTDLLNFGATTNTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTASDNV 240  
DB 181 lngigstltdllnfgattntndvtddekkraasvkdvlmagwnikgvkpgttasdnv 240

QY 241 DFRVRYDVFELFADTKTTNVNVEKDKNGKTEVKIGAKTSVIEKDKGLVTGKGDENG 300  
DB 241 dfrvrydvtvelfadtkttnvnveskdngkktevkgaktsviekdkglvtgkgdeng 300

QY 301 SSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTGOADKRETVTSGTNVTFASGKGTTA 360  
DB 301 sstdegeglvtakevidavnkagwrmtntangqtgoadkretvtsgtnvtfasgkgtta 360

QY 361 TVSKDDQGNITVKYDYNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKGMD 420  
DB 361 tvskddqgnitvkydynvgdalnvnlqnsqwnldskavagssgkvisgnvpskgmd 420

QY 421 TVNINAGNNIETRNKKNIDIAATSMAPQFSSVSLGAGADAPTLSDDEGALNVGSKDNTK 480  
DB 421 tvninagnnietrnknidiatmapqfssvslgagadaptlsvddegalnvgskdntk 480

QY 481 PVRIITNAPGVKEGDTNVAQLKGVAQLNNRDNVGNARAGIAQATATAGLVAQYLP 540  
DB 481 pvriitnappgvkedtnvaqlkgvaqlnnrldnvgnaragiagataglvaylpg 540

QY 541 KSMMAIGDGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYQW 594  
DB 541 ksmmaigdgtyrgeagyaigyssisdggnwiikgtasnsrhfgasasvgyqw 594

## RESULT 3

AA06177  
ID AA06177 standard; Protein; 598 AA.

AC AA06177;

DT 08-SEP-1999 (first entry)

XX A surface protein of *Neisseria meningitidis*.

XX Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.

XX *Neisseria meningitidis*.

XX W0931132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

XX (UYOU) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

XX DR N-PSDB; AAX85794.

XX *Neisseria meningitidis* surface proteins useful for treating *N.*

PT meningitidis infections

PS Claim 1; Page 108-110; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria meningitidis* which is approximately 62 kDa. The *N. meningitidis* surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of *N. meningitidis* infection in humans. The *N. meningitidis* surface glycoproteins can also be used to prevent or treat *N. meningitidis* infection in humans, especially in the form of vaccines. The proteins and antibodies can also be used to identify immunoreactive peptides.

SQ Sequence 598 AA;

Query Match 98.3%; Score 2971; DB 20; Length 598;

Best Local Similarity 98.0%; Pred. No. 6.1e-172;

Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 1 MNKIYRIIWNLSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATDDDDLYLE 60

DB 1 mnkiyriiwnlsalnawvvvseltnrhtrkrasatvatvatltilfatvqanaddddlyle 60

QY 61 PVQRTAVVLSFRSDKEGTEGEGEDSNWAVYFDEKRVLKAGAILKAGDNLIKQNTNE 116

DB 61 pvrtravvlsfrsdkegtegedsnwavyfdekrvllkagailkagdnlikqntne 120

QY 117 NTNENTDSSFTYSLKDLTDLTSVETELSGANGKNYITSDTKGLNFAKETAGTNGD 176

DB 121 ntntndsfysylkdltdltsvetelsfgangknynitsdtkglnfaketagngd 180

QY 177 PVTHLNGTSTLTDLLNFGATTNTNDVTDDEKRAASVKDVLNAGWNIKGVKPGTTA 236

DB 181 pvthlngtstltdllnfgattntndvtddekkraasvkdvlmagwnikgvkpgtta 240

QY 237 SDNVDFVRYDVFELFADTKTTNVNVEKDKNGKTEVKIGAKTSVIEKDKGLVTGK 296

DB 241 sdnvdfvrydvtvelfadtkttnvnveskdngkktevkgaktsviekdkglvtgk 300

QY 297 DENGSTDEGGLVTAKEVIDAVNKGWRMKTNTANGQTGOADKRETVTSGTNVTFAS 356

DB 301 dengsstdegeglvtakevidavnkagwrmtntangqtgoadkretvtsgtnvtfas 360

QY 357 GTTATVSKDDQGNITVKYDYNVGDALNVNQLQNSGWNLDKAVAGSSGKVISGNVSPSKG 416

DB 361 gttatvskddqgnitvkydynvgdalnvnlqnsqwnldskavagssgkvisgnvpskg 420

QY 417 KMDETVNIINAGNNIETRNKKNIDIAATSMAPQFSSVSLGAGADAPTLSDDEGALNVGSK 476

DB 421 kmdeetvniinagnnietrnknidiatmapqfssvslgagadaptlsvddegalnvgsk 480

QY 477 DTNKPVRITNAPGVKEGDTNVAQLKGVAQLNNRDNVGNARAGIAQATATAGLVAQ 536

DB 481 dtnkpvritnappgvkedtnvaqlkgvaqlnnrldnvgnaragiagataglvaylpg 540

QY 537 YLPKGSMAAIGDGTYRGEAGYAGYSSISDGGNWIITKGTASGNSRHFASASVGYQW 594

DB 541 ylpkgssmaaigdgtyrgeagyaigyssisdggnwiikgtasnsrhfgasasvgyqw 598

## RESULT 4

AA06177

ID AA06177 standard; Protein; 598 AA.

XX AA06177;

XX 24-OCT-2001 (first entry)

XX *N. meningitidis* H15 surface antigen NHA peptide sequence.

XX Surface antigen NHA; meningococcal disease; meningitis vaccine.



```
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1: Page 91-93; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX Sequence 598 AA;
SQ
Query Match 97.5%; Score 2948; DB 20; Length 598;
Best Local Similarity 97.3%; Pred. No. 1.5e-170;
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;
QY 1 MNKIYRIIWSALNAWVVSSELTRNTRKASATVATVATLTLFATVQANATDDDDLYLE 60
Db 1 MNKIYRIIWSALNAWVVSSELTRNTRKASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PQVORTAVLSFRSDKRGTEGTEGSDNNAVVFDEKRVLKAGAITLKAGDNLKIKQ- --- 116
Db 61 PQVORTAVLSFRSDKRGTEGTEGSDNNAVVFDEKRVLKAGAITLKAGDNLKIKQ- --- 116
QY 117 NTNENTNDSFYSYSLKKDITLDTSVTEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
Db 117 NTNENTNDSFYSYSLKKDITLDTSVTEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
QY 177 PTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGVKPGTGA 236
Db 177 PTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNIGVKPGTGA 236
QY 237 SDNVDFRVTYDVEFLSADTKTTNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 296
Db 237 SDNVDFRVTYDVEFLSADTKTTNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 296
QY 297 DENGSTDEGEGLVTAKEVIDAVNKAQWTKTTTANGOTCOADKFTETVTSMTNVTFA 356
Db 297 DENGSTDEGEGLVTAKEVIDAVNKAQWTKTTTANGOTCOADKFTETVTSMTNVTFA 356
QY 301 GENGSTDEGEGLVTAKEVIDAVNKAQWTKTTTANGOTCOADKFTETVTSMTNVTFA 360
Db 301 GENGSTDEGEGLVTAKEVIDAVNKAQWTKTTTANGOTCOADKFTETVTSMTNVTFA 360
QY 357 GTTATVSKDDQGNITVKYDVNVDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKG 416
Db 357 GTTATVSKDDQGNITVKYDVNVDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKG 416
QY 361 GTTATVSKDDQGNITVKYDVNVDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKG 420
Db 361 GTTATVSKDDQGNITVKYDVNVDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKG 420
QY 417 KMDETVNIAGNNIETRNKKNIDTATSNAPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476
Db 417 KMDETVNIAGNNIETRNKKNIDTATSNAPOFSSVSLGAGADAPTLSDVDEGALNVGSK 476
QY 477 DFNKPVRIITNAPGVKREGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQATATGLVOA 536
Db 477 DFNKPVRIITNAPGVKREGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQATATGLVOA 536
QY 481 DANKPVRIITNAPGVKREGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQATATGLVOA 540
Db 481 DANKPVRIITNAPGVKREGDVTNVAQLKGVAQNLNRRIDNVGNARAGIAQATATGLVOA 540
QY 537 YLPKSNMAIGDITYRGEAGYAIYSSISDGGNWIITKGTASGNSRGRHFGASASVGYQW 594
Db 537 YLPKSNMAIGDITYRGEAGYAIYSSISDGGNWIITKGTASGNSRGRHFGASASVGYQW 594
QY 541 YLPKSNMAIGDITYRGEAGYAIYSSISDGGNWIITKGTASGNSRGRHFGASASVGYQW 598
Db 541 YLPKSNMAIGDITYRGEAGYAIYSSISDGGNWIITKGTASGNSRGRHFGASASVGYQW 598
RESULT 6
AAU06178
ID AAU06178 standard; Protein: 598 AA.
XX
AC AAU06178;
XX
XX 24-OCT-2001 (first entry)
XX
DE N. meningitidis B210 surface antigen NhhA polypeptide sequence.
```

```
XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.
KW Neisseria meningitidis strain B210.
XX
OS Neisseria meningitidis strain B210.
XX
FH Key Location/Qualifiers
FT Region 1..50
FT /label= C1
FT /note= "Conserved region 1"
FT Region 51..104
FT /label= V1
FT /note= "Variable region 1"
FT Region 105..116
FT /label= C2
FT /note= "Conserved region 2"
FT Region 117..130
FT /label= V2
FT /note= "Variable region 2"
FT Region 131..194
FT /label= C3
FT /note= "Conserved region 3"
FT Region 195..216
FT /label= V3
FT /note= "Variable region 3"
FT Region 217..235
FT /label= C4
FT /note= "Conserved region 4"
FT Region 236..242
FT /label= V4
FT /note= "Variable region 4"
FT Region 243..598
FT /label= C5
FT /note= "Conserved region 5"
XX
PN WO200155182-A1.
XX
XX 02-AUG-2001.
XX
XX 25-JAN-2001; 2001WO-AU00069.
XX
XX 25-JAN-2000; 2000US-0177917.
XX
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX
XX WPI; 2001-488774/53.
XX
XX N-PSDB; AAS09168.
XX
XX New NhhA surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen NhhA
XX (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen NhhA
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
XX Sequence 598 AA;
```

```
Query Match      97.5%; Score 2948; DB 22; Length 598;
Best Local Similarity 97.3%; Pred. No. 1.5e-170;
Matches 582; Conservative 2; Mismatches 10; Indels 4; Gaps 1;

QY 1 MNKIYRIIWNLSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 mnkisirliwnsalnawvvsveltrnhtkrasatvatvatltilfatvqanatdddddyle 60

QY 61 PVORTAVVLFSRDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKO--- 116
DB 61 pvtartavvlfsrdskegtgekedtsnwaavyfdekrvllkagaitllkagdnllkikntne 120

QY 117 NTNENTNDSSFTYSLKDDI/PDLTSVETEKLSFGANGKNVITSDTKGLNPAKETAAGTNGD 176
DB 121 ntentndssftysllkddildtsveteklsfgangknvitsdtkglnfaketaagtagnd 180

QY 177 PTVHLNGIGSTLDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIKGVPGETTA 236
DB 181 ptvhlngigstltdtllntgattnvtndvdekkraasvkdvlalnagwnikgvpgetta 240

QY 237 SDNVDFVRTYDTVEFLSADTKTTNNVESKNGKTEVKIGAKTSVKEKDKGLVTCKGK 296
DB 241 sdnvdfvrtvdtveflsadtkttnnveskngktevkiaktsvikekdglvtckgk 300

QY 297 DENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTQADKFETVTSNTVTFASGK 356
DB 301 dengssddegglvtakevidavnkgwrmtttfngotqadkfetvtsntvtfasgn 360

QY 357 GTTATVSKDDOGNITVKYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSKG 416
DB 361 gttatvskddognitvkydvnvgdalnvqlnsgnwldskavagssgkvsgnvspsgk 420

QY 417 KMDETVNIAGNIEITRNKNIDTSMAPQSSVSLGAGADAPTLSDVDEGALNVGSK 476
DB 421 kmdetvniagnieitrngknidtsmtppqssvslgagadaptlsvddegalnvgsk 480

QY 477 DTNKPVRITNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQA 536
DB 481 dtnkpvrntnvapgvkegdvntvnaqlkgvaqnlnrindnvgnaragiaaiataglaqa 540

QY 537 YLPKSKMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
DB 541 ylpkksmmaiggytyrgeagyaigyssisdggnwniigktasgnsrghfgtsasvgyqw 598

RESULT 7
AAV23740
ID AAY23740 standard; Protein; 594 AA.
XX
AC AAY23740;
XX
XX 08-SEP-1999 (first entry)
XX
DE A surface protein of Neisseria meningitidis.
XX
KW Surface protein; surface glycoprotein; infection; vaccine;
KW immunoreactive peptide.
XX
OS Neisseria meningitidis.
XX
PN WO9931132-A1.
XX
XX 24-JUN-1999.
XX
XX 14-DEC-1998; 98WO-AU01031.
XX
XX 12-DEC-1997; 97GB-0026398.
XX
XX (ISIS-) ISIS INNOVATION LTD.
XX (UYQU ) UNIV QUEENSLAND.
XX
XX Jennings MP, Moxon ER, Peak IRA;
PI
XX
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```
DR WPI; 1999-418754/35.
XX N-PSDB; AAX85792.
XX Neisseria meningitidis surface proteins useful for treating N.
PT meningitidis infections
XX
XX Claim 1; Page 100-101; 132pp; English.
XX
CC The present sequence represents a surface protein of Neisseria
CC meningitidis which is approximately 62 kDa. The N. meningitidis
CC surface glycoproteins, nucleic acids, the primers and optionally
CC a thermostable polymerase, or antibodies are useful in a kit for
CC the detection or diagnosis of N. meningitidis infection in humans.
CC The N. meningitidis surface glycoproteins can also be used to
CC prevent or treat N. meningitidis infection in humans, especially
CC in the form of vaccines. The proteins and antibodies can also
CC be used to identify immunoreactive peptides.
XX
XX Sequence 594 AA;
SQ
```

```
Query Match      95.1%; Score 2874; DB 20; Length 594;
Best Local Similarity 95.6%; Pred. No. 4.5e-166;
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 mnkiryiwnsalnawvvsveltrnhtkrasatvatvatltilfatvqastdddddyle 60

QY 61 PVORTAVVLFSRDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
DB 61 pvtartavvlfsrdskegtgekedtsnwaavyfdekrvllkagaitllkagdnllkikqntne 120

QY 121 NTNDSSTYSIKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAAGTNGDPTVH 180
DB 121 ntnassftysllkddildtsveteklsfgangknvitsdtkglnfaketaagtagnd 180

QY 181 LNGIGSTLDTLLNTGATTNVTNDVDEKKRAASVKDVLNAGWNIKGVPGETTASDNV 240
DB 181 lngigstltdtllntgattnvtndvdekkraasvkdvlalnagwnikgvpgettasdnv 240

QY 241 DFVRTYDTVEFLSADTKTTNNVESKNGKTEVKIGAKTSVKEKDKGLVTCKGKDENG 300
DB 241 dfvrtvdtveflsadtkttnnveskngktevkiaktsvikekdglvtckgkde 300

QY 301 SSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTQADKFETVTSNTVTFASGKGTTA 360
DB 301 sstdekglvtakevidavnkgwrmtttfngotqadkfetvtsntvtfasgkgtta 360

QY 361 TVSKDDOGNITVKYDVNVGDALNVQLNSGNWLDKAVAGSSGKVISGNVSPSKGRMDE 420
DB 361 tvskddognitvkydvnvgdalnvqlnsgnwldskavagssgkvsgnvspsgk 420

QY 421 TVTNAGNIEITRNKNIDTSMAPQSSVSLGAGADAPTLSDVDEGALNVGSKDNTK 480
DB 421 tvtnagnieitrngknidtsmtppqssvslgagadaptlsvddegalnvgskdank 480

QY 481 PVRTNVAPGVKEGDTVNTVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLP 540
DB 481 pvrntnvapgvkegdvntvnaqlkgvaqnlnrindnvgnaragiaaiataglvaylp 540

QY 541 KSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594
DB 541 ksmmaiggytyrgeagyaigyssisdggnwniigktasgnsrghfgasasvgyqw 594
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```
RESULT 8
AAV57044
ID AAY57044 standard; Protein; 594 AA.
XX
XX AAY57044;
XX
XX 21-FEB-2000 (first entry)
DT
```

XX BASB029 amino acid sequence from N. meningitidis strain ATCC13090.  
XX  
KW BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;  
KW infection; treatment; prevent; antibacterial drug.  
XX  
OS Neisseria meningitidis.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 104 /note= "Encoded by AATC"  
FT  
XX  
PN W09958683-A2.  
XX  
PD 18-NOV-1999.  
XX  
XX 07-MAY-1999; 99WO-EP03255.  
PF  
XX 13-MAY-1999; 98GB-0010276.  
PR (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.  
PA  
PA Ruelle J;  
PI  
XX WPI; 2000-053103/04.  
DR N-PSDB; AA239864.  
DR  
XX  
XX New polypeptide from neisseria meningitidis useful for diagnosis,  
PT treatment or prevention of bacterial infections in mammal -  
XX  
XX Claim 4; Fig 2; 74pp; English.  
XX  
XX This is the Neisseria meningitidis BASB029 amino acid sequence from  
CC serogroup B strain ATCC13090. The BASB029 protein is homologous to the  
CC Haemophilus influenzae surface fibril (HSF) protein. The invention  
CC relates to BASB029 polynucleotide sequences (AA239864-Z39865) and  
CC polypeptide sequences (AA57044-Y57045) and their immunogenic fragments.  
CC BASB029 polypeptides are useful in a method of diagnosing a Neisseria  
CC meningitidis infection in a mammal. Compositions containing a Neisseria  
CC polynucleotides and polypeptides are useful for generating an immune  
CC response in an animal. A therapeutic composition comprising an antibody  
CC directed against BASB029 is useful in treating humans with Neisseria  
CC meningitidis disease. The polynucleotide is useful in the diagnosis of  
CC the stage of infection, type of infection, susceptibility to an  
CC infection which results from increased or decreased expression of the  
CC polynucleotide, and for therapeutic or prophylactic purposes.  
CC particularly genetic immunisation. Antibodies against BASB029  
CC polynucleotides and polypeptides are also useful for treating infections  
CC particularly bacterial infections. The protein is useful in the  
CC screening and development of antibacterial drugs. Fused recombinant  
CC protein is useful for the stimulation of the immune system of an organism  
CC receiving the protein.  
XX  
SQ Sequence 594 AA;

Query Match 95.1%; Score 2874; DB 21; Length 594;  
Best Local Similarity 95.6%; Pred. No. 4.5e-166;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIMNSALNMAVWVSELTNRHTRKASATVATVATLTLFAIVQANATDDDDLYLE 60  
Db 1 mnkiyriiwnsalnawvavseltrnrhtkrasatvatvatltilfatvqastddldlyle 60  
QY 61 PVORTAVWLSFRSDKGTGKTEGKTESNNAVYFDEKRVLKAGAITLKAGNLKIKQNTNE 120  
Db 61 pvdrtavvlsfrsdkgtegektevtdsnwgyfdkkgvltagtitlkagdnlkikgntne 120  
QY 121 NTNDSSFTYSLLKKDLTDLTSVTEKLSFGANGKNVNTSDTKGLNFAKTAGTNGDPTVH 180  
Db 121 ntndssftysllkkdltdltsvtekteklsfsgangknvntsdtkglntfakktagtgngdptvh 180  
QY 181 LNGIGSTLTDLTLTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTASDNV 240  
XX

Db 181 lngigstltdlntgattntndvtddekkraasvkdvlnagwnkvgkpgttasdnv 240  
QY 241 DFVRYTDTVEFLSADTKTTNVNVEKDNKGKTEVKIGAKTSVKEKDGKLVTCGKDGDEG 300  
Db 241 dfvrytdtveflsadtktttvnveskdngkrtevkigaktsvkekdgklvtgdkgend 300  
QY 301 SSTDEGEGLVTAKEVIDAVNKAQWRMKTTTTANGOTGOADKFETVTSGTNVTFASGKGTTA 360  
Db 301 sstdkgeglvtakevidavnkagwrmttttangotgqadkfetvtsgtnvtfasgkgtta 360  
QY 361 TVSKDDQGNITVKYDVNVGDALNVNQLQNSWNLDKAVAGSSGKVISGNVSPSKGKMD 420  
Db 361 tvskddqgnitvmydvnvgdalnvnqlqnswnldskavagssgkvisgnvspskgkmd 420  
QY 421 TVNINAGNIEITRNKGNIDDIATSMAPQPSVSLGAGADAPTLSVDEGALNVGSKDNTK 480  
Db 421 tvninagnieltrngknidiaatcmtppqfssvslgagadaptsvdegalnvvgskdank 480  
QY 481 PVRITNVAPGVKREGDVTNVAQLKGVQNLNNDVGNARAGIAQAIATPAGLVQAYLPG 540  
Db 481 pvrntnvapgvkegdvtlnvaqlkgvqnlndvndgnaraglaiaataglvqaylpg 540  
QY 541 KSMMAIGDITYRGEAGYATGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 594  
Db 541 ksmmaigggtyrgeagyatgyssisdggwnwikgtasgnsrghfgasasvgyqw 594

RESULT 9  
AAU06174  
ID AAU06174 standard; Protein; 594 AA.  
XX  
AC AAU06174;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis EG327 surface antigen Nhma polypeptide sequence.  
XX  
KW Surface antigen Nhma; meningococcal disease; meningitis vaccine.  
XX  
OS Neisseria meningitidis strain EG327.  
XX  
FH Key Location/Qualifiers  
FT Region 1..50 /label= C1  
FT /note= "Conserved region 1"  
FT Region 51..104 /label= V1  
FT /note= "Variable region 1"  
FT Region 105..116 /label= C2  
FT /note= "Conserved region 2"  
FT Region 117..126 /label= V2  
FT /note= "Variable region 2"  
FT Region 127..190 /label= C3  
FT /note= "Conserved region 3"  
FT Region 191..212 /label= V3  
FT /note= "Variable region 3"  
FT Region 213..231 /label= C4  
FT /note= "Conserved region 4"  
FT Region 232..238 /label= V4  
FT /note= "Variable region 4"  
FT Region 239..594 /label= C5  
FT /note= "Conserved region 5"  
XX  
PN W0200155182-A1.  
XX

PD 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-AU00069.  
XX 25-JAN-2000; 2000US-0177917.  
XX (UYQU ) UNIV QUEENSLAND.  
XX Peak IRA, Jennings MP;  
XX WPI; 2001-488774/53.  
XX N-PSDB; AAS09164.  
XX  
PT New Nhha surface antigen polypeptides and polynucleotides from  
PT Neisseria meningitidis, useful in producing vaccines for treating or  
PT preventing broad spectrum of Neisseria meningitidis -  
XX  
PS Claim 9; Fig 1; 9lpp; English.  
XX  
CC The present invention relates to the isolation of novel Neisseria  
CC meningitidis mutant polypeptides of the surface antigen Nhha  
CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
CC characterised by deletions of non-conserved amino acids, particularly  
CC the deletion of variable regions. The deletion mutants are useful in  
CC diagnostics, therapeutic and prophylactic vaccines against a broader  
CC spectrum of N. meningitidis, and in designing and/or screening of  
CC medicaments. The mutant proteins when used as a vaccine can effectively  
CC immunise against a broader spectrum of N. meningitidis strains than  
CC would be expected from a corresponding wild-type surface antigen.  
CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain EG327 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
XX the present invention.  
XX  
SQ Sequence 594 AA;

Query Match 95.1%; Score 2874; DB 22; Length 594;  
Best Local Similarity 95.6%; Pred. No. 4.5e-166;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

Qy 1 MNKYRIIWNALNAWVVSSELTRNHTKRASATVATVATLILFATVOANATD-DDDLYLE 60  
Db 1 mnkyriiwnsalnawvavseltrnhtkrasatvatavlatilfatvqastddldyle 60  
Qy 61 PQVQTAIVLSFRSDEKGTGEGTSDSNWVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
Db 61 pvtatvlsfrsdekgtegevedtsnwgvyfddkkgvltagttikagdnkikqntne 120  
Qy 121 NTNDSSTFYSLLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGDPTVH 180  
Db 121 ntnassfyslkkdltdltsvgtelksfnsankvnitsdtkglnfaketaetngdttvh 180  
Qy 181 LINGISLTDLTLNTGATTNTNVDDEKRAASVKDVLNAGWNKGVKPGTTASDNV 240  
Db 181 lngisgltldlntgattntvndtdekkraasvkdvlmagwnlkgvkgpgttasdnv 240  
Qy 241 DFVRTYDFEFLSADTKTTTNNVSKONGKKEVIGAKTSVKEKDGKLVTKGKDENG 300  
Db 241 dfvrtvdfelsadtkttttnvskongkrtvkgaktsvkekgdglvkgkdgnd 300  
Qy 301 SSTDEGLEVLTAKEVIDAVNKGWRMTTANGOTGOADKFETVTSCTNVTFAFGKGTGA 360  
Db 301 sstdkgelvtakevidavnkagwrmttangotgqadkfetvtsctnvtfaskgtga 360  
Qy 361 TVSKDDQGNITVYDVNVGDALNVQNLONSGWNLDSRAVAGSSKGVISGNVSPSGKMD 420  
Db 361 tvskddqgnitvymdvngvdalnvnqnlqsgwnldskavagssgkvvisgnvpskgmde 420  
Qy 421 TVNINAGNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSDDEGALNVGSKDTNK 480  
Db 421 tvninagnieitrngknidiatsmtpqfssvslgagadaptlsvddegalnvgskdank 480

Qy 481 PVRITNVAPGVKEGDTNVAQLKGVANLNINRDNVDGNARAGIAQAIATAGLVQAYLPG 540  
Db 481 pvrntnvpvgvkegdvtnvaqlkgvaqlnnhndvndgnaragiataglvqaylpg 540  
Qy 541 KSMMAIGDFTYRGEAGYAGYSSISDGGNWIITKTASGNSRCHFGASASGVQW 594  
Db 541 ksmmaig99tyrgeagyalgysissdgggnwiikgtasgnsrghfgasasgvqw 594

RESULT 10.  
AAI23743

ID AAY23743 standard; Protein; 599 AA.

XX AAY23743;

XX 08-SEP-1999 (first entry)

XX A surface protein of Neisseria meningitidis.

XX Surface protein; surface glycoprotein; infection; vaccine;  
XX immunoreactive peptide.

XX Neisseria meningitidis.

XX WO9931132-A1.

XX 24-JUN-1999.

XX 14-DEC-1998; 98WO-AU01031.

XX 12-DEC-1997; 97GB-0026398.

XX (ISIS-) ISIS INNOVATION LTD.

XX (UYQU ) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI; 1999-418754/35.

XX N-PSDB; AAX85795.

XX Neisseria meningitidis surface proteins useful for treating N.  
XX meningitidis infections

XX Claim 1; Page 114-115; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
XX meningitidis which is approximately 62 kDa. The N. meningitidis  
XX surface glycoproteins, nucleic acids, the primers and optionally  
XX a thermostable polymerase, or antibodies are useful in a kit for  
XX the detection or diagnosis of N. meningitidis infection in humans.  
XX The N. meningitidis surface glycoproteins can also be used to  
XX prevent or treat N. meningitidis infection in humans, especially  
XX in the form of vaccines. The proteins and antibodies can also  
XX be used to identify immunoreactive peptides.

XX Sequence 599 AA;

Query Match 92.7%; Score 2802.5; DB 20; Length 599;  
Best Local Similarity 92.5%; Pred. No. 9.6e-162;  
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;

Qy 1 MNKYRIIWNALNAWVVSSELTRNHTKRASATVATVATLILFATVOANATD-DDDLYLE 59  
Db 1 mnkyriiwnsalnawvavseltrnhtkrasatvatavlatilfatvqanadedeeel 60  
Qy 60 EPVORTAVVLSFRSDEKGTGEGTSDSNWVYFDEKRVLKAGAITLKAGDNLKIKQ--- 116  
Db 61 epvrsalvlqfmidkegngengestngwsiyydnhnhtlbgatvltkagdnkikqntn 120  
Qy 117 -NTNENTNDSSTFYSLLKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNG 175  
Db 121 kntnentndssftysllkdltdltsveteklsfgangknvnitsdtkglnfaketagtng 180



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QY 176 DPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGNNIKGVKPGTT 235
DB 181 dtvhlngigstltdtllntgattvndvtdckkkaasvkvdlngagwnlkgvkgpgct 240
QY 236 ASDNVDFVRTYDVBFLSADTKTTTNNVESKDKGKTEYKIGAKTSVIREKDGKLVTKGK 295
DB 241 asdnvdfvhtydtvflsadtktttvnnveskdngkrtvkvigaktsvirekdgkclvtgk 300
QY 296 KDNSSSTDEGEGLVTAKEVIDAVNKAGHRMKTITTTANGOTGOADKFEVTSGTNVTFASG 355
DB 301 kgengsstdegeglvtakevidavnkagwrmtttcangtgqadkfetvtsgtntvfag 360
QY 356 KGTATVSKDDOGNTVYKDYDNNVGDALNNOLNSGNWLDKAVAGSSGKVISGNVSPSK 415
DB 361 kgtatvskddogntvkvdydnnvgdnlvnglqnsagnwldskavagssgkvisgnvpsk 420
QY 416 GKMDETVNTNAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDDEGALNVGS 475
DB 421 gkmdetvnnagnnieitrngknidiatsmtpfssvslgagadapltlsvddkgalnvgs 480
QY 476 KDTNKPVRITNVPAGVKEGDVTNVAQLKGYAQNLRINDVNGNARAGIAQAIAITAGLVQ 535
DB 481 kdtnkpvrntnvpagvkegdvtnvaqlkgvaqnlrindvngnragiaqalaglvq 540
QY 536 AYLPGKSMMAIGDTRVGEAGYAIGVSSISDGGNWIITKGTASGNSRGHFGASASVGYOW 594
DB 541 aylpgksmmaiggytrgeagyaigyssisdggnwiikgtasgnsrghfgasasvgyow 599

RESULT 11
AAU06176
ID AAU06176 standard; Protein; 599 AA.
XX AC AAU06176;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis H38 surface antigen Noha polypeptide sequence.
XX KW Surface antigen Noha; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain H38.
XX FH Key
XX FT Location/Qualifiers
XX FT 1..50 /label= C1
XX FT 51..105 /note= "Conserved region 1"
XX FT 106..117 /label= V1
XX FT 118..131 /note= "Conserved region 2"
XX FT 132..195 /label= V2
XX FT 196..217 /note= "Conserved region 3"
XX FT 218..236 /label= V3
XX FT 237..243 /note= "Conserved region 4"
XX FT 244..599 /label= V4
XX FT /note= "Conserved region 5"
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PN WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYOU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
XX WPI; 2001-488774/53.
XX N-PSDB; AAS09166.
XX New Noha surface antigen polypeptides and polynucleotides from
XX preventing broad spectrum of Neisseria meningitidis -
XX Claim 9; Fig 1; 91pp; English.
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Noha
XX (AAU06182-AAU06186). The modified or mutant Noha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX immunisations. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Noha
XX from N. meningitidis strain H38 is 1 of 10 Noha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX Sequence 599 AA;
XX SQ
XX Query Match 92.7%; Score 2802.5; DB 22; Length 599;
XX Best Local Similarity 92.5%; Pred. No. 9.6e-162;
XX Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;
QY 1 MNKIYRIWNSALNAWVYSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLVL 59
DB 1 mkiyriwnsalnawvyseltrnhtkrasatvkvavlattllfatvqanadedeeel 60
QY 60 EPVQRTAVVLSFRSDKEGTGEKGTEDSNWAVYFDEKRVLKAGAITLKAGDNLKIKO--- 116
DB 61 epvrsalvlqfmidkegenestgnigwsiyddnhtlhgatvtlkgadnlkikqntn 120
QY 117 -NTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNG 175
DB 121 kntnentndssftyslkkdltdltsveteklsfgangknvntsdtkglnfaketagtn 180
QY 176 DPTVHLNGIGSTLDTLLNTGATTNVTNDVTDDEKRAASVKDVLNAGNNIKGVKPGTT 235
DB 181 dtvhlngigstltdtllntgattvndvtdckkkaasvkvdlngagwnlkgvkgpgct 240
QY 236 ASDNVDFVRTYDVBFLSADTKTTTNNVESKDKGKTEYKIGAKTSVIREKDGKLVTKGK 295
DB 241 asdnvdfvhtydtvflsadtktttvnnveskdngkrtvkvigaktsvirekdgkclvtgk 300
QY 296 KDNSSSTDEGEGLVTAKEVIDAVNKAGHRMKTITTTANGOTGOADKFEVTSGTNVTFASG 355
DB 301 kgengsstdegeglvtakevidavnkagwrmtttcangtgqadkfetvtsgtntvfag 360
QY 356 KGTATVSKDDOGNTVYKDYDNNVGDALNNOLNSGNWLDKAVAGSSGKVISGNVSPSK 415
DB 361 kgtatvskddogntvkvdydnnvgdnlvnglqnsagnwldskavagssgkvisgnvpsk 420
QY 416 GKMDETVNTNAGNNIEITRNGKNIDIATSMAPQFSSVSLGAGADAPTLSVDDDEGALNVGS 475
DB 421 gkmdetvnnagnnieitrngknidiatsmtpfssvslgagadapltlsvddkgalnvgs 475
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PN W09936344-A2.  
XX 22-JUL-1999.  
XX 14-JAN-1999; 99WO-IB00103.  
XX 09-OCT-1998; 98GB-0022143.  
PR 14-JAN-1998; 98GB-0000760.  
PR 01-SEP-1998; 98GB-0019015.  
XX (CHTR-) CHIRON SPA.  
XX Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;  
XX WPI: 1999-444400/37.  
DR N-PSDB; AAX99124.  
XX New protein and its nucleotide sequence, useful in vaccines or  
PT diagnostic compositions for treating and/or preventing *Neisseria*  
PT meningitidis infections  
XX  
XX Claim 1; Page 62; 123pp; English.  
XX  
XX The invention provides proteins (AAY27201-245) from *Neisseria*  
CC meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)  
CC encoding the proteins. Compositions comprising the protein, nucleic acid  
CC or antibody specific to the protein are useful as pharmaceuticals, e.g. a  
CC vaccine composition or a diagnostic composition. The composition is also  
CC useful for treating or preventing an infection due to *Neisseria*  
CC bacteria, especially *Neisseria meningitidis*.  
XX  
XX Sequence 591 AA;

Query Match 90.7%; Score 2740.5; DB 20; Length 591;  
Best Local Similarity 92.1%; Pred. No. 5.3e-158;  
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;  
QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
DB 1 mnkiyriiwsalnawvvsselftrnhtkrasatvktavltilfatvqasaneedl 60  
QY 58 YLEPQVORTAVVLSFRSDKEGTGEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116  
DB 61 yldpqrtvavilvnsdkegtgekeveensdwavynfnekgvltareitlkagdnlikq 120  
QY 117 NTNENTNDSSTYSLKKDLTLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 176  
DB 121 -----ngntfyslkkdltdltsvgtklsfsangknvntsdtkglnfaketagngd 174  
QY 177 PTVHLNIGIGSTLTDLTLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236  
DB 175 tlvhlnigistldtlnltgattnvndvntddekrraasvkdvlagnwnkvgkpgtta 234  
QY 237 SDNVDFVRYDTVEFLSADTKTTTVNESKDKGKTEVKIGAKTSVKEKDKGLVTGKKG 296  
DB 235 sdnvdfvrydtveflsadtktttvneskdngkktvkgigaktsvikekgdglvtgkkg 294  
QY 297 DENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSGTNVTFSAGK 356  
DB 295 gengstdegeglvtakevidavnkagwrmtttangqfqtgqadkfetvtsgtntvtfsagk 354  
QY 357 GTTATVSKDDQGNITVKYDVNVGDALNVQNLQNSGWNLDKSAVAGSGKVISGNVSPSKG 416  
DB 355 gttatvskddqgnitvmydvngdnlvnlqngswlnldskavagsgkvisgnvpskg 414  
QY 417 KMDETVNIAGNIEITRNKNDIATSMAPQFSSVSLGAGADAPTLVSDDEGALNVGSK 476  
DB 415 kmdetvniagnieitrngkndiatcsmtpqfssvslgagadaptlsvdgd-alnvgsk 473  
QY 477 DTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDVNDGNARAGIAQAIATAGLVQA 536  
DB 474 kdnkpvritnvapgvkegdvtnvaqlkgvaqnlnnridvndgnaragiataglvqa 533

QY 537 YLPKSMMAIGDGYRGEAGYATGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594  
DB 534 ylpksmmaiggyrgeagyaigyssisdgggnwilkgtasgnsrgrhfgasasvgyqw 591  
RESULT 14  
AAY23746  
ID AAY23746 standard; Protein; 591 AA.  
XX AAY23746;  
XX  
XX 08-SEP-1999 (first entry)  
XX A surface protein of *Neisseria meningitidis*.  
DE  
DE  
XX Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
XX *Neisseria meningitidis*.  
OS  
XX W09931132-A1.  
XX  
XX 24-JUN-1999.  
XX  
XX 14-DEC-1998; 98WO-AU01031.  
XX  
XX 12-DEC-1997; 97GB-0026398.  
XX  
XX (ISIS-) ISIS INNOVATION LTD.  
PA (UYOU ) UNIV QUEENSLAND.  
XX  
XX Jennings MP, Moxon ER, Peak IRA;  
PI  
XX WPI: 1999-418754/35.  
DR N-PSDB; AAX85798.  
XX  
XX *Neisseria meningitidis* surface proteins useful for treating N.  
PT meningitidis infections  
XX  
XX Claim 1; Page 127-128; 132pp; English.

XX The present sequence represents a surface protein of *Neisseria*  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.  
XX  
XX Sequence 591 AA;

Query Match 90.7%; Score 2740.5; DB 20; Length 591;  
Best Local Similarity 92.1%; Pred. No. 5.3e-158;  
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;  
QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
DB 1 mnkiyriiwsalnawvvsselftrnhtkrasatvktavltilfatvqasaneedl 60  
QY 58 YLEPQVORTAVVLSFRSDKEGTGEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116  
DB 61 yldpqrtvavilvnsdkegtgekeveensdwavynfnekgvltareitlkagdnlikq 120  
QY 117 NTNENTNDSSTYSLKKDLTLTSVETKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 176  
DB 121 -----ngntfyslkkdltdltsvgtklsfsangknvntsdtkglnfaketagngd 174  
QY 177 PTVHLNIGIGSTLTDLTLNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNKGVKPGTTA 236  
DB 175 tlvhlnigistldtlnltgattnvndvntddekrraasvkdvlagnwnkvgkpgtta 234

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Db 175 ttvhlngigstldtllntgattntvndvtddekkraasvkdvlagnwnikvgkpgtta 234
QY 237 SDNVDFVRTYDTVEFLSADTKTTNNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 296
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Db 235 sdndvfrtydtveflsadtktttnvneskdngkkttevkigaktsvikekdglvtgkdk 294
QY 297 DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTttTANGQTGOADKFEFVTSGTNVTFA 356
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Db 295 gengsstdegeglvtakevidavnkagwrmttttangtggadkfetvtsgtntvtfasgk 354
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Db 355 gttatvskddqgnltvmydvngdnlvngqlqnsqwnldskavagssgkvisgnvpskg 414
QY 417 KMDETVINAGNNIEITRNKGNIDIAFSMAPOFSSVSLGAGADAPTLVSDDEGALNVGSK 476
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QY 477 DTNKPVRITNVAPEKGVGDVNTNVAQLKGVAQNLNNRDNDVGNARAGIAQAIATAGLVQA 536
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Db 474 kdnkpvritnvaqvgkegdvtnvaqlkgvaqnlndvgnaraglaqaiataglvqa 533
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Db 534 ylpqksmmaigggtyrgeadyaigyssisdggnwllkgtasgnsrghfgasasygyq 591

RESULT 15
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ID AAU06171 standard; Protein; 591 AA.
XX AC AAU06171;
XX DT 24-OCT-2001 (first entry)
XX DE N. meningitidis PMC21 surface antigen NhhA polypeptide sequence.
XX KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX OS Neisseria meningitidis strain PMC21.
XX PH
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    /note= "Predicted mature protein, specifically claimed in claim 12"
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FT FT /label= C5
XX XX /note= "Conserved region 5"
PN PN
XX XX WO200155182-A1.
PD PD 02-AUG-2001.
XX XX
XX XX 25-JAN-2001; 2001WO-AU00069.
XX XX
XX XX 25-JAN-2000; 2000US-0177917.
XX XX (UYQU ) UNIV QUEENSLAND.
XX XX
XX XX Peak IRA, Jennings MP;
XX XX WPI: 2001-488774/53.
XX XX N-PSDB; AAS09161.
XX XX
XX XX New NhhA surface antigen polypeptides and polynucleotides from
    Neisseria meningitidis, useful in producing vaccines for treating or
    preventing broad spectrum of Neisseria meningitidis -
    Claim 9; Fig 1; 91pp; English.
XX PS
XX CC The present invention relates to the isolation of novel Neisseria
    meningitidis mutant polypeptides of the surface antigen NhhA
    (AAU06182-AAU06186). The modified or mutant NhhA polypeptides are
    characterised by deletions of non-conserved amino acids, particularly
    the deletion of variable regions. The deletion mutants are useful in
    CC diagnostics, therapeutic and prophylactic vaccines against a broader
    CC spectrum of N. meningitidis, and in designing and/or screening of
    CC medicaments. The mutant proteins when used as a vaccine can effectively
    CC immunise against a broader spectrum of N. meningitidis strains than
    CC would be expected from a corresponding wild-type surface antigen.
    CC The present sequence representing the wild type surface antigen NhhA
    (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
    the present invention.
XX XX Sequence 591 AA;
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Query Match 90.7%; Score 2740.5; DB 22; Length 591;
Best Local Similarity 92.1%; Pred. No. 5.3e-158;
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;

QY 1 MNKIYRIIWNLSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDD 57
    |||||
Db 1 mnkiyriiwnlsalna wvvseltrnhtrhkrsatvktavlatllfatvqasannee 60
    |||||

QY 58 YLEPVPQRTAVVLSFRSDKEGTGEGTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIKQ 116
    |||||
Db 61 ylpvqrtavvllvnsdkegtgekeveensdwavyfnekgvltareitlkagdnlkikq 120
    |||||

QY 117 NTNENTNDSSTYSLSKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 176
    |||||
Db 121 -----ngtftytslkkdltdltsvgteklsfsgangknvitsdtkglnfaketag 174
    |||||

QY 177 PTVHLNGIGSTLTDLTLLNTGATTNTVNDTDDKKRAASVKDVLNAGWNKGVKPGTTA 236
    |||||
Db 175 ttvhlngigstldtllntgattntvndvtddekkraasvkdvlagnwnikvgkpgtta 234
    |||||

QY 237 SDNVDFVRTYDTVEFLSADTKTTNNVESKDNKGKTEVKIGAKTSVKEKDGKLVTKGK 296
    |||||
Db 235 sdndvfrtydtveflsadtktttnvneskdngkkttevkigaktsvikekdglvtgkdk 294
    |||||

QY 297 DENGSSTDEGEGLVTAKEVIDAVNKAGWRMKTttTANGQTGOADKFEFVTSGTNVTFA 356
    |||||
Db 295 gengsstdegeglvtakevidavnkagwrmttttangtggadkfetvtsgtntvtfasgk 354
    |||||

QY 357 GTTATVSKDDGGNTVKYDYNVGDALVNOLONSGWNLDKAVAGSSGKVISGNVSPSKG 416
    |||||
Db 355 gttatvskddqgnltvmydvngdnlvngqlqnsqwnldskavagssgkvisgnvpskg 414
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Qy 417 KMDTVNINAGNIEITRNGKNIDIATSMAPOFSSVSLGAGADAPTLSDDEGALNVGSK 476  
Db 415 kndetvniinagmnieitrngknidiatsmtpqfssvsigagadapclsvdgd-alnvgsk 473  
Qy 477 DTNKPVRITNVAPGVKEGDTVNTVAOLKGYAQNLRNDRIDNVGNARAGIAQAIAATAGLVQA 536  
Db 474 kdnkpvrntnvapgvkegdtvnvaqlkgvaqnlrnrdrdnvgnaraglaqalataglvqa 533  
Qy 537 YLPKSMMAIGGDTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGRFGASASVGYQW 594  
Db 534 ylpkksmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrgrhfgasasvgyqw 591

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Job time: 321 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:37:10 ; Search time 39.66 seconds  
(without alignments)  
365.830 Million cell updates/sec

Title: US-09-771-382-9  
Perfect score: 3023  
Sequence: 1 MNKIYRIIWSALNAWVVS.....TASGSRGHFGASVGYQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 2442594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pap.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	3023	100.0	594	4	US-09-669-974-7 Sequence 7, Appli
3	2971	98.3	598	4	US-09-377-155-13 Sequence 13, Appl
4	2971	98.3	598	4	US-09-669-974-13 Sequence 13, Appl
5	2948	97.5	598	4	US-09-377-155-5 Sequence 5, Appli
6	2948	97.5	598	4	US-09-669-974-5 Sequence 5, Appli
7	2874	95.1	594	4	US-09-377-155-9 Sequence 9, Appli
8	2874	95.1	594	4	US-09-669-974-9 Sequence 9, Appli
9	2802.5	92.7	599	4	US-09-377-155-15 Sequence 15, Appl
10	2802.5	92.7	599	4	US-09-669-974-15 Sequence 15, Appl
11	2740.5	90.7	591	4	US-09-377-155-21 Sequence 21, Appl
12	2740.5	90.7	591	4	US-09-669-974-21 Sequence 21, Appl
13	2733	90.4	592	4	US-09-377-155-2 Sequence 2, Appli
14	2733	90.4	592	4	US-09-669-974-2 Sequence 2, Appli
15	2721.5	90.0	591	4	US-09-377-155-11 Sequence 11, Appl
16	2721.5	90.0	591	4	US-09-669-974-11 Sequence 11, Appl
17	2664	88.1	592	4	US-09-377-155-17 Sequence 17, Appl
18	2664	88.1	592	4	US-09-669-974-17 Sequence 17, Appl
19	2573.5	85.1	589	4	US-09-377-155-19 Sequence 19, Appl
20	2573.5	85.1	589	4	US-09-669-974-19 Sequence 19, Appl
21	1330.5	44.0	2353	4	US-09-377-155-33 Sequence 33, Appl
22	1330.5	44.0	2353	4	US-08-913-942-4 Sequence 4, Appli
23	1330.5	44.0	2353	4	US-09-669-974-33 Sequence 33, Appl
24	1329.5	44.0	2354	4	US-09-268-347-47 Sequence 47, Appl
25	1295.5	42.9	2411	1	US-09-268-347-30 Sequence 30, Appl
26	1263	41.8	607	1	US-08-409-995-6 Sequence 6, Appli
27	1263	41.8	607	3	US-08-685-467-6 Sequence 6, Appli

28	1263	41.8	607	4	US-08-913-942-6	Sequence 6, Appli
29	1263	41.8	1912	1	US-08-409-995-4	Sequence 4, Appli
30	1263	41.8	1912	3	US-08-685-467-4	Sequence 4, Appli
31	1079	35.7	1094	4	US-09-268-347-32	Sequence 32, Appl
32	1050	34.7	1098	1	US-08-409-995-2	Sequence 2, Appli
33	1050	34.7	1098	3	US-08-685-467-2	Sequence 2, Appli
34	1050	34.7	1098	4	US-09-377-155-32	Sequence 32, Appl
35	1050	34.7	1098	4	US-08-913-942-2	Sequence 2, Appli
36	1050	34.7	1098	4	US-09-669-974-32	Sequence 32, Appl
37	1050	34.7	1098	4	US-09-268-347-44	Sequence 44, Appl
38	1031	34.1	658	1	US-08-409-995-5	Sequence 5, Appli
39	1031	34.1	658	3	US-08-685-467-5	Sequence 5, Appli
40	1031	34.1	658	4	US-08-913-942-5	Sequence 5, Appli
41	1011.5	33.5	679	4	US-08-913-942-15	Sequence 15, Appl
42	1011.5	33.5	679	4	US-09-268-347-26	Sequence 26, Appl
43	757	25.0	1002	4	US-09-268-347-24	Sequence 24, Appl
44	756	25.0	1004	4	US-09-268-347-30	Sequence 30, Appl
45	709	23.5	1104	4	US-09-268-347-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1

US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
; US-09-377-155-7

Query Match	100.0%	Score	3023	DB	4	Length	594
Best Local Similarity	100.0%	Pred. No.	8.7e-236	Mismatches	0	Indels	0
Matches	594	Conservative	0	Gaps	0		
QY	1	MNKYRIIWSALNAWVVS	ELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE	60			
Db	1	MNKYRIIWSALNAWVVS	ELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE	60			
QY	61	PVORTAVVLSFRSDKEGTEGTEDSNNAVYFDEKRVLKAGAITLKAGDNLIKONTNE	120				
Db	61	PVORTAVVLSFRSDKEGTEGTEDSNNAVYFDEKRVLKAGAITLKAGDNLIKONTNE	120				
QY	121	NTNDSFTYSLAKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH	180				
Db	121	NTNDSFTYSLAKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH	180				
QY	181	LANGISTLDTLLNTGATTNVTNDNVVDDEKKRAASVDVNLNAGWNKGVKPGTTASDNV	240				
Db	181	LANGISTLDTLLNTGATTNVTNDNVVDDEKKRAASVDVNLNAGWNKGVKPGTTASDNV	240				
QY	241	DFVRYIDVFEFLSADTKTTTVNVESKDNGKTEVIGAKTSVIKEKDGKLVTKGKDENG	300				
Db	241	DFVRYIDVFEFLSADTKTTTVNVESKDNGKTEVIGAKTSVIKEKDGKLVTKGKDENG	300				
QY	301	SSTDEGLEVTAKVIDAVNKAGWRMKTTTTANGQTQADKFEETVTSGTNVTWTFASGKGTTA	360				

Db 301 SSTDEGELVTAKEVIDAVNKAGRMKTTTANGOTGOADKFEVTSNTVTFASGKGTTA 360  
QY 361 TVSKDDOGNITVYDYVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420  
Db 361 TVSKDDOGNITVYDYVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420  
QY 421 TVNINAGNIEITRNGKNIDIATSMAPQFSVSLGAGADAPTLSVDDDEGALNVGSKDTNK 480  
Db 421 TVNINAGNIEITRNGKNIDIATSMAPQFSVSLGAGADAPTLSVDDDEGALNVGSKDTNK 480  
QY 481 PVRTNTPVAPGKGDVTNVAQLKGVAQNLANNRIDNVGDNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRTNTPVAPGKGDVTNVAQLKGVAQNLANNRIDNVGDNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMAAIGDITYRGEAGYAICYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594  
Db 541 KSMAAIGDITYRGEAGYAICYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594

## RESULT 2

US-09-669-974-7  
; Sequence 7, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669, 974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-7

Query Match 100.0%; Score 3023; DB 4; Length 594;  
Best Local Similarity 100.0%; Pred. No. 8.7e-236;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNAWVWVSELTRNHTKRASATVATAVLATLFLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWVWVSELTRNHTKRASATVATAVLATLFLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTGEGTEDSNWAYFDEKRVLKAGAITLKAGNLIKQNTNE 120  
Db 61 PVQRTAVVLSFRSDKEGTGEGTEDSNWAYFDEKRVLKAGAITLKAGNLIKQNTNE 120  
QY 121 NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGDPTVH 180  
Db 121 NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGDPTVH 180  
QY 181 LINGISFTLDTLLNTGATTNVDNVTDDDEKRAASVKDVLNAGWNIKGKPGTASDNV 240  
Db 181 LINGISFTLDTLLNTGATTNVDNVTDDDEKRAASVKDVLNAGWNIKGKPGTASDNV 240  
QY 241 DFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKDENG 300  
Db 241 DFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKDENG 300  
QY 301 SSTDEGELVTAKEVIDAVNKAGRMKTTTANGOTGOADKFEVTSNTVTFASGKGTTA 360

Db 301 SSTDEGELVTAKEVIDAVNKAGRMKTTTANGOTGOADKFEVTSNTVTFASGKGTTA 360  
QY 361 TVSKDDOGNITVYDYVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420  
Db 361 TVSKDDOGNITVYDYVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKME 420  
QY 421 TVNINAGNIEITRNGKNIDIATSMAPQFSVSLGAGADAPTLSVDDDEGALNVGSKDTNK 480  
Db 421 TVNINAGNIEITRNGKNIDIATSMAPQFSVSLGAGADAPTLSVDDDEGALNVGSKDTNK 480  
QY 481 PVRTNTPVAPGKGDVTNVAQLKGVAQNLANNRIDNVGDNARAGIAQAIAATAGLVQAYLPG 540  
Db 481 PVRTNTPVAPGKGDVTNVAQLKGVAQNLANNRIDNVGDNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMAAIGDITYRGEAGYAICYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594  
Db 541 KSMAAIGDITYRGEAGYAICYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594

## RESULT 3

US-09-377-155-13  
; Sequence 13, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-13

Query Match 98.3%; Score 2971; DB 4; Length 598;  
Best Local Similarity 98.0%; Pred. No. 1.4e-231;  
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVWVSELTRNHTKRASATVATAVLATLFLFATVQANATDDDDLYLE 60  
Db 1 MNKIYRIIWSALNAWVWVSELTRNHTKRASATVATAVLATLFLFATVQANATDDDDLYLE 60  
QY 61 PVQRTAVVLSFRSDKEGTGEGTEDSNWAYFDEKRVLKAGAITLKAGNLIKQNTNE 116  
Db 61 PVQRTAVVLSFRSDKEGTGEGTEDSNWAYFDEKRVLKAGAITLKAGNLIKQNTNE 120  
QY 117 NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 176  
Db 121 NTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKNVNTSDTKGLNFAKETAGTNGD 180  
QY 177 PTVHLNIGISFTLDTLLNTGATTNVDNVTDDDEKRAASVKDVLNAGWNIKGKPGTTA 236  
Db 181 PTVHLNIGISFTLDTLLNTGATTNVDNVTDDDEKRAASVKDVLNAGWNIKGKPGTTA 240  
QY 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKG 296  
Db 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKG 300  
QY 297 DENGSSSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGOADKFEVTSNTVTFASGK 356  
Db 301 DENGSSSTDEGEGLVTAKEVIDAVNKAGRMKTTTANGOTGOADKFEVTSNTVTFASGK 360  
QY 357 GTTATVSKDDOGNITVYDYVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416





Db	421	KMDETVINAGNNIETTRNCKNKIDIIATSMTPQFSSVSLGAGADAPTLSSVDDEGALNVGSK	480
Qy	477	DTNKPVRTINAPGVCKEGDVTNVAQLKGVAQNLNRRIDNVGDNARAGIAQAIATAGLVOA	536
Db	481	DANKPVRTINAPGVCKEEDVTNVAQLKGVAQNLNRRIDNVGDNARAGIAQAIATAGLAQA	540
Qy	537	YLPCKSMAIIGGDTYRGEAGYATGYSSISDGGNNIIKGTASGNSRGHFGASASVGYQW	594
Db	541	YLPCKSMAIIGGGTYRGEAGYATGYSSISDGTGNWIKGTASGNSRGHFGTSASVGYQW	598

RESULT 6  
US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent NO. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

	Query Match	97.5%;	Score 2948;	DB 4;	Length 598;	
	Best Local Similarity	97.3%;	Pred. No. 9.9e-230;			
	Matches 582; Conservative	2;	Mismatches 10;	Indels 4;	Gaps	
Qy	1	MNKYRIIWNLSALNAWVVVSELFRNHTKRASATVATAVLATLTLFATVQAANATDDDLYLE	60			
Dd	1	MNKLSRIIWNLSALNAWVVVSELFRNHTKRASATVATAVLATLTLFATVQAANATDDDLYLE	60			
Qy	61	PVQRATVVLFSRDKETGEBKEGTSDSNWAAYVFDEKRVLKAGAITLLKAGDNLKIQ----	116			
Dd	61	PVQRATVVLFSRDKETGEBKEGTSDSNWAAYVFDEKRVLKAGAITLLKAGDNLKIQTNE	120			
Qy	117	NTNENTNDSSFTYSLKDLLDTLTSVETEKLSPGANGKNVNITSDTKGLNFPAKETAGTNGD	176			
Dd	121	NTNENTNDSSFTYSLKDLLDTLTSVETEKLSPGANGKNVNITSDTKGLNFPAKETAGTNGD	180			
Qy	177	PTVHLNGIGSTLTDLTLANTGATTNVTDNDVTDDKKRAASVKDVLNAGWNIKGVPCTTA	236			
Dd	181	PTVHLNGIGSTLTDLTLANTGATTNVTDNDVTDDKKRAASVKDVLNAGWNIKGVPCTTA	240			
Qy	237	SDNDVFRVTVDFEFLSADTKTTTVNVYESKDNGKKTEVIKCAKTSVIKEKDGKLVTKGK	296			
Dd	241	SDNDVFRVTVDFEFLSADTKTTTVNVYESKDNGKKRTVEIKAKTSVIKEKDGKLVTKGK	300			
Qy	297	DENGSSSTDEBEGLVTAKEVIDAVNKAQRWKMTTANGQTCQADKFETVTSGMTVNTFASK	356			
Dd	301	GENGSSSTDEBEGLVTAKEVIDAVNKAQRWKMTTANGQTCQADKFETVTSGMTVNTFASN	360			
Qy	357	GTTATVSKDDOGNTTVKYDVNVGDALNVQLQNSGNWLDSKAVAGSGGKVISGNVSPSKG	416			
Dd	361	GTTATVSKDDOGNTTVKYDVNVGDALNVQLQNSGNWLDSKAVAGSGGKVISGNVSPSKG	420			
Qy	417	KMDETVAINAGNNIEITRNCKNIDIAITSMAPQFSSVSLGAGADAPTLTSDVDEGALNVGSK	476			

Db	421	KMDTVMINAGNNIETRNCKNKIDIIATSWTPQSPSSVSLGAGADAPTLSDVDDGALNVGSK	480
QY	477	DTNKPVRIITNVAPOGVKGGDVTNVAUKGVAQNLNRRIDNVNDGNARAGIAQAIAITAGLVQA	536
Db	481	DANKPVRIITNVAPOGVKGGDVTNVAUKGVAQNLNRRIDNVNDGNARAGIAQAIAITAGLAQA	540
QY	537	YLPCKSMMAIGGGDTYRGEAGYAIGYSSISDGGNWIKTGTASGNSRGHFCAASVGYQW	594
Db	541	YLPCKSMMAIGGGDTYRGEAGYAIGYSSISDTGNWIKGTASGNSRGHFCAASVGYQW	598

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RESULT      7
US-09-377-155-9
> Sequence 9, Application US/09377155
> Patent No. 6197312
> GENERAL INFORMATION:
> APPLICANT: PEAK, Ian Richard Anselm
> APPLICANT: JENNINGS, Michael Paul
> APPLICANT: MOXON, E. Richard
> TITLE OF INVENTION: NOVEL INVASION ANTIGEN
> FILE REFERENCE: 065064/0128
> CURRENT APPLICATION NUMBER: US/09/377,155
> CURRENT FILING DATE: 1999-08-19
> PRIOR APPLICATION NUMBER: PCT/AU98/01031
> PRIOR FILING DATE: 1998-12-14
> PRIOR APPLICATION NUMBER: GB 9726398.2
> PRIOR FILING DATE: 1997-12-12
> NUMBER OF SEQ ID NOS: 33
> SOFTWARE: PatentIn Ver. 2.0
> SEQ ID NO 9
> LENGTH: 594
> TYPE: prt
> ORGANISM: Neisseria meningitidis
US-09-377-155-9

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Query Match	95.1%	Score 2874;	DB 4;	Length 594;
Best Local Similarity	95.0%;	Pred. No. 9.1e-224;		
Matches 568; Conservative	5;	Mismatches 221;	Indels	0; Gaps
Qy	1	MNKYRIIWNLSALNAWVVSSELTRNHTKRASATVATAVLATLLFATVQANATDDDLYLE	60	
Db	1	MNKYRIIWNLSALNAWVVSSELTRNHTKRASATVATAVLATLLFATVQASTDDDLYLE	60	
Qy	61	PVQRTAVVLSFRSDKEGTGEKETSNSWAVYFDEKRVLKAGAITLLKAGDNLKIKQNTNE	120	
Db	61	PVQRTAVVLSFRSDKEGTGEKETSNSWGYFDKKGVLTAGTITLLKAGDNLKIKQNTNE	120	
Qy	121	NTNDSSTFYSLKKDLTDLTTSVETEKLSFGANGKNKVNITSDTKGLNFAKETAGTNGDPTVH	180	
Db	121	NTNASSETFYSLKKDLTDLTTSVGTKEKLSFSANSKNVNITSDTKGLNFAKKTAEETNGDPTVH	180	
Qy	181	LNGIGSTLTDFLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNILKGVPGTASDNV	240	
Db	181	LNGIGSTLTDFLLNTGATTNVTNDNVTDDEKKRAASVKDVLNAGWNILKGVPGTASDNV	240	
Qy	241	DFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEVIGAKTSVIEKDKGLVTGKGDENG	300	
Db	241	DFVRTYDVEFLSADTKTTTVNVESKDNGKRTVEVIGAKTSVIEKDKGLVTCKDKGEND	300	
Qy	301	SSTDDEGLVTAKEVIDAVNKGWRMKTTTANGOTGOADKFETVTSCTNNVTFASGKGTTA	360	
Db	301	SSTDKGELVTAKEVIDAVNKGWRMKTTTANGOTGOADKFETVTSCTNNVTFASGKGTTA	360	
Qy	361	TVSKDDOGNITVVKDYNVGDALNVNQLQNSGWNLDLSKAVAGSSGKVIISGNVSPSKGMDE	420	
Db	361	TVSKDDOGNITVMYDYNVGDALNVNQLQNSGWNLDLSKAVAGSSGKVIISGNVSPSKGMDE	420	
Qy	421	TVNINAGNNIEITRNGKNIDIAATSMAPQFSSVSLGACADAPTLTSDDEGALNVGSKDINK	480	
Db	421	TVNINAGNNIEITRNGKNIDIAATSMTPQFSSVSLGACADAPTLTSDVDEGALNVGSKDANK	480	
Qy	481	PVRTINVPAGYKEGDVTNVNQLKGVAQNLLNRRINDVDSGNARAGIAQAIATAGLVQAYLPG	540	

Db 481 PVRITNVPVKGEGDVTNVAQLKGVAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMWATGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594  
Db 541 KSMWATGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594

RESULT 8  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1998-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 95.1%; Score 2874; DB 4; Length 594;  
Best Local Similarity 95.6%; Pred. No. 9.1e-224;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;  
QY 1 MNKIYRIIWNLSALNANWVSELTNRHTKRASATVATVATLTLFATVQANATDDDLYLE 60  
Db 1 MNKIYRIIWNLSALNANWVSELTNRHTKRASATVATVATLTLFATVQASTTDDDLYLE 60  
QY 61 PVQRTAVLSFRSDKGEKTEGSDSNWVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
Db 61 PVQRTAVLSFRSDKGEKTEGSDSNWVYFDEKRVLKAGAITLKAGDNLKIKONTNE 120  
QY 121 NTNDSFTYSLKDLTLDTLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180  
Db 121 NTNDSFTYSLKDLTLDTLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVH 180  
QY 181 LNGIGSTLDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240  
Db 181 LNGIGSTLDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240  
QY 241 DFVRTYDTVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGKDG 300  
Db 241 DFVRTYDTVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGKDG 300  
QY 301 SSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTQADKFEVTSCTNVTFASGKGTGA 360  
Db 301 SSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTQADKFEVTSCTNVTFASGKGTGA 360  
QY 361 TVSKDQGNITVYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSKMDE 420  
Db 361 TVSKDQGNITVYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSKMDE 420  
QY 421 TVNINAGNIEITRNKNIDDIATSMAPQSSVSLGAGADAPTLVSDEGALNVGSKDTNK 480  
Db 421 TVNINAGNIEITRNKNIDDIATSMPTQSSVSLGAGADAPTLVSDEGALNVGSKDKANK 480  
QY 481 PVRITNVPVKGEGDVTNVAQLKGVAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540

Db 481 PVRITNVPVKGEGDVTNVAQLKGVAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQAYLPG 540  
QY 541 KSMWATGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594  
Db 541 KSMWATGGDTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594

RESULT 9  
US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 92.7%; Score 2802.5; DB 4; Length 599;  
Best Local Similarity 92.5%; Pred. No. 5.4e-218;  
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;  
QY 1 MNKIYRIIWNLSALNANWVSELTNRHTKRASATVATVATLTLFATVQANATD-DDDLYL 59  
Db 1 MNKIYRIIWNLSALNANWVSELTNRHTKRASATVATVATLTLFATVQANATDEDEEL 60  
QY 60 EPQRTAVLSFRSDKGEKTEGSDSNWVYFDEKRVLKAGAITLKAGDNLKIKO--- 116  
Db 61 EPVRSALVQLQFMIDKEGNESTGNIWSIYDHNHTLHGATVTLKAGDNLKIKONTN 120  
QY 117 -NTNENTNDSSFTYSLKDLTLDTLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 175  
Db 121 KNTNENTNDSSFTYSLKDLTLDTLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180  
QY 176 DPTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNIKGVPKGT 235  
Db 181 DPTVHLNGIGSTLDTLLNTGATTNTVNDVTDDEKRAASVKDVLNAGWNIKGVPKGT 240  
QY 236 ASDNVDFVRYDTVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGK 295  
Db 241 ASDNVDFVRYDTVEFLSADTKTTVNVESKDNKGKTEVKIGAKTSVKEKDKGLVTGK 300  
QY 296 KDENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTQADKFEVTSCTNVTFASG 355  
Db 301 KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTITANGOTQADKFEVTSCTNVTFASG 360  
QY 356 KGTATVSKDQGNITVYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 415  
Db 361 KGTATVSKDQGNITVYDVNVGDALNVQNSGNWNLDSKAVAGSSGKVISGNVSPSK 420  
QY 416 GKMDETVNIINAGNIEITRNKNIDDIATSMAPQSSVSLGAGADAPTLVSDDGALNVGS 475  
Db 421 GKMDETVNIINAGNIEITRNKNIDDIATSMPTQSSVSLGAGADAPTLVSDDGALNVGS 480  
QY 476 KDTNKKPVRTITNAPVKGEGDVTNVAQLKGVAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQ 535  
Db 481 KDKANKPVRTITNAPVKGEGDVTNVAQLKGVAQNLNHNHIDNVDGNARAGIAQAIAATAGLVQ 540  
QY 536 AYLPGKSMMAIGDGTYRGEAGYATGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYQW 594

Db 541 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 599  
|||||

RESULT 10  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 92.7%; Score 2802.5; DB 4; Length 599;  
Best Local Similarity 92.5%; Pred. No. 5.4e-218;  
Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;  
Qy 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVATVATLTLFATVOANATD-DDDLXL 59  
Db 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVATVATLTLFATVOANATDEEDEL 60  
Qy 60 EPVQRTAVLSFRSDKEGTEGKEDTSNNVAVFDEKRVLKAGAITLTKAGDNLIKQ--- 116  
Db 61 EPVRSALVLFQMDIKKEGNGENESTGNGWSIYYDNNHTLHGATVTLKAGDNLIKONTN 120  
Qy 117 -NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 175  
Db 121 KNTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 180  
Qy 176 DPTVHLNGIGSTLTDLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKGVKPGTT 235  
Db 181 DPTVHLNGIGSTLTDLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKGVKPGTT 240  
Qy 236 ASDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGK 295  
Db 241 ASDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGK 300  
Qy 296 KDNGSSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFEFVTSGTNVTFASG 355  
Db 301 KGNGSSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFEFVTSGTNVTFASG 360  
Qy 356 KGTATVSKDDQGNITVKYDVNVDALNVLQNSGWNLDKSAVAGSGKVIYSGNVSPSK 415  
Db 361 KGTATVSKDDQGNITVKYDVNVDALNVLQNSGWNLDKSAVAGSGKVIYSGNVSPSK 420  
Qy 416 GKMDETVINAGNNEIETRNKNIDTSMAPQFSVSLGAGADAPTLSDVDEGALNVGS 475  
Db 421 GKMDETVINAGNNEIETRNKNIDTSMTPQFSVSLGAGADAPTLSDVDDKALNVGS 480  
Qy 476 KDNKPVRIITNVPAGVKEGDDVTNVAQLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 535  
Db 481 KDNKPVRIITNVPAGVKEGDDVTNVAQLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 540  
Qy 536 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 594  
|||||

Db 541 AYLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 599  
RESULT 11  
US-09-377-155-21  
; Sequence 21, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 90.7%; Score 2740.5; DB 4; Length 591;  
Best Local Similarity 92.1%; Pred. No. 5.3e-213;  
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;  
Qy 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVATVATLTLFATVOANATD---DDDL 57  
Db 1 MNKIYRIIWSALNANWVSELTRNHTKRASATVATVATLTLFATVOASANNQEDEL 60  
Qy 58 YLEPVQRTAVLSFRSDKEGTEGKEDTSNNVAVFDEKRVLKAGAITLTKAGDNLIKQ 116  
Db 61 YLDPVQRTAVLSFRSDKEGTEGKEDTSNNVAVFDEKRVLKAGAITLTKAGDNLIKQ 120  
Qy 117 NTNENTNDSFTYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 176  
Db 121 -----NGTFYTSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG 174  
Qy 177 PTVHLNGIGSTLTDLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 175 TTVHLNGIGSTLTDLLNTGATTNVTNDVDDKKRAASVKDVLNAGWNKGVKPGTTA 234  
Qy 237 SDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGK 296  
Db 235 SDNVDFVRYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVIKEKDKGLVTGK 294  
Qy 297 DENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFEFVTSGTNVTFASG 356  
Db 295 GENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFEFVTSGTNVTFASG 354  
Qy 357 GTTATVSKDDQGNITVKYDVNVDALNVLQNSGWNLDKSAVAGSGKVIYSGNVSPSK 416  
Db 355 GTTATVSKDDQGNITVKYDVNVDALNVLQNSGWNLDKSAVAGSGKVIYSGNVSPSK 414  
Qy 417 KMDETVINAGNNEIETRNKNIDTSMAPQFSVSLGAGADAPTLSDVDEGALNVGSK 476  
Db 415 KMDETVINAGNNEIETRNKNIDTSMTPQFSVSLGAGADAPTLSDVGD-ALNVGSK 473  
Qy 477 DTNKPVRITNVPAGVKEGDDVTNVAQLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 536  
Db 474 KDNKPVRIITNVPAGVKEGDDVTNVAQLKGAQNLNRRIDNVDGNARAGIAQAATAGLVQ 533  
Qy 537 YLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 594  
Db 534 YLPGKSMMAIGGTYRGEAGYAIGYSSISDGGNWIITKTASGNSRGRHFGASASVGYQW 591  
|||||

RESULT 12

US-09-669-974-21  
; Sequence 21, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-21

Query Match 90.7%; Score 2740.5; DB 4; Length 591;  
Best Local Similarity 92.1%; Pred. No. 5.3e-213;  
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;

QY	1	MNKYRIIWNLSALNWWVYSELTRNHTKRASATVATVAVLATLFLFATVQANATD---DDDL	57
DB	1	MNKYRIIWNLSALNWWVYSELTRNHTKRASATVATVAVLATLFLFATVQANNEEEDL	60
QY	58	YLEPVORTAVLSFRSDKEGTEGEGED-SNWAYFDEKRVLKAGAITLKAGDNLKIK	116
DB	61	YLDPVORTAVLVNSDKEGTEGKEKEVENSOWAVYFNEKGVLTAREITLKAGDNLKIK	120
QY	117	NTNENTNDSFYSYLSKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD	176
DB	121	-----NGTNFYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD	174
QY	177	PTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKIGVKPGCTTA	236
DB	175	TTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKIGVKPGCTTA	234
QY	237	SDNVDPVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIKEKDKGLVTGKG	296
DB	235	SDNVDPVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIKEKDKGLVTGKDK	294
QY	297	DENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGOADKPFETVTSGTNTVTFASG	356
DB	295	GENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGOADKPFETVTSGTNTVTFASG	354
QY	357	GTTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDLSKAVAGSSGKVISGNVSPSKG	416
DB	355	GTTATVSKDDQGNITVYDVNVGDALNVQLNSGWNLDLSKAVAGSSGKVISGNVSPSKG	414
QY	417	KMDETVINAGNNIETTRNGKNIDIATSMAPOFSSVSLGAGADAPTLSDVDEGALNVGSK	476
DB	415	KMDETVINAGNNIETTRNGKNIDIATSMTPOFSSVSLGAGADAPTLSDVGD-ALNVGSK	473
QY	477	DTNKPVRTINAPGVKEGDTVNTVAQLKVAQNLLNRIDNVDGNARAGIAQAATAGLVQA	536
DB	474	KDNKPVRTINAPGVKEGDTVNTVAQLKVAQNLLNRIDNVDGNARAGIAQAATAGLVQA	533
QY	537	YLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW	594
DB	534	YLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW	591

RESULT 13

US-09-377-155-2

; Sequence 2, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-2

Query Match 90.4%; Score 2733; DB 4; Length 592;  
Best Local Similarity 91.8%; Pred. No. 2.2e-212;  
Matches 550; Conservative 10; Mismatches 27; Indels 12; Gaps 4;

QY	1	MNKYRIIWNLSALNWWVYSELTRNHTKRASATVATVAVLATLFLFATVQANATDD---DD	56
DB	1	MNKYRIIWNLSALNWWVYSELTRNHTKRASATVATVAVLATLFLFATVQASANNRPKKD	60
QY	57	YLEPVORTAVLSFRSDKEGTEGEGED-SNWAYFDEKRVLKAGAITLKAGDNLKIK	115
DB	61	YLDPVORTAVLVNSDKEGTEGKEKEVENSOWAVYFNEKGVLTAREITLKAGDNLKIK	120
QY	116	QNTNENTNDSFYSYLSKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG	175
DB	121	Q-----NGTNFYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNG	174
QY	176	DPVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKIGVKPGTT	235
DB	175	DTVHLNGIGSTLTDLLNTGATTNTVNDVTDDEKKRAASVKDVLNAGWNKIGVKPGTT	234
QY	236	ASNDVPVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIKEKDKGLVTGKG	295
DB	235	ASNDVPVRTYDVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVIKEKDKGLVTGKD	294
QY	296	KDENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGOADKPFETVTSGTNTVTFASG	355
DB	295	KGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTGOADKPFETVTSGTNTVTFASG	354
QY	356	KGTATVSKDDQGNITVKYDVNVGDALNVQLNSGWNLDLSKAVAGSSGKVISGNVSPSK	415
DB	355	KGTATVSKDDQGNITVYDVNVGDALNVQLNSGWNLDLSKAVAGSSGKVISGNVSPSK	414
QY	416	GRMDETVINAGNNIETTRNGKNIDIATSMAPOFSSVSLGAGADAPTLSDVDEGALNVGS	475
DB	415	GRMDETVINAGNNIETTRNGKNIDIATSMTPOFSSVSLGAGADAPTLSDVGD-ALNVGS	473
QY	476	KDNKPVRTINAPGVKEGDTVNTVAQLKVAQNLLNRIDNVDGNARAGIAQAATAGLVQ	535
DB	474	KDNKPVRTINAPGVKEGDTVNTVAQLKVAQNLLNRIDNVDGNARAGIAQAATAGLVQ	533
QY	536	AYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW	594
DB	534	AYLPKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW	592

RESULT 14

US-09-669-974-2  
; Sequence 2, Application US/09669974  
; Patent No. 6333173

GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-2

Query Match 90.4%; Score 2733; DB 4; Length 592;  
Best Local Similarity 91.8%; Pred. No. 2,2e-212;  
Matches 550; Conservative 10; Mismatches 27; Indels 12; Gaps 4;  
  
Qy 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDD---DD 56  
Db 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASANNERPKKD 60  
  
Qy 57 LYLEPVQRTAVVLSFRSDEKTEGKECTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIK 115  
Db 61 LYLEPVQRTAVVLSFRSDEKTEGKECTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIK 120  
  
Qy 116 QNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG 175  
Db 121 Q-----NGTFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG 174  
  
Qy 176 DPTVHLNGIGSTLTDLTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTT 235  
Db 175 DTTVHLNGIGSTLTDLTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTT 234  
  
Qy 236 ASDNVDFVRYTDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGK 295  
Db 235 ASDNVDFVRYTDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGK 294  
  
Qy 296 KDENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFFETVTSGTNVTFA 355  
Db 295 KGENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFFETVTSGTNVTFA 354  
  
Qy 356 KGTATVSKDDQGNITVYDYNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 415  
Db 355 KGTATVSKDDQGNITVYDYNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 414  
  
Qy 416 GKMDETVINAGNIEITRNKNIDIAATSMAPQSSVSLGAGADAPTLSDVDEGALNVGS 475  
Db 415 GKMDETVINAGNIEITRNKNIDIAATSMAPQSSVSLGAGADAPTLSDVDEGALNVGS 473  
  
Qy 476 KDNKPVRTITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQ 535  
Db 474 KDNKPVRTITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQ 533  
  
Qy 536 AYLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594  
Db 534 AYLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 592

RESULT 15  
US-09-377-155-11  
; Sequence 11, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 11  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-11

Query Match 90.0%; Score 2721.5; DB 4; Length 591;  
Best Local Similarity 91.6%; Pred. No. 1.8e-211;  
Matches 548; Conservative 12; Mismatches 27; Indels 11; Gaps 4;  
  
Qy 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
Db 1 MNEILRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASANNEEQEEDL 60  
  
Qy 58 YLEPVQRTAVVLSFRSDEKTEGKECTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIK 116  
Db 61 YLEPVQRTAVVLSFRSDEKTEGKECTED-SNNAVYFDEKRVLKAGAITLKAGDNLKIK 120  
  
Qy 117 QNTNENTNDSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG 176  
Db 121 -----NGTFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG 174  
  
Qy 177 PTVHLNGIGSTLTDLTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 236  
Db 175 TTVHLNGIGSTLTDLTLNTGATTNVTNDVTDDEKRAASVKDVLNAGWNKGVKPGTTA 234  
  
Qy 237 SDNVDFVRYTDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGK 296  
Db 235 SDNVDFVRYTDTVEFLSADTKTTTVNVEKDKGKTEVKIGAKTSVKEKDKGLVTGK 294  
  
Qy 297 DENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFFETVTSGTNVTFA 356  
Db 295 GENGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFFETVTSGTNVTFA 354  
  
Qy 357 GTTATVSKDDQGNITVYDYNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 416  
Db 355 GTTATVSKDDQGNITVYDYNVGDALNVNQLNSGNWLDKAVAGSGKVISGNVSPSK 414  
  
Qy 417 KMDETVINAGNIEITRNKNIDIAATSMAPQSSVSLGAGADAPTLSDVDEGALNVGS 476  
Db 415 KMDETVINAGNIEITRNKNIDIAATSMAPQSSVSLGAGADAPTLSDVDEGALNVGS 473  
  
Qy 477 DTKNPVRTITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQ 536  
Db 474 KDNKPVRTITNVPAGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQ 533  
  
Qy 537 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 594  
Db 534 YLPCKSMMAIGGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGRHFGASASVGYQW 591

Search completed: July 3, 2002, 08:37:11  
Job time: 337 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:38:24 ; Search time 58.79 Seconds  
(without alignments)  
970.863 Million cell u

Title: US-09-771-382-9  
perfect score: 3023  
Sequence: 1 MNKIYRIIWNALNAWVVS.....TAGNSRGHEGASASVGYOW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues  
Total number of hits satisfying chosen parameters: 283138

```

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                  Maximum Match 10%
                  Listing first 45

```

```
Database : PIR_71:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query		DB	ID	Description
		Match	Length			
1	2740.5	90.7	591	2	G81133	adhesin NMB0992 [i
2	2552	84.4	592	2	A81888	probable surface f
3	635	21.0	298	2	I64138	adhesin homolog HI
4	404	13.4	2059	2	D82671	surface protein XF
5	392.5	13.0	1190	2	A83615	surface protein XF
6	371	12.3	1107	2	A80976	probable autotrans
7	356	11.8	1588	2	AC6036	probable adhesin Z
8	356	11.8	1588	2	H91188	probable adhesin E
9	338	11.2	658	2	AH0110	probable surface p
10	260	8.6	1004	2	C82672	surface-exposed ou
11	240	7.9	1091	2	G64964	hypothetical prote
12	230	7.6	1286	2	S28634	adhesin AIDA-I pre
13	221.5	7.3	1910	2	AF0394	probable adhesin h
14	217.5	7.2	3705	2	AD0123	probable autotrans
15	216	7.1	949	2	D08003	Aida-1 adhesin-lik
16	216	7.1	1005	2	H85611	probable adhesin Z
17	213.5	7.1	4919	2	T31105	hypothetical prote
18	211	7.0	5291	2	F90696	hypothetical prote
19	207.5	6.9	1343	2	D85724	hypothetical prote
20	207	6.8	5188	2	B85547	probable RTX fami
21	206.5	6.8	1109	2	A56143	surface-array prot
22	206.5	6.8	1325	2	A64905	ydxK protein - Esc
23	204.5	6.8	1343	2	E90893	hypothetical prote
24	204.5	6.8	1417	2	A83080	hypothetical prote
25	204	6.7	1536	2	A43855	high-molecular-we
26	203	6.7	1018	2	H83135	probable adhesin P
27	201	6.6	2551	2	E98047	hypothetical prote
28	200.5	6.6	961	2	AD0548	puative autotransp
29	199	6.6	1361	2	T03415	S-layer protein -

## ALIGNMENTS

```

RESULT      1
adhesin NMB0992 [imported] - Neisseria meningitidis (strain MC58 serogroup B)
G81133
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: G81133
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen,
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.
ri, H.; Qian, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandt, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.;
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755
A:Accession: G81133
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-591 <TET>
A:Cross-references: GB:AE002450; GB:AE002098; NID:g7226229; PIDN:AAF41395.1; PID:g7226229
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0992

```

Query Match	90.7%	Score	2740.5;	DB 2;	Length	591;			
Best Local Similarity	92.1%;	Pred.	No. 4.8e-131;						
Matches	551;	Conservative	11;	Mismatches	25;	Indels	11;	Gaps	4;
Qy	1	MNKYRIWNSALNANVVVSELTRNHKTKRASATVATVATLFLFATVOAANTD---DDDL	57						
							:	:	:
Db	1	MNKYRIWNSALNANVVVSELTRNHKTKRASATVKTAVTATLFLFATVOASANNEEQEDL	60						
Qy	58	YLEPQRTAVVLSPRSOKEGTGEKGTED-SNWAVYDEKRVLKAGAITLKAGNLKIQ	116						
					:		:	:	:
Db	61	YLDPQRTAVVILVNSOKEGTGEKVEENSOWAFNEKGVLTAIREITLKAGNLKIQ	120						
Qy	117	NTNENTVDSSTYSISKDLTDLTSVETEKLSFGGANKKNVITSDTKGLNFAKETAGTAGND	176						
		:							
Db	121	-----NGTNFTYSLKKDLTDLTSVGTEKLFSFGANGKNVITSDTKGLNFAKETAGTAGND	174						
Qy	177	PTVHLNGIGSPLDTLLNTGATTNNVDNVTDDDEKRAASVKDVNLNAGWNITKGVPGGTTA	236						
Db	175	TTVHLNGIGSPLDTLLNTGATTNNVDNVTDDDEKRAASVKDVNLNAGWNITKGVPGGTTA	234						
Qy	237	SDNVDFVRTYDTVFELSAADTKTTVNYESKDNGKKTVEKIGAKTSVIKEKDGLVTCGKG	296						
Db	235	SDNVDFVRTYDTVFELSAADTKTTVNYESKDNGKKTVEKIGAKTSVIKEKDGLVTCGDK	294						
Qy	297	DENGSSSTDEGBGLVTAKEVIDAVNKAGRMMKTTTTANGOTGOADKFETVTSCTNVTTFASGK	356						
Db	295	GENGSSSTDEGBGLVTAKEVIDAVNKAGRMMKTTTTANGOTGOADKFETVTSCTNVTTFASGK	354						
Qy	357	GTTATVSCKDDOGCNTIVKYDVNVGVDAIYNVOLQNSGWNIJLDSKAVAGSSSKVISGNVSPSGK	416						

Db 355 GTTATVSKDDQGNITVMDYVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNSPSKG 414  
|||||  
Qy 417 KMDVTVINAGNNEITRNKNDIATSMAPQSSVSLGAGADAPTLVSDDGALNVGSK 476  
|||||  
Db 415 KMDVTVINAGNNEITRNKNDIATSMPTQFSSVSLGAGADAPTLVSDDG-ALNVGSK 473  
|||||  
Qy 477 DTNKPVRITNVAPGKGDVTVNAQLKGVAQNLRNIDNVGNARAGIAQIAIATAGLVQA 536  
|||||  
Db 474 KDNKPVRTNVAPGKGDVTVNAQLKGVAQNLRNIDNVGNARAGIAQIAIATAGLVQA 533  
|||||  
Qy 537 YLPKSKMAIGDGYRGEAGYAGYSSISDGGNWIIRKGTASGNSRGHFGASASVGYQW 594  
|||||  
Db 534 YLPKSKMAIGGTYRGEAGYAGYSSISDGGNWIIRKGTASGNSRGHFGASASVGYQW 591  
|||||

RESULT 2  
A81888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2249  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: A81888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel  
; Holroyd, S.; Jørgens, K.; Leather, S.; Mungall, K.; Quail, M.A.; Rajandream,  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis 22491.  
A:Reference number: A81775; MUID:20222556  
A:Accession: A81888  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737989  
A:Experimental source: serogroup A, strain 22491  
C:Genetics:  
A:Gene: NMA1200

Query Match 84.4%; Score 2552; DB 2; Length 592;  
Best Local Similarity 86.8%; Pred. No. 1-5e-121;  
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;  
Qy 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLXL 59  
|||||  
Db 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL 60  
|||||  
Qy 60 EPVORTAVLFSRDSKGTGKEG-----TEDSNWY--YFDEKRVLKAGAITLKAGDNL 112  
|||||  
Db 61 ESVR-SVSGISQASMGSGELETISLMTNDSKEFDPYI-----VVTUKAGDNL 110  
|||||  
Qy 113 KIKONTNENTNDSFTYSLKKDLTSLVETEKLSFGANGKNVITSDTKGLNFAKETAG 172  
|||||  
Db 111 KIKONTNENTNASSFTYSLKKDLTLINVEKLSFGANGKNVITSDTKGLNFAKETAG 170  
|||||  
Qy 173 TNGDPTVHLNGIGSTLTDTLTNGATNTVNDVNTDEKRAASVKDVLNAGWNIKGVK 232  
|||||  
Db 171 TNGDPTVHLNGIGSTLTDTLTLAGSSASVHDAGNOST--HYTRAASIKDVLNAGWNIKGVK 228  
|||||  
Qy 233 GTTA--SDNVDFRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDGKL 290  
|||||  
Db 229 GSTTGQSENDFRTYDTVEFLSADTKTTNVNVEKDKGKRTVEVKIGAKTSVKEKDGKL 288  
|||||  
Qy 291 VTGKGDENGSSDTDEGGLVTAKEVIDAVNKGWRMKTTTANGQTGQADKFEVTSCTNV 350  
|||||  
Db 289 VTGKKGKENGSSDTDEGGLVTAKEVIDAVNKGWRMKTTTANGQTGQADKFEVTSCTNV 348  
|||||  
Qy 351 TFASGKTTATVSKDDGNTITVKYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVTSGN 410  
|||||  
Db 349 TFASGKTTATVSKDDGNTITVMYDVNVGDALNVQNLQNSGWNLDKAVAGSSGKVTSGN 408  
|||||  
Qy 411 VSPSKGMDVTNINAGNNEITRNKNDIATSMAPQSSVSLGAGADAPTLVSDDGGA 470  
|||||  
Db 409 VSPSKGMDVTNINAGNNEITRNKNDIATSMAPQSSVSLGAGADAPTLVSDDGGA 468  
|||||

Qy 471 LNVGSKDTNKPVRITNVAPGKGDVTVNAQLKGVAQNLRNIDNVGNARAGIAQIAIAT 530  
|||||  
Db 469 LNVGSKDANKPVRITNVAPGKGDVTVNAQLKGVAQNLRNIDNVGNARAGIAQIAIAT 528  
|||||  
Qy 531 AGLVQAYLPKSKMAIGDGYRGEAGYAGYSSISDGGNWIIRKGTASGNSRGHFGASASV 590  
|||||  
Db 529 AGLVQAYLPKSKMAIGGTYRGEAGYAGYSSISDGGNWIIRKGTASGNSRGHFGASASV 588  
|||||  
Qy 591 GYQW 594  
|||||  
Db 589 GYQW 592  
|||||  
RESULT 3  
I64138  
adhesin homolog HI1732 - Haemophilus influenzae (strain Rd KW20)  
C:Species: Haemophilus influenzae  
C:Date: 18-Aug-1995 #sequence\_revision 18-Aug-1995 #text\_change 24-Oct-1997  
C:Accession: I64138  
R:Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage  
; Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman  
; D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M.  
Science 269, 496-512, 1995  
A:Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter  
A:Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.  
A:Reference number: A64000; MUID:95350630  
A:Accession: I64138  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-298 <TIGR>  
A:Cross-references: GB:U32846; GB:L42023; NID:g1574588; PID:g1574589; TIGR:HI1732

Query Match 21.0%; Score 635; DB 2; Length 298;  
Best Local Similarity 47.8%; Pred. No. 2.9e-25;  
Matches 151; Conservative 42; Mismatches 88; Indels 36; Gaps 9;  
Qy 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDLYLE 60  
|||||  
Db 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVQANATVQVQ----- 49  
|||||  
Qy 61 PVORTAVLFSRDSKGTGKEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEGTEG 119  
|||||  
Db 50 -INDAGTFVVKVQSTEDIEDSAATKDDN-----KQALKAGDPTLTKAGKNLAKL--- 99  
|||||  
Qy 120 ENTNDSFTYSLKKDLTSLVETEKLSFGAN-----GNKNVITSDTKGLNFAKETAG 172  
|||||  
Db 100 -DOGGKSVTALAKDLVDKAKVSDTLTIGNTPAAGATPKVSVITSTADGLKAK---G 155  
|||||  
Qy 173 TNGDPTVHLNGIGSTLTDTLTNGATNTVNDVNTDEKRAASVKDVLNAGWNIKGVK 232  
|||||  
Db 156 TNGDPTVHLNGLASTLPDVTNTGASTSVT-FSPSDIEKTPAATIKDVLNAGWNIKGVK 214  
|||||  
Qy 233 GTTASDNVDFRTYDTVEFLSADTKTTNVNVEKDKGKTEVKIGAKTSVKEKDKGLVT 292  
|||||  
Db 215 AGGNTENVLDVAGYDNVEFTGDKNTLDVVLTAKEGKTEVKEFTPKTSVIKDNNGKILT 274  
|||||  
Qy 293 GK-GKEN-GSSDDEGE 307  
|||||  
Db 275 GKQLKDANTGTATNATE 291  
|||||

RESULT 4  
D82671  
surface protein XF1529 [imported] - Xylella fastidiosa (strain 9a5c)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: D82671  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq  
Nature 405, 151-157, 2000  
A:Title: the genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below



```
Db 963 ----NVADAKEAT--DAVNLQRLDRVAODANRYVDNKNKTESLSEGQTF----- 1003
Qy 421 TVTNAGNNEIETRNKKNIDIAATMAPOFSSVSLGAGADA-----PTLSVDDEG 469
Db 1004 -VKVNSLNN-----SATPIAGVATAIGVGATASCAUSIAMGNKASASADNAV 1051
Qy 470 AL-----NVGSKDNKPKVRITNVAPGVKEGDTNVVAQLKGVAQNLRIDNWD 517
Db 1052 AIGNHSVADRANTVSGSAGSER--QVTVNAAGTADTDAVNVSQLNQCLITAKQYTDGV 1109
Qy 518 GNAR----AGTAAQATATAGLVOAYLPKSMMAIGDGYRGEAGYAGVSSISDGNWLIK 573
Db 1110 GSLRDTDGGVAAATATANLPQATIPGRGMTSVGVSSYRGQSAITAVGVSSVSEGRWVFK 1169
Qy 574 GTASGNSRGHFCASASVGYQW 594
Db 1170 FSGSANTRSQVIGAGVGYQW 1190

RESULT 6
AC0976
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar Typhimurium
C:Species: Salmonella enterica subsp. enterica serovar Typhi
C:Note: This species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 09-Nov-2001
C:Accession: AC0976
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Mouton, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, J.; Connor, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, J.; Mouton, S.; O'Garra, P.
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhimurium
A:Reference number: AB0502; PMID:11677608
A:Accession: AC0976
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1107 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:gl6504923; GSPDB:GN00176
C:Genetics:
A:Gene: sapB

Query Match 12.3%; Score 371; DB 2; Length 1107;
Best Local Similarity 22.0%; Pred. No. 3.2e-11;
Matches 184; Conservative 105; Mismatches 263; Indels 286; Gaps 31;

Qy 27 TKRASATVAT---AVLATLIFAT---VQANATDDDLYLEPQVORTAVVLSFRSDKEGTG 79
Db 286 TNLAAGLTAASTDAVNGSQLYETNQKVDQNTSAIDINTSITNLSSDNLSSNETTNSFS 345

Qy 80 EKEGTEDSNWAVYFDEKRVLKAGAITLKAGD-----NLKIKONT----- 118
Db 346 ASHGSSSTN-----KTNVAAGELSESTDAVNGSQLFETNEKRVQDQNTTIAANTTNIT 399

Qy 119 -----NENTNDSFTYSLKKDLTD---LPSVETEKLSFGANGKNVNTSDTKGLNPAK 168
Db 400 QNSAIEANLNTSVSDINTSI-TGLTDNALLWDEDTGAPSANHGGSSTKITNVAAALSED 458

Qy 169 ETAGTNGDPTVHLNGIGSTLTDL--LNTGATTNVTNDVTDDEKKRAASVKVDVNLGAWN 226
Db 459 STDAVNGSQLYETNQKVDQNTSAIDINT-SITNLGTDALSDDDEEGAFSASHTGSGTNK 517

Qy 227 IKGVKPGTTASDNDVDFV---RTYDT-----VEFLSADTKTTTVN-----VES 265
Db 518 ITNVAAGEIASDSTAINGSQLYETNMLISQYNESISQAGDTSETYITENGTVGKYIRT 577

Qy 266 KDNKKTE-----VKIGAKTSVKEK-----DGKLVYTGKGDEN----- 299
Db 578 NDNGLEGODAYATGATGATVAVGASGACGLAQNSSSSIEGSIAGLGSSTSNRAITT 637

Qy 300 ----GSSTDEGGL--VTAKEVIDAVNKA---GWRMKTITANGQTCQADKFFETVSGT 348
Db 638 GIRETSATSDGVWIGYNTTDRLLGAUSLGTGDSYROIITNWADG--SEADAVTVROLQ 695
```

```
Qy 349 NVTFASCKGTTATYSKDDQGNIT-----VKYDVNVGDALNVNQLQN 389
Db 696 NAIGA---VTTTPTKYYHANSTEDSLAVGCTDSLAMGAKTIVNADAGIGLNTLVWAD 751
Qy 390 --SGWNLDSKAVAGSSGKVISGNVSP-----SKGMD---E 420
Db 752 AINGIATGNSNARANHANSIAMNGSQTTTRGAQTDYTAYNMDTPQNSVGEFSVSGSDGQ 811
Qy 421 TVTNAGN-----NIEITRNKNI-----DIATS 444
Db 812 ITNVAAGSADTDAVNVGQLKYTDQAQVSRTQSIINLTQVSNLDRVTNIEINGDIYVT 871
Qy 445 MAPOF-----SSVSLGAGADAP-----TSLVDDE-GALNVGSKDKTNK 480
Db 872 GSTKYFKTNTDGDANAGGADSAIGSGSIAAENSVALGTSNVADEANTVSGSSTQQR 931
Qy 481 PVRITNVAPGVKEGDTNVVAOLK----- 503
Db 932 --RITNVAAGVNTDAVNVVAOLKASEAGSVRYETNADGSVNVSVNLGLDGGSGTTRIGNV 989
Qy 504 -----GVAO-----NLNRIIDVGNARAGIAQAIAATAGLVQA 536
Db 990 SAAVNDTDAVNVVAOLKRSVEEANTYTDOKMGEMNSKIKGIENKMSGGSIASAMAGLPOA 1049
Qy 537 YLPKSMMAIGDGYRGEAGYAGVSSISDGNWLIKGTASGNSRGHFGASASVGYQW 594
Db 1050 YAPGANMTSAGGTFCGESAVAGVSMVYSEGWWYKLGQTSNSGGDYSAALGAGFQW 1107

RESULT 7
A86036
probable adhesin 25029 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:Species: Escherichia coli
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A86036
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May
Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A86036
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1588 <STO>
A:Cross-references: GB:AE005174; NID:gl2518349; PIDN:AAG50749.1; GSPDB:GN00145; UWGP:
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: 25029

Query Match 11.8%; Score 356; DB 2; Length 1588;
Best Local Similarity 25.8%; Pred. No. 2.9e-10;
Matches 149; Conservative 81; Mismatches 240; Indels 108; Gaps 21;

Qy 111 NLKIKONT---NENTNDSFTYSLKKDLTDLTSTVET---EKLSTF-----GANGKNKVNITS 159
Db 1025 NMWIEQNTQIIINQLAGNTDAY-IQEGAGINYVVRTNDGLAENFNDASAAQGVGATAGVNS 1083

Qy 160 DTGKLNFAKETAGTNGDPTVHLNGIGSTLTDLTNTGA-TTNVTNDNV-----TDDEKK 212
Db 1084 VAKGDSVVAIQGGSYSVDVDTGIALGSSSVSRVIAKGRSDTSITENGVIYDITDCELL 1143

Qy 213 RAASVKD-----VLNAGWNKGVKPGCTTASDNDVDFVRYTDTVEFLSADTKTTTVNVESK 266
Db 1144 GALSIGDDGKYRQIIN-----VADGSEADAVT-VROLQAICAVATTTKTFHANST 1195

Qy 267 DNGK-----KTEVKICAKTSVKEKDGKLVTKGDKDENGSSSTDEGEGLVTAKEVIDAVNKA 322
Db 1196 EEDSLAVGCTDSLAMGAKTIVNGDKGIGYGAYVDANALN---GTAIGSNAQVIVHNSIA 1252

Qy 323 GWRMKTITANGQTCQADKFFETVSGT---GQAD-----KFEVTVSGTNVTFASCKG--- 357
```

Db 1253 IGGSTTTTGAQTNTAYNMDAPQNSVGEFSVGSADGQRQITNVAAGSADTDVAVNGQLK 1312  
QY 358 -TTATVSKDDQGNIT-----VKYDVNVGDAL-----NVNQLQNSGN 393  
Db 1313 VTAQVQSNTQ-SITLNDNRVTNLDNRVTNIENGIGDVTGTSTKYFKTNTDGVDAQAQ 1371  
QY 394 LSKAVAGSGKVISGNVSPSKGM---DETVMNAGNIEITRN---GKNIDIATSMAP 447  
Db 1372 KDSVAIGSGSIAAADNSVALGTSGVATEENTISVGSSTNORRITNVAAGKNATDAVNAQ 1431  
QY 448 QPSSVSLGAGADAPTLVSVDDEGALNVGSKDTNPKPRITNVAPOVKEGDVTNVAQLKGVAQ 507  
Db 1432 LKSSEAGGVRYDTKADGSDIDYSNITLGG-GNGGTTTRISNVSGVNNNDVNVYAQLKQSVQ 1490  
QY 508 -----NLNNRIDNVGNARAGIAQAATAGLVOAYLPKGSMAAIGGDTYRGEAG 556  
Db 1491 ETKQYTDQRMVEMDNKLSKTESKLSGSIASAMAMTGLPQAYTPGASMASIGGTYNGESA 1550  
QY 557 YAIYSSISDGGNWIILKTASGNSRHFAGSASVGYQW 594  
Db 1551 VALGVSMSVANGRWYKLOGSTNSQGEYSAAALGAGIQW 1588  
RESULT 8  
H91188  
probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno  
A:Reference number: A99629; PMID:21156231; PMID:11258796  
A:Accession: H91188  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA037903.1; PID:g13363955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs4480

Query Match 11.8%; Score 356; DB 2; Length 1588;  
Best Local Similarity 25.8%; Pred. No. 2.9e-10;  
Matches 149; Conservative 81; Mismatches 240; Indels 108; Gaps 21;  
QY 111 NLKIKONT---NENTNDSPFYSKKDLTDLTSVET--EKLSP-----GANGKNYNTS 159  
Db 1025 NMIEQNTQIINOLAGNTDATY-IOENGAGINVRTNDGCLAENDASAQGVGATAIGYNS 1083  
QY 160 DTGKLNFAKETAGTNGDPTVHLNGIGSTLTDLLNTGA-TTNVTNDNV-----TDDEKK 212  
Db 1084 VARGDSSVAIGQSGSDVDTGIALGSSSVSRVIAKGRSDTSITENGWVIGYDTTDELL 1143  
QY 213 RAASVD-----VLNAGNINIKVPGCTTASDNVDFVRYDTVEFLSADTKTTTVNVESK 266  
Db 1144 GAUSIGDGGKRYOIN-----VADGSEAHDAVT-VROLQNAIGAVATPTTKYFHANST 1195  
QY 267 DNKG-----KTEVRIGAKTSVIKEDGKLVTKGKDENGSTDEGGLVTAKEVIDAVNKA 322  
Db 1196 EEDSLAVGTDLSLAKGAKTVNGDKIGIGVAYVDANALN---GIAIGSNAQVIHNSIA 1252  
QY 323 GWRMKTNTANGOT-----GQAD-----KFETVTSNTVTFASGKG--- 357  
Db 1253 IGGSTTTTGAQTNTAYNMDAPQNSVGEFSVGSADGQRQITNVAAGSADTDVAVNGQLK 1312  
QY 358 -TTATVSKDDQGNIT-----VKYDVNVGDAL-----NVNQLQNSGN 393  
Db 1313 VTAQVQSNTQ-SITLNDNRVTNLDNRVTNIENGIGDVTGTSTKYFKTNTDGVDAQAQ 1371  
QY 394 LSKAVAGSGKVISGNVSPSKGM---DETVMNAGNIEITRN---GKNIDIATSMAP 447

Db 1372 KDSVAIGSGSIAAADNSVALGTSGVATEENTISVGSSTNORRITNVAAGKNATDAVNAQ 1431  
QY 448 QPSSVSLGAGADAPTLVSVDDEGALNVGSKDTNPKPRITNVAPOVKEGDVTNVAQLKGVAQ 507  
Db 1432 LKSSEAGGVRYDTKADGSDIDYSNITLGG-GNGGTTTRISNVSGVNNNDVNVYAQLKQSVQ 1490  
QY 508 -----NLNNRIDNVGNARAGIAQAATAGLVOAYLPKGSMAAIGGDTYRGEAG 556  
Db 1491 ETKQYTDQRMVEMDNKLSKTESKLSGSIASAMAMTGLPQAYTPGASMASIGGTYNGESA 1550  
QY 557 YAIYSSISDGGNWIILKTASGNSRHFAGSASVGYQW 594  
Db 1551 VALGVSMSVANGRWYKLOGSTNSQGEYSAAALGAGIQW 1588  
RESULT 9  
AH0110  
probable surface protein (partial) YPO0902 [imported] - Versinia pestis (strain CO92)  
C:Species: Versinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Versinia pestis, the causative agent of plague.  
A:Reference number: AB0001; PMID:21470413; PMID:11586360  
A:Accession: AH0110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0902

Query Match 11.2%; Score 338; DB 2; Length 658;  
Best Local Similarity 23.8%; Pred. No. 7.5e-10;  
Matches 154; Conservative 84; Mismatches 236; Indels 174; Gaps 28;  
QY 27 TKRASATVAT---AVLATLILFATVQ-----ANATDDDDLLYLPVQRTAV----- 67  
Db 105 TNLAPATISSTSDAVVGSQLYNLVODGTRYFHANSVNPDTSLASGLETTIAGVPATVVSQ 164  
QY 68 -----VLSFRSDKEGTG-----EKEGTEDSNWAVTFDEKRVL 99  
Db 165 DNGVGIGNTALVGAAATGGIAIGFTQVTAAGATAIGSAAQAQGA-----QSLAL 214  
QY 100 KAGAITLKAGDNLKIKONTNENTNDSFT-YSLKKDLTDLTSVETEKLSFG-ANGNKVNI 157  
Db 215 GAGAVTSQANSIALGAASINTVGAQSSYSAYAL-----TAPQASVGLGIGTALGNR-KI 268  
QY 158 TSDTKGLNFAKETAGTNGDPTVHLNGIGSTLTDLLNTGATTVTN--DNVTDEKKRAA 215  
Db 269 TGVAAQ-----SASSDANVNAQLTAVGDQVQON-----TANITSLGRVTTIE---G 312  
QY 216 SVKDVNLNAGNIKGVPGCTTASDNVDFVRYDTVEFLSADTKTTTVNVESKDKNGKKT--- 272  
Db 313 SMASIANGG-GVKYFHANSTQPSV-----ASGTSNVAIGPASLASNAALAS 359  
QY 273 ---EVKIGAKTSVIKEDGKLVTKGKDENGSTDEGGLVTAKEVIDAVNKAQWRMKT 329  
Db 360 GAGAVAILG--DGAASADGSAVIGQSGDNGRGVENVIG-----KYSN 400  
QY 330 TANGQTQADKFETVTSNTVTFASGKGTATVTSKDDQGNITVKYDVNVGDALNVQLQN 389  
Db 401 ASNTSSG-----TVSVGNAT-----GETRTVSNVADG-----LQATDAVNLRLQDQ 442  
QY 390 SGWNLDSKAVAGSGKVISGNVSPSKGMDETVMNAGNINI-EITRNGKKIDLI--ATPSA 446  
Db 443 -----IAASIVVENNVNQLQNTDGMFQVNNSSGLAKPSATGANSATGGAGSVA 492

[illegible]

Query Match	8.6%;	Score 260;	DB 2;	Length 1004;	
Best Local Similarity	22.2%;	Pred. No. 1.1e-05;			
Matches 164;	Conservative 103;	Mismatches 260;	Indels 212;	Gaps	
QY	2	NKYIRIWNALNANWVVVSELTRN-----	HTKRASATVATAVLATLILFATVQANAT	52	
Db	4	:    :    :    :    :    :	:    :    :    :    :		
QY	4	QNIYKFPWNLGWSVASHMTNDGGCDVYLRHSGVRNRLVLAIGLALTSVT-----	57		
QY	53	DDDDLXLEPQRTAVILSFR-----	SDKEGTEGEGTE-----	85	
Db	58	-----HAQSVKSPAWVTASVVAHVDSQVNRDTADRIPTG-----	DGSELTHMHALDWKFFFP	110	
QY	86	-DSNWAY-YFDEKRVLLKAGAITLKAGDNLIKIKONTNENTNDSFTYSKKDLTDLTTSVT	143		
Db	111	GNNSIAGIYF-SKAFAPNAL- GYNSSVTSQANGV-----	ALGSNST-VSGVNS	158	
QY	144	EKLSFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLNGIGSTLPDITLLNTGATNTVNTN	203		
Db	159	VALCAGSWMASELANVISYGGG-----	DGVTGPAVRRIINVVG-----	DGIGNNDVANKSOL	207
QY	204	DNYTDEKKAASVKDVL-----	NAGWNIKGVKPGTTA-SDNVDFVRIYDTVE	250	
Db	208	DGVTAASVNDVAASVKITLALTNQVTSVSAASKESTAIGSQAQAVADN-----	TTA	259	
QY	251	F-----LSADT-----	KTTTNNVESKD-----	NGKKTEKIG	277

Db	260	FGGRATIANAVCASALGFDSDSHAKGINSTTGTSVSLGGQGVSLGYNSFVGSGSFNGLAIG	319
Qy	278	AKTSVIKEKDGKLVTKG-----KDENGSSDDEGBGL--VTAKEVI-----DAVNKAG	323
Db	320	SNSLVLQQVDVSVALGSGSMASPNVVSVCSGDGLRCPARRIVNVYDGTIGNNDAYNKSQ	379
Qy	324	WRMKTTTANGOTGOADKFETV--TSGTNVTFASGKGTTAT--YSKDDQGNTIKYDVNVDG	380
Db	380	LDGVTASVNDWVASVKNIACAIQITGSGVASVSGDSQAAGSAQAAGSSIA---LGA	435
Qy	381	ALNVNLONGSWILD-----SKAVAGSSGKVISGNVSPSKCKMDETYNINAGNNIET	433
Db	436	RSRANATGSSALGVGDHALGANSTALGGOSTATISEGTSLG----YNSFVQSQTATNGIALG	492
Qy	434	RNGKNIDIATSMAPOFSSVSLGAGADPTLSVDEGALNVGSKD--TNKPV-RITNVAPG	490
Db	493	SN-----AIVSYGNSVALGAGSVASELNV-----ISVGGDGYTPAVRRIVNVGDG	539
Qy	491	VKEGDTNVNALKGVGAONLNN---RIDNVDGNAR---AGTAQAI-----ATAGLVQAVLPQK	541
Db	540	IGNDAVNKSOLDGVTASVNDVAASKVKIVGTIIQTGSGVASAIGKDXSTATGASAQAVGD	599
Qy	542	SMAIG-----GPTYGEAGYAIGYSSISDGGNWLIK-----G	574
Db	600	SSVALGTRATANAGSSVLGVDSRRARGINSTALGROSNAIGDGSVSLGFNSFVROSGEHH	659
Qy	575	TASGNSRGHFGA-SASVGY	592
Db	660	VALGTAGVSGKDSIALGY	678
RESULT 11			
G64964			
hypothetical protein b2000 - Escherichia coli			
C;Species: Escherichia coli			
C;Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 02-Feb-2000			
C;Accession: G64964			
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.			
.A.; Rose, D.J.; Mau, B.; Shao, Y.			
Science 277, 1453-1462, 1997			
A>Title: The complete genome sequence of Escherichia coli K-12.			
A;Reference number: A6720; MUID: 97426617			
A;Accession: G64964			
A>Status: nucleic acid sequence not shown; translation not shown			
A:Molecule type: DNA			
A;Residues: 1-1091 <BLAST>			
A;Cross-references: GB:AE000291; GB:U00096; NID:gl1788298; PIDN:AAC75061.1;			
A;Experimental source: strain K-12, substrain MG1655			
C;Keywords: nucleotide binding; P-loop			
F;683-690/Region: nucleotide-binding motif A (P-loop)			
Query Match 7.9%; Score 240; DB 2; Length 1091;			
Best Local Similarity 23.7%; Pred. No. 0.00013;			
Matches 149; Conservative 57; Mismatches 210; Indels 212; Gaps			
Qy	1	MNKYIRIWNALNAVYVVSSELNRHTKRASATVATAVLATLLFATVQANATDDDDLYLE	60
Db	57	LNTCYRLVNHMTGAFVVASELARARGKGVAAVLSLAAVTSPLVLA-----DIVVH	110
Qy	61	PVQRTAVVLSFRSDKETGETGEDSDSNWAYVFDEKRVLKAGAITILKAGDNLKIKONTNE	120
Db	111	P-----GE-----TWNGG--TLANHNDNQTVFTTNG	134
Qy	121	NTNDSPTYSILKDLTDLTSVETEKLFSFGANGKNVNTSDTKGLNFAKETAGTAGNGPTVH	180
Db	135	MTISTGLEYPDNE----ANTGGWQDGGTANKTIWTSG--GLQ--RVNPGSVSDTVI	186
Qy	181	LNGIGSTL----TDTLNTG-----ATTNVTNDVNTDDEKKRAASVKOVNLNAGWI	227
Db	187	SAGGGSQLOGRAVNTTLNGGEQWHEGAIATGVINDK-----GWQV	228

Qy	228	KGVKPGTASDNVDFVRT-----YDVEFELSADTKTTTNNVESKONGKKTEVKIG	277
		: :	
Db	229	--VKPGTAVTDVT--VNTGAEGGPAENGDTCQFVRGDAVRTTIN---KNGRQIVRAEG	280
		: :	
Qy	278	-AKTSVTIKEKGLVTKGKDE--NGSSSTDEGGLVTAKEVIDAVNKAGWR-----K	327
		: :	
Db	281	TANTVVYAGGDTVIGHALDTTLNGGYQYVING--GTASDTV--VNSDQWQIVKNGGVAG	337
		: :	
Qy	328	TTTANGOTGQADKEFTVCTNNVTFASG----KGTATVYSKDDOOGNITVKYDVNVGDALN	383
		: :	
Db	338	NTTVN-QKGRL-QVDAGGTATNTLKGQCALVSTAATVT-----G	376
		: :	
Qy	384	VNQLNSGNWMLDSKAVAGSGKVI SGNVSPSKGKMDETVNNAGNNBITRNGKNIDIAT	443
		: : :	
Db	377	INRL-----GAFSVBEGKADNV-----LENGGRGLDVL	405
		: :	
Qy	444	SMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDTNKPVRTNVAPGVKEGDVTNVAQLK	503
		: :	
Db	406	-----GHTATWTRVDDGGLDVRNGGTATTVSMGN--GGVLLAD-----S	443
		: :	
Qy	504	GVAQNLNRIIDNNGNARAGIAQAATAGLVQAYL--PKGSMAATGGDT-----Y	551
		: :	
Db	444	GAA-----VSGTRSDGKAFCIG-GQADALMLEKGSFTLNAAGDTATDTTVNGGLF	493
		: :	
Qy	552	RBGAGYAIGVSSISDCGNWIIKGTASGN	579
		: :	
Db	494	TARGGTLAGTTTLNNGAILTSLGKTWNN	521
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RESULT 12
S28634
adhesin AIDA-I precursor - Escherichia coli plasmid pIB6
C:Species: Escherichia coli
C:date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 08-Oct-1999
C:Accession: S28634: S22680: S28881: S72657

```

A;Benz, I.;  
submitted to the EMBL Data Library, March 1992  
A;Reference number: S28634  
A;Accession: S28634  
A;Molecule type: DNA  
A;Residues: 1-1286 <BEN>  
A;Cross-references: EMBL:X65022; NID:G42254; PIDN:CANA6156.1; PID:942255  
R;Benz, I.; Schmidt, M.A.  
Mol. Microbiol. 6, 1539-1546, 1992  
A;Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeal pathogen *E. coli* serotype O157:H7  
A;Reference number: S28638  
A;Accession: S28638  
A;Molecule type: DNA  
A;Residues: 1-1286 <BEN>  
A;Cross-references: EMBL:X65022; NID:G42254; PIDN:CANA6156.1; PID:942255  
R;Benz, I.; Schmidt, M.A.  
Mol. Microbiol. 6, 1539-1546, 1992  
A;Title: AIDA-I, the adhesin involved in diffuse adherence of the diarrhoeal pathogen *E. coli* serotype O157:H7  
A;Reference number: S28638  
A;Accession: S28638  
A;Molecule type: DNA  
A;Residues: 1-1286 <BEN>

A:Accession: S22080  
A:Status: nucleic acid sequence not shown  
A:Molecule type: DNA  
A:Residues: 839-1286 <BE2>  
A:Cross-references: EMBL:X65022  
A:Experimental source: strain 2787  
A:Accession: S28881  
A:Molecule type: protein  
A:Residues: 50-56 <BE3>  
A:Experimental source: strain 2787  
R:Suhr, M.; Benz, I.; Schmidt, M.A.  
Mol. Microbiol. 22, 31-42, 1996  
A:Title: Processing of the AIDA-I precursor: removal of AIDA and evidence  
A:Reference number: S72657; MUID:97055419  
A:Accession: S72657  
A:Molecule type: protein  
A:Residues: 847-856 <SUH>  
A:Experimental source: DAEC strain 2787  
C:Genetics:  
A:Genome: plasmid pIB6  
C:Keywords: membrane protein  
F:1.49/Domain: signal sequence #status predicted <SIG>  
F:50-1286/Product: adhesin AIDA-I #status predicted <NAT>

Query Match	7.6%;	Score 230;	DB 2;	Length 1286;
Best Local Similarity	17.0%;	Pred. No. 0.0005;		

	Matches	156;	Conservative	106;	Mismatches	291;	Indels	364;	Gaps								
Qy	1	MNKYRIIWS	NSALNAWV	WSELRNH-----TKRASATVATA--VLATLLEATVQA	NS	51											
Db	1	MNKAYSII	WSHRQAVI	SELARGHGFVLA	KKNTLLVAVVSTIGNAF	AVNISGTVSSG	60										
Qy	52	TDDDDLY	LEPVQTA	VVLSPFRDKEGTGE	KEGTE-----	85											
Db	61	TVSSG-----	ETQIVISGR	SGNSATVNSGGTQIVNNG	GKTTATTVNSSGSQNVGTSGA	113											
Qy	86	-----	DSNWAYV	FEDEKVKL	KAGAIT---	105											
Db	114	TISTIVNS	GGIQRVSS	CGVASATNL	SGCAQNIYNLGHASNTV	IFSGCGNTIFSGGTTDT	173										
Qy	106	-LKADN	LKIQN---T	NENTNDSSFTY	LSKKD---LTDLTS	VETEKLSPFGANGK	NVIT	158									
Db	174	NISSGGO	ORVSSG	VGASNTTINS	GAGNILSEGAISTHSSG	NOYISAGANATETIVN	233										
Qy	159	SDTKGL	NFAKETAG	TNCDP	VPVHLNG-----IGSTL	TDTLN	194										
Db	234	SG-----	GQVRNSG	AVATGTVL	SGGTONVSSG	GSATSTSVNSGVQTVFAGATV	TDVTN	289									
Qy	195	TGATTNT	NDNVTD	DDEKKRA	SVKDVNLNAG---WNIGK	-----	229										
Db	290	SGGNQ	NISSG	GISETTV	NTVSGTQNIYSG	SALSANIKGSQIVNSE	CTAINTLVSDG	QY	349								
Qy	230	-VKP	GTASDN	VDVPTDY	TFEFLSADTKTT	VTVNESKDKNGKTEYKIGAKTS	VIKE--K	286									
Db	350	HIRNG	GIASGTIV	NOSGY-----	VNISGGV	AEASTIINSG	TLRLVSLD	SGVA	395								
Qy	287	DGKL	VTCKGD	-ENG	S-----STDEG	EGLVTAKEVIDAV	NKAG	----	323								
Db	396	RGTIL	NSGREN	SVNGSV	YNAMITGGNOYIYSDGE	ATAAIVNTSGFORINS	GGTAPVQ	455									
Qy	324	-----	WRMKT	TTTANGO	-----TG	336											
Db	456	NSVVV	TRVSSA	KPDAEYV	SGGKTQVYLWRGI	WISNFLTAVWSMPPG	TASGANV	NL	515								
Qy	337	QADK	FETV	TSGTNT-----	FASGKGT	TATVSKDDOGNTITVYDVNV	GDALNMV	NOLQ--	388								
Db	516	RLN	FAGNV	VVGTIL	NBEGROYVYISG	TATSTVGNNEGREYVLSGGITD	GTIVNSG	GLQAV	575								
Qy	389	NSGN	NLDSK	VAGSSGRVI--	SGNVSP	SKGMDETVINAGN--NIE	TRGNK	NI	DIAT	443							
Db	576	SSGK	KASATV	INEGGAOFV	YDGGQVGTN	IKNGGTIRVDSGASAL	NIALSSGN	LEPTSTG	635								
Qy	444	SMAPQ	FSV-----	SLGAGAD-----	APTLSV	DDGALN--	472										
Db	636	ATL	PELT	MAALSV	QNSHASN	IVLEN	GGLLRVTS	SGGTATDTTVNS	AGR	LRID	GGT	INGT	695				
Qy	473	-----	VGSKD	NKP	RVITN	VP-----	489										
Db	696	TTINAD	GIVAGT	NIQNDGN	FLNLAENY	DPETELSG	SVLKV	KDNTGIMTYAGT	LT	QAQV	755						
Qy	490	GVKEG-----	DVTN	VAOLK	VQAON-----LNN	RIDNV	DGNAR	523									
Db	756	NVK	NGGIF	DSAVV	NADMV	NQNAV	INISQ	PAITSVN	NGSIV	INN	ST--ING	NI	TD	813			
Qy	524	IAQ	ATAG	IFGL	VOAYLP	PKSM-----	MAITGGDT-----	YRGEAG	YAIGY	SSISD	GG	568					
Db	814	ADLS	FGT	AKLL	SATVNS	GLVNNK	NIILNP	T	KESAG	N	TLTVS	NTGT	PGSV	SILG	GV	LE	873
Qy	569	N-----	WI	IK	TAS	GN	580										
Db	874	NSL	TD	RL	V	V	K	G	T	S							

RESULT 13  
AF0394  
probable adhesin hmwa [imported] - Yersinia pestis (strain C092)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AF0394



R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Hoiden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AF0394  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1910 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC92482.1; PID:gl5981183; GSPDB:GN00175  
C:Genetics:  
A:Gene: hmwA

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Query Match          7.3%; Score 221.5; DB 2; Length 1910;
Best Local Similarity 21.5%; Pred. No. 0.0022;
Matches 153; Conservative 86; Mismatches 271; Indels 201; Gaps 30;

Qy 14 NAWVVSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLEPVQ-----R 64
Db 898 NATITANNISMN---GNITANDAVLMTNFTLAKGDIKTD---LTSPTKGLWFRNGGM 950

Qy 65 TA---VWLSFRSDKEGTEGSDSNWVYFDEKRV-LKAGATLKGADNLKIKQNTNE 120
Db 951 TAANNILLVANSTSGETVKINASSSNKMNITAGKDIIAGNSKTATGPNINT-ENYNI 1009

Qy 121 NTNDSSTFYSLLKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGCDPVH 180
Db 1010 ETNNGNFT-----TNGITSTWLSGVNVASANG--VDITSNSTG-----TGGVILDNTNI 1055

Qy 181 LINGISTLTLANTGATTNTNDVTDDEKRAASVKDV-----LNAGNINKGV--KPGT 234
Db 1056 LTTVGD-----INT-IVTNSSGKIWKISNSTLNSNKDITLVGVSAGQN-EGVLIQSS 1107

Qy 235 TASDNDVPRYDVVEFLSADTKTTTVNVESKNGKKTEVKIG--AKTSVKEKDGKLV 292
Db 1108 DASRN-----NISAQGNITLIGKMGNGSGQHSILNLGNVSLTS-----S 1146

Qy 293 GKGDENGSSDDEGBGLVTAKEVIDAVNKAGWRMKTFTA-----NGOTGQADK 340
Db 1147 GRNIDINGSSAGTGDVYTFNVELNATAGNVSIYAETKTALSTSLNAVLSLGNNSIKAQN 1206

Qy 341 FETVSGTNTVFAGKGTATVSKDDQGNITVK-----YDYNVGDALVN 385
Db 1207 GWLICKAPNTQAGIGFRANSSLSVDGNIILKGETGVGATRKIDFYGANTLNIKGS 1266

Qy 386 QLQNSWNLDSKAVG----- 401
Db 1267 QLSLLENGKGAQDTAGGNGISYTSIAKLTVNNGSLKMEGRSTSGTINFPSSNNTLVFN 1326

Qy 402 -----SSGKVISGNVSPSKGMD-----ETVNNIAGN 428
Db 1327 GDGDTLKGSSVAGTGAAGISGVVNNSTGPMTEIGISTDCAGVHIFSABHRIDRINVTGSS 1386

Qy 429 ----NIEITRNGKNIDIA-TSMAPQFSSVSLGA--GADAPTLSDDEGALNWSKDTNKP 481
Db 1387 THAEGRLISGNAIIVDTTLTKSINGSQVKIDSLPGSSVVRVSLVDNATLN-GSSSSCKG 1445

Qy 482 VRITNAPGVKEGVTWVAQLKGAQNLNRRIDNDVGNARAG--IAQAIATAGLVQVAYLP 539
Db 1446 VEITSDINGIHSSINGTTGTGTGIDIGEN-SNVITGTSEADLLILQGVATTG-----T 1498

Qy 540 GKSMMAIGDGYRGEA-----GVAIGYSS-ISDGGNWIILKGTASGNSRG 582
Db 1499 GTGKILGNNDLSNTSLNSSAVDGIADITGFLANQGVNILNGTASGSGIG 1549
```

RESULT 14  
AD0123

probable autotransporter protein yaph [imported] - *Yersinia pestis* (strain CO92)

C:Species: *Yersinia pestis*

C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001

C:Accession: AD0123  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Hoiden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AD0123  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-3705 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89847.1; PID:gl5979073; GSPDB:GN00175  
C:Genetics:  
A:Gene: yaph

```
Query Match          7.2%; Score 217.5; DB 2; Length 3705;
Best Local Similarity 20.6%; Pred. No. 0.0083;
Matches 164; Conservative 85; Mismatches 272; Indels 277; Gaps 36;

Qy 2 NKIYRIIWNLSALNAWVVSELTRNHTKRASATVATVATLFLFATVQANATDDDDLYLEP 61
Db 364 NVIYNLGTGSILKA-----TWGILAT-----KNANNASDIYRS 398

Qy 62 VORTAVVLSFRSDKEGTG-----EKEGTEDSNWVYFDEKRVLKA-----GATLKGAD 110
Db 399 AGDITAAATGISATHTGTGVKIKNDGTTTSTAGIAISSASIKSIVSDTGTITATAGT 458

Qy 111 NLKIKQ-----NTNENTNDSSFTYSI-KKDLTDLTSVETEKLSFG---ANGNKV 155
Db 459 GVNVLASAILNLFGGTINTSATANGITFAGTEGGHTLTDLT---INLGTGIALSNVAGV 515

Qy 156 NITSDTKGLNFAKETA-----GTNGDPTVHLN--GIGSTLTDTLNT----- 195
Db 516 NLTLNVTNLNTLNGTALNSLTGLTLYVDSLNGRNTINIEGAGIGIAATNTELTDPDAEALD 575

Qy 196 -----GATTNVTNDVTDDEKRAASVKOVNLNAGWNI-KGVKPGTPTASDNVDF-VRTYD 247
Db 576 INVNAGIGIQATGGVNLASNLIIINVANTLGTALQITDGTIDNTTTIGNETQLNAENAT 635

Qy 248 TVEFLSADTKTTTVNVEKONG--KKTEVKIGAKTSVIEK---DGKLVTCGKDE---- 298
Db 636 AINFLGSSSKTL-----NNGTIGKSVIFAGVADHIIINNNGTLDGTLTTGAGNDTLVLD 689

Qy 299 -----NGSSTDEGEGLVTAKEVIDAVNKAGWRM 326
Db 690 SSSOSNDVINLGDGNNSVTIONGATVSSIITGNGDFTTINGMSVGSYTLGSLD-ACITGL 748

Qy 327 KTTTANGOTGO-----ADKFETVTSQTNV----- 350
Db 749 NTLNPNASTDELAATAATSLQGFTNINLVDSHITLVSDDNIGSGMVNIDSSSELLFGSTFDG 808

Qy 351 ----TFASGKGT-----TATVSKDDQGNITVKYDVNVGDAL---NVNQLQNS-----GW 392
Db 809 ILHATLGAAGTSAIVNNSANVSLSEQASMFAGTQVWNOGCGALTASNSNLGSAKIGLDGTL 868

Qy 393 NLDSKAVAGSGKVIYGNVSPSKGMDETVINAGNNTIEITRNGKNIDIA-TSMAPQFSSV 452
Db 869 NLDNAL---FNHVLGTNGT-----LNVAKNLATTA---PDFGSTVGVGAFSGI 910

Qy 453 -----SLGAGAD-----APTLSDDEGALNVGSKD----- 477
Db 911 VNLTKTTTFALSADNAALASATLKSDDSVTTGVTGTTDLTGLDLSGCTLIFDGAVPQSQ 970

Qy 478 TNKPVRTNVPVKEGVDV-----TNYAQLK-----GVAQNLLNRRIDNDVGG 518
Db 971 TSGVVTYTDLA--LNSGTVNITGSGSWNDTPLATNVSIILEODRAGSTLELIN-ATNVTG 1027

Qy 519 NARA-----GIAQAIATAGLVQVYLPCKSMMA-----IGGDTYRCEAGYAIYS--- 562
Db 1028 DIDALDLLVNGTATISGTQGVQSAIQOQGSIVANAHHVGLASSNSNGDSGLVYNYTLA 1087

Qy 563 ---SISDGGNWIILKGTASG 578
```











CC	EMBL; X65022; CAA46156.1; -	
DR	PIR; S28634; S28634.	
KW	Cell adhesion; Signal; Outer membrane; Plasmid.	
FT	SIGNAL 1 49	
FT	CHAIN 50 ?	ADHESIN AIDA-I.
FT	PROPEP ?	1286
SQ	SEQUENCE 1286 AA; 132271 MW; B2A00F72AC05FB34 CRC64;	
Query Match		
Best Local Similarity 7.6%; Score 230; DB 1; Length 1286;		
Matches 156; Conservative 106; Mismatches 291; Indels 364; Gaps 31;		
QY	1 MNKIYRIIWNLSALNVAWVSELTNRH-----TKRASATVATA--VLATLLFATVOANA 51	
DB	1 MNKAYSIIHSHSQIAIVASELARGHGFVLAKNTLLVLAVVSTIGNAFVAVNISGTVSSGG 60	
QY	52 TDDDLLEPVPQRTAVLVLSFRSDEKGTGEKTE-	
DB	61 TVSSG-----ETQIVYSGRGSNATVNSGGTQIVNNGGKTATTVNSSGSONVCTSGA 113	
QY	86 -----DSNWAYFDEKRVLKAGAIT--- 105	
DB	114 TISTIVNSGGIORVSSGGVASATNLSSGAQNIYNLGHASNTTIFSGNQITFSGGITDST 173	
QY	106 -LKAGDNLKIQN---TNEINTDSSFTYSLKGD---LTDLTSVETEKLSFGANGKVNIT 158	
DB	174 NTSSGQQRVSSGGVASNTTINSSGAQNIILSEGAISTHSSGNGQYISAGANATETIVN 233	
QY	159 SDPKGLNFAKETAGTNGDPTVHLNG-----IGSTLTDTLLN 194	
DB	234 SG---GFQVNSGAVATGTVLSGGTQNVSSGSAISTSVNSGVQTVFAGATVTDTTVN 289	
QY	195 TGATTNVTNDVTDDEKRAASVKDVLNAG----WNIGK----- 229	
DB	290 SGCNQNISSGGIVSETTVNSGQNTYISGGSALSALSIQVINSSEGTINTLVSDGGYQ 349	
QY	230 -VKPGTTASDNVDFTYDTVEPLSADTKTTTVNVEKDKGKTEVKIGAKTSVIRE--K 286	
DB	350 HIRNGIAGSTVNSQSGY-----VNISGGYAEETIINSGLTVLSDGYA 395	
QY	287 DGKLVTKGKD--ENGSS-----STDEGEGLVTAKEVIDAVNKGAG----- 323	
DB	396 RGTILNSGRNVNGSVSNAMINTGGQYIYSDGEATAIIVNTSGFORINSGGTAPVQ 455	
QY	324 -----WRKMTTANQ-----TG 336	
DB	456 NSYVTVRTVSSAAKPFDAEYISGGKQTVYIWRGIWYSNFLTAVWMSFPFGTASGANVLSG 515	
QY	337 QADKFEVTVSGTNVT-----FASGKGTATVSKDQGNITVKYDYNVGDALNVNOLQ-- 388	
DB	516 RLNAFAGNVVGTLLNDEGRQYVYSGATATSTVGNNGREYVLSGGITDGTVLNSGGQLAV 575	
QY	389 NSGNWLDKSAVAGSSGKVI--SGNVSPRSKGMDETINAGN---NIEITRNGKNIDIAI 443	
DB	576 SSGKASATVINBGAQFVYDGGQVGTGNTKNGGTIRVDSGASALNALSSGGLNLTSTG 635	
QY	444 SNAPQFSSV-----SLGAGAD-----APTLSVDDEGALN-- 472	
DB	636 ATLPELTMAALSVSONHASNIIVLENGLLRVTSGGTATDTTVNSAGRLRIDGGGTINGT 695	
QY	473 -----VGSKDTNKPVRITNVAP----- 489	
DB	696 TTNADGIVAGTNIQDNGFILNLAENYDFETELSSGVLVKDNTGIMTYAGFLTQAQGV 755	
QY	490 GKVEG-----DVTNVAQLKVAQN-----LNNRIDNVDGNARAG 523	
DB	756 NVKNGGIIFDSAVVNADMAVNQININISDOATINGSVNNNGSIVNNSI--INGNITND 813	
QY	524 IAQAIAATAGLVQALYLPKSKM-----MATGGDT-----YRQBAGYAIGYSSISDGG 568	
DB	814 ADLSFGTAKLLSATVNGSLVNNKNIILNPTKESAGNTLTVSNYTGTPGVSISLGGVLEGD 873	

QY	569 N-----WIIKGTASGNS 580	
DB	874 NSLTDLRLVVKGNTSGQS 890	
RESULT 3		
ID	YDEK_ECOLI	STANDARD; PRT; 1325 AA.
AC	P32051; P77168;	
DT	01-OCT-1993 (Rel. 27, Created)	
DT	01-NOV-1997 (Rel. 35, Last sequence update)	
DT	16-OCT-2001 (Rel. 40, Last annotation update)	
DE	Hypothetical lipoprotein ydek precursor (ORET).	
GN	YDEK OR ORF OR BI510.	
OS	Escherichia coli	
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;	
OC	Escherichia	
OX	NCBI_TaxID=562;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=K12 / MG1655;	
RX	MEDLINE=97426617; PubMed=9278503;	
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,	
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,	
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,	
RA	Mau B., Shao Y.;	
RT	"The complete genome sequence of Escherichia coli K-12.";	
RL	Science 277:1453-1474(1997).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=K12;	
RX	MEDLINE=97251357; PubMed=9097039;	
RA	Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,	
RA	Kasai H., Kashimoto K., Kimura S., Kitagawa M., Kitagawa M.,	
RA	Makino K., Mikii T., Mizobuchi K., Mori H., Mori T., Motomura K.,	
RA	Nakade S., Nakamura Y., Nishimoto H., Nishio Y., Oshima T., Saito N.,	
RA	Sampeki G., Seki Y., Silvasundaram S., Tagami H., Takeda J.,	
RA	Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;	
RT	"A 570-kb DNA sequence of the Escherichia coli K-12 genome	
RT	corresponding to the 28.0-40.1 min region on the linkage map.";	
RL	DNA Res. 3:363-377(1996).	
RN	[3]	
RP	SEQUENCE OF 595-1325 FROM N.A.	
RX	MEDLINE=94100243; PubMed=8274505;	
RA	Cartwright P.J., Timms M.W., Lithgow T., Hoeg P.B., Hoogenraad N.J.;	
RT	"An Escherichia coli gene showing a potential ancestral relationship	
RT	to the genes for the mitochondrial import site proteins ISP42 and	
RT	MOM38.";	
RL	Biochim. Biophys. Acta 1153:345-347(1993).	
CC	- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor	
CC	(Potential).	
CC	- SIMILARITY: TO E.COLI YEAL.	
CC	- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS	
CC	ISP42 AND MOM38.	
CC	- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A	
CC	FRAMESHIFT IN POSITION 653.	
CC	-----	
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).	
CC	-----	
DR	EMBL; AE000248; AAC74583.1; -	
DR	EMBL; D90793; BAA15190.1; ALT_INIT.	
DR	EMBL; D90794; BAA15197.1; ALT_INIT.	
DR	EMBL; X73295; CAA51730.1; ALT_FRAME.	
DR	PIR; S34315; S34315.	
DR	EcoGene; EG11780; ydek.	
DR	PROSITE; PS00013; PROKAR_LIPOPROTEIN; 1.	









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CC -----
DR EMBL: X16353; CAA34403.1; -
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Präm: PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1333 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1334 1654 32 KDA BETA PEPTIDE.
FT DOMAIN 1181 1188 POLY-THR.
SQ SEQUENCE 1654 AA; 168184 MW; D7AB70FB7087F618 CRC64;

Query Match 6.3%; Score 189.5; DB 1; Length 1654;
Best Local Similarity 21.7%; Pred. No. 0.035;
Matches 148; Conservative 85; Mismatches 284; Indels 165; Gaps 34;

QY 15 AWVVSELFRNHTKRA-----SATVATAVLATL-----LFAVQA-NATDDD 55
Db 181 ASTLVENLANPTQKAPLILGDNAVANGVNTLNVNCFGIVQVSNKSFATVKAINIADGQ 240
QY 56 DYLEVPQRTAVVLSFR-----SDKEGTGEK-----EGTESNNAVYF 93
Db 241 GIIFNTDANNANLNIQAGGTTINFTGDTGRLVLLSKHAAATNFNITGLSGNLKGV 300
QY 94 DEKRVLKAGAITLKAGDNLKIKQNTENTNDSSFTYSLKDLTDLTSVETEKLSFGANG 153
Db 301 EFNVAVDGOLTNAGAAANAVICNGAGRAAGFVVSVD-----NGK 342
QY 154 KVNITSDTKGLNFAKTAGTNGDPTV-HLNGIGSTLTDLTLLTGATTNVTNDN--VTDDE 210
Db 343 VATIDGQVAKDMVIOQSANATGOVNFRIHVDVGADGTAPKTAASKVTITQDSNFGNTDF 402
QY 211 KKAASVK--DVLNAGWNIGK--VKPGTTRASDNVDFVRYD--TVEFLSADKTTTVN- 262
Db 403 GNLAQIKVFNATLTGNETGDSNFGNTAG-----VITFDANGTLESADANAVAVTN 457
QY 263 ---VESKDNQ-----KKEVEIGAKTSVKEKDKGLVTGK-----GKDENGSTD 304
Db 458 ITAIEASGAGVQVLSGTHAEELRIGNAGSIFKLADGTVINGKYNQVALGGLAAGTITL 517
QY 305 EGELVTAKEVIDAVNKGAWRMKTTTANGOTGQADKFETV-SGTNVTFASG-----K 356
Db 518 DGSATITGD--IGNAGGAALQRITLAN-----DAKKTTLTGANIIGAGGTTIDLOAN 569
QY 357 GTTATVSKDDQGNITVYKDYVNVG-DALNVNQLQNSGNWLDKAVAGSSGKVISGNVSPSK 415
Db 570 GGTIKLT-SPQNNIVDFDLAIATDQTV-----VDASLTNAQTITNGKIG-TI 618
QY 416 GKMDTV-NINAGNNIETRNG---KNIDIATSMAPQF-----SSVSLGAGA--- 458
Db 619 GANNKTLGQFNIGSSKTVLSNGVNAINELVIGNDGAVQFAHDYTLTRTNAAAGQGIIF 678
QY 459 -----DAPTLSDVDEGALNVGSKDTPKVRITNVPAGVKECDVTNVAQLKGVAQNLNRI 513
Db 679 NPVVNNCTTLA---AGTNLGS-A-TNPLAEINFGSGVNVVDVLNVGE--GVNLXATN-I 730
QY 514 DNVDGHRAGIAQAIAT---AGLV-----QAYLPKSKMAATGGDYRGEAGYAG 560
Db 731 TTTDANYGSFVFVAGGTNIVSGTVGGQGNKFNVALENGTTVKFLGNATFNNGNTTIAAN 790
QY 561 YSSISDGGNNIIKGTASGNSRG 582
Db 791 -STLQIGGNTYADCVASADGTG 811

RESULT 8
```

```
OMPB_RICCN STANDARD; PRT; 1655 AA.
ID OMPB_RICCN 09KX98; 09XC45;
AC OMPB_RICCN 09KX98; 09XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (ScA5) (rOmpB)
DE (Surface protein antigen) (Cell surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide).
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RA MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
RA Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M.,
RA Raoult D.;
RT Mechanisms of evolution in Rickettsia conorii and R. prowazekii.;
RL Science 293:2093-2098(2001).
RN [2]
RP SEQUENCE OF 33-1649 FROM N.A.
RC STRAIN=Indian tick typhus, and Malish 7;
RX MEDLINE=20393643; PubMed=10939649;
RA Roux V., Raoult D.;
RT Phylogenetic analysis of members of the genus Rickettsia using the
RT gene coding the outer-membrane protein rOmpB (ompB).";
RL Int. J. Syst. Evol. Microbiol. 50:1449-1455(2000).
RN [3]
RP SEQUENCE OF 353-1655 FROM N.A.
RC STRAIN=Malish 7;
RA Stenos J., Walker D.;
RT "The rickettsial outer membrane protein A and B genes of Rickettsia
RT australis, the most divergent rickettsia of the spotted fever group.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC -----
DR EMBL: AE008659; AAL03623.1; -
DR EMBL: AF123721; AAF34124.1; -
DR EMBL: AF123726; AAF34129.1; -
DR EMBL: AF149110; AAD39533.1; -
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Präm: PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall; Complete proteome.
FT CHAIN 1 1334 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1335 1655 32 KDA BETA PEPTIDE.
FT VARIANT 61 61 P -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 75 75 G -> S (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 78 78 K -> N (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 251 251 V -> A (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 413 413 N -> D (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 959 959 I -> V (IN STRAIN INDIAN TICK TYPHUS).
FT VARIANT 988 988 A -> T (IN STRAIN INDIAN TICK TYPHUS).
```

FT VARIANT 1139 1139 R -> L (IN STRAIN INDIAN TICK TYPHUS).  
FT CONFLICT 353 354 KD -> GH (IN REF. 3).  
FT CONFLICT 776 776 F -> S (IN REF. 3).  
FT CONFLICT 1159 1159 E -> D (IN REF. 3).  
FT CONFLICT 1177 1177 G -> S (IN REF. 3).  
FT CONFLICT 1492 1492 H -> R (IN REF. 3).  
SQ SEQUENCE 1655 AA; 168342 MW; E49E19377D5FCE37 CRC64;

Query Match 6.2%; Score 188.5; DB 1; Length 1655;  
Best Local Similarity 22.3%; Pred. No. 0.039;  
Matches 146; Conservative 76; Mismatches 298; Indels 135; Gaps 28;

Qy 10 NSALNAYVVVSELTRNHRKASATVATLALLFATVQANATDDLLYLPVQRTAVVL 69  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 211 NGTLN-----VINGFKVSSKSFATVNVINGDQGQIMNTDADNVNTLNQANGATI 263  
Qy 70 SFRDSKEGTG-----EKEGTEDSNNAYVFEKRVKAGAITLKAGDNLIK 115  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 264 TF-NGTGTGRVLVLSKNAAATDFNVTSGLGNLKGITFEFTVAVNGOLKANAGANA 322  
Qy 116 QNTNENTNDSSTYSLLKDLTSLTSVETKLSFGANGKNVITSDTKLGNFAKETAGTNG 175  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 323 GTNNGAGRAAGFVVSVD-----NGKVATIDGQVYAKDVMVQSANAVG 364  
Qy 176 DPT-----VHLANGIGSTLTDLLNTGATNTVNDVTDDEKKRAASVKD---V 228  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 365 QVNFRIHVDTGDTAPKTAASKVAITQNSFGTDPGNLAAQIIVNTWTLNGNFTGD 424  
Qy 229 GVKPGTASDNVDFRTYD---TVEFLSADTKTTTVN-----VESKNG----- 274  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 425 ASNPGNTAG-----VITFDANGTLASADANAVTNNITAEASGAGVQVLSGTHAAEL 479  
Qy 275 KIGAKTSVIEKDKGLVTGK-----GKDEGSSSTDEGELVTAKEVIDAVNKAGWRM 326  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 480 RLGNAGSVFKLADGTVINGKNVQALVGALAGTITLDGSAITG-----DIGNAGG--- 532  
Qy 327 KTTTANGOTGADKFETV-----SGTNVTFASGKGTATVSKDDQGNITVKYDV- 376  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 533 -AAALQGITLANDATKTLTGGLGANGITGOTINFGANGTITKLTSTQNNIVVDFDLA 589  
Qy 377 -----NVGDALNVNOLNSGWNLDKSAVAGSSKVISGNVSPSKGM-DETVNIN--- 426  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 590 IATDQGTGVVDASSLTNAQTLINGKIGTVGANNKTLGQFNIGSSKTVLSDGDVAINE 649  
Qy 427 GNN--IEITRNGKNIDIAATNAPO-----FSSV-----SLGAGADAPTLSD 475  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 650 GNNGAVQFAHTYLLITRTTNAAGOGKIIFNPVNNNTTLATGTLNLS-ATNPLAEINFGS 708  
Qy 476 KDTNKPVRITNVAPVKEGCVTVNVAQLKGVAQNLNRRIDNVDG-NARAGIAQAATAGLV 534  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 709 KGAANVDVTLNVGKGVNL-YATNITTTDA---NVGSFIFNAGGNTIVSG----- 758  
Qy 535 Q-----AYLPKGSMAAIGDGTGGEAGYAGYSSISDGGNWIKGTASNSRG 582  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 759 QGNKNTVALDNGTIVKPLGNATENGNTTIAAN-STLIQIGNYTADEFVASADGTG 812

## RESULT 9

ID ICEN\_XANCT STANDARD; PRT; 1567 AA.  
AC P18127;  
DT 01-NOV-1990 (Rel. 16, Created)  
DT 01-NOV-1990 (Rel. 16, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Ice nucleation protein.  
GN INAX.  
OS Xanthomonas campestris (pv. translucens).  
OC Bacteria; Proteobacteria; gamma subdivision; Xanthomonas group;  
OC Xanthomonas.  
OX NCBI\_TaxID=343;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=X56S;  
RX MEDLINE=91080859; PubMed=2259339;  
RA Zhao J., Orser C.S.;  
RT "Conserved repetition in the ice nucleation gene inax from  
Xanthomonas campestris pv. translucens.";  
RL Mol. Gen. Genet. 223:163-166(1990).  
CC -|- FUNCTION: ICE NUCLEATION PROTEINS ENABLE BACTERIA TO NUCLEATE  
CRYSTALLIZATION IN SUPERCOOLED WATER.  
CC -|- SUBCELLULAR LOCATION: Outer membrane (By similarity).  
CC -|- DOMAIN: CONTAINS 153 IMPERFECT REPEATS OF THE CONSENSUS  
OCTAPEPTIDE A-G-Y-G-S-T-L-T; FURTHER ON A 16-RESIDUE AND A  
REGIONAL 48-RESIDUE PERIODICITY IS SUPERIMPOSED.  
CC -|- MISCELLANEOUS: A STRUCTURAL MODEL IS SUGGESTED IN WHICH THE ICE  
NUCLEATION PROTEIN DISPLAYS A SYMMETRY RELATED TO THAT OF ICE.  
CC -|- SIMILARITY: BELONGS TO THE BACTERIAL ICE NUCLEATION PROTEIN  
FAMILY.  
CC  
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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
CC EMBL; X52970; CAA37140.1; -.  
DR PIR; S11672; S11672.  
DR HSP; P06620; LINA.  
DR InterPro; IPR000258; Ice\_nucleatn.  
DR Pfam; PF00818; Ice\_nucleation; 81.  
DR PRINTS; PR00327; ICENUCLEATN.  
DR PROSITE; PS00314; ICE\_NUCLEATION; 57.  
KW Ice nucleation; Repeat; Outer membrane.  
SQ SEQUENCE 1567 AA; 152548 MW; C8B451D959ECAD63 CRC64;

Query Match 6.2%; Score 188; DB 1; Length 1567;  
Best Local Similarity 20.3%; Pred. No. 0.039;  
Matches 117; Conservative 82; Mismatches 263; Indels 114; Gaps 19;

Qy 77 GTGKEGTEDSNWAVYFDEKRVKAGAITLKAG-----DNLKIK--QNTNENTNDSF 127  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 735 GSTQTSGLSLTLAGYGTQARKGSDVTAGYGTGTAGADSTLIAGYGTQTSGLSS 794  
Qy 128 TYSLLKDLT-----DLTSVETKLSFGA-----NGNKVNITSDTKLGNFAKE 169  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 795 TAGYGTQARKGSDIYAGYGTGTAGADSTLIAGYGTQTSGLSSLTAGYGTQATARE 854  
Qy 170 -----TAGTNGDPTVHLNGIGSTLT---DTLLNTGATNTVNDVTDDEKKRAASV 217  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 855 GSDVTAGYGTGTAGADSTLISGYGTQTAGSDSLTLAGYGTQARKGSD----- 905  
Qy 218 KDVNLNAGNNIKGVPGTTASDNVDFRTYDVEFLSADTKTTTVNVEKDKNGKTEVKIG 277  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 906 ---VTAGYGTG-----TAGADSTLIAGYGTQTSGLSSLTAGYGTQARKGSDMTAG 957  
Qy 278 AKTSVIEKDKGLVTGKGDENGSSSTDEGELVTAKEVIDAVNKAGWRMKTITANGQTG 337  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 958 YGSTGTAGADSTLIAGYGTQTSGLSS-----DSSLTLAGYGTQATAREGSDVT 1003  
Qy 338 ADKFETVTSNTVTFASGKGTATVSKDDQGNITVKYDVNVYGDALNVNQLNSGWNLD 397  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1004 AGYGTGTAGADSTLIAGYGTQTAGSD--SSLTAGY----GSTQARQSDVTAGYGT 1057  
Qy 398 AVAGSSKVISGNVSPSKGMDETVNINAGNNIETRNGKNIDIAATNAPOFSSVSLG-- 455  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1058 GTAGADSTLIAGYGTQTAGSDSLTLAGY-----STQARQSDIYAGY 1103  
Qy 456 ----AGADAPTLSDVDEGALNVGSKDTPKVRITNVAPVKEGCVTVNVAQLKGVAQNLN 511  
| | | | | : | | | | | : | | | | | : | | | | | : | | | | | :  
Db 1104 STGTAGADSSLLIA--GYGSTGTAGYDLSNLTAGYGTQATAREDSSLTLAGYGTSTAGHDS 1161  
Qy 512 RIDNVGNARAGIAQAATATA-GLVQAYLPKGSMAAIGDGTGGEAGY----AIGYSSISD 566

```
Db 1162 LIAGYGTGCTAGYNSILITGGYGTGTQTAQESSILTAGYGT--STAGYDSTLTAGYGTOT 1219
QY 567 GG--NWIKGTAGSNRGH-----FGASASVGQ 593
Db 1220 AGYKSTLTAGYGSNSTAGHESLIAGYGTQIAGYE 1255

RESULT 10
HLIA_PROMI
ID HLIA_PROMI STANDARD: PRT: 1577 AA.
AC P16466;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN HPMA.
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Proteus.
OX NCBI_TaxID=584;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 30-43.
RC STRAIN-ISOLATE 477-12;
RX MEDLINE=90170827; PubMed=2407716;
RA Uphoff T.S., Welch R.A.;
RT Nucleotide sequencing of the Proteus mirabilis calcium-independent hemolysin genes (hpma and hpmb) reveals sequence similarity with the Serratia marcescens hemolysin genes (shla and shlb).";
RL J. Bacteriol. 172:1206-1216(1990).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. HPMA REQUIRES HPMB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- MISCELLANEOUS: THE CONSERVED AMPHIPATHIC DOMAINS IN SHLA AND HPMA MAY BE RESPONSIBLE FOR PORE FORMATION.
CC -!- SIMILARITY: TO S.MARCESCENS HEMOLYSIN (SHLA).
CC -----
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CC -----
DR EMBL; M30186; AAA25657.1; -.
DR PIR; A35140; A35140.
KW Hemolysis; Toxin; Outer membrane; Signal.
FT SIGNAL 1 29
FT CHAIN 30 1577 HEMOLYSIN.
SQ SEQUENCE 1577 AA; 165869 MW; 175975E0C924B2D9 CRC64;

Query Match 6.1%; Score 184; DB 1; Length 1577;
Best Local Similarity 21.5%; Pred. NO. 0.062;
Matches 142; Conservative 80; Mismatches 253; Indels 186; Gaps 30;

QY 22 LTRNHTKRASATVATVATLFLATVQANATD--DDDLLEPVQRTAVVLSFRSDKEGTG 79
Db 317 LFKTELKGNITLVAS-----SHNQIKASDLMGDDITLQAGDLTI-----DGKQLQ 362
QY 80 EKEGTDSNW-----AVYDEKRVLKAG-----AITLRAGDNL 112
Db 363 QKETDIDNWFYSWKYDVYTKKEKEIQIGSQIDAKNNATLTATKGVTLDAKINAGNML 422
QY 113 KI-----KQNTNENNTNDSSTYSLLK-----DLTDLT----- 139
Db 423 AINANKDIHINGLVEKESRSENGKRNHTRSLESWSNSHOTETLKASELTAGKDLGLD 482
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QY 140 ---SVETELSEFGANGKNVITSDTKGLNFAKETAGTNGDPTVHLN-----GIGSTLTDT 191
Db 483 AOGSTTAQAGAKLHANENVLVNAKDNLNVQK-----TNNDKTVTDHNVWVGIGGQGNK 538
QY 192 LLNTGATTNTVNDVTDDEKKRAASVYKDLNAGWNKIG-----VKPGTTASDNVDFVRTY 246
Db 539 NNNQQVSHAT--QLTADGQLLLAADNNVNVITGSQVKGNOGAFVK--TTQGDVVIDNALS 594
QY 247 DTVEFLSAD-----TKTTTVNVESKDNKKTEYKIGAKTSVIREKD-----GKLVTKGK 295
Db 595 ETISKIDERTGTAFTNITKSSHKNETNKOTSTGSELISDAQLTVVSGNDVNVIGSLIKSAD 654
QY 296 K-----DENGST-----DEGGLVT---AKEVIDAVNKAAGWMTKTTANGOTGOA 338
Db 655 KLGIIHSLGDLNVKSAQOVTKIDDEKTSLAITGHAKVEDEKQYSAGPHIHTTNKNTSTET 714
QY 339 DKFETVTSCTNVTFSAGKGTATTVS--KDDOQNTVYKDVNVGDALNVLOLQNSGNWLD 396
Db 715 EQANSTISGANVDLQANKDVTTFAGSDLKTTAGNASITGD--NVAFVSTENKKQTD--NTDT 771
QY 397 KAVAGSSGKVISGNVSPSKGMD-----ETVNNAGNNIEIT----- 433
Db 772 TISGGFS-----YTGVDVKVSKADFOYDKQHTQTEVTKNRGSQTEVAGDLTITANKDLLHE 828
QY 434 -----RNGKNID-IATSMAPQFSVSLGACADAPTLSVDDEGALNVGSKDTNKP 481
Db 829 GASHHVEGRYQSGENIQLHAVNDSSTKTSLSLNVGIDV-----GVNLDYSGVTKP 879
QY 482 VR-----ITNVAPGVKEGDTVNAQLKGVAQNLRNIDNVGNARAGIAQAATAGLVQ 535
Db 880 VKKAIEDGVNTTKPG--NNTDLTKKVTARDAIANLAN--LSNLE--TPNVGVEVGKGGGSOQ 936
QY 536 A 536
Db 937 S 937

RESULT 11
OMPA_RICCN STANDARD: PRT: 2021 AA.
AC Q52657; P95591; P95592; P95593; P95594; Q52667; Q52668; Q52669;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface antigen) (rOMPA) (rOMPA).
GN OMPA OR RC1273.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=94171067; PubMed=8125327;
RX Crocquet-Valdes P.A., Weiss K., Walker D.H.;
RT "Sequence analysis of the 190-kDa antigen-encoding gene of Rickettsia conorii (Malish 7 strain).";
RL Gene 140:115-119(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V., Samson D., Roux V., Cossart P., Weissenbach J., Claverie J.-M., Raoult D.;
RT "Mechanisms of evolution in Rickettsia conorii and R. prowazekii.";
RL Science 293:2093-2098(2001).
RN [3]
RP SEQUENCE OF 8-204 FROM N.A.
RC STRAIN=Indian tick typhus, M1, Malish 7, and Moroccan;
RX MEDLINE=97015921; PubMed=8862558;
```



## RESULT 12

OMP8\_RICTY STANDARD; PRT; 1645 AA.

AC P96989;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Outer membrane protein B precursor (168 kDa surface-layer protein)

DE (Surface protein antigen) (Cell surface antigen 5) (Scas5) (rOMP8)

DE (rOMP B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].

GN OMPB OR SLP.

OS Rickettsia typhi.

OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;

OC Rickettsiaceae; Rickettsiae; Rickettsia.

OX NCBI\_TaxID=785;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=WILMINGTON;

RX MEDLINE=94040787; PubMed=8224886;

RA Hahn M.-J., Kim K.-K., Kim I., Chang W.-H.;

RT "Cloning and sequence analysis of the gene encoding the crystalline surface layer protein of Rickettsia typhi.";

RL Gene 133:129-133(1993).

RN [2]

RP PARTIAL SEQUENCE.

RC STRAIN=WILMINGTON;

RX MEDLINE=92114896; PubMed=1370573;

RA Ching W.M., Carl M., Dasch G.A.;

RT "Mapping of monoclonal antibody binding sites on CNBr fragments of the S-layer protein antigens of Rickettsia typhi and Rickettsia prowazekii.";

RT Mol. Immunol. 29:95-105(1992).

RN [3]

RP IDENTIFICATION OF CLEAVAGE SITE.

RX MEDLINE=92104668; PubMed=1729180;

RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;

RT "Evidence for proteolytic cleavage of the 120-kilodalton outer membrane protein of rickettsiae: Identification of an avirulent mutant deficient in processing.";

RT Infect. Immun. 60:159-165(1992).

CC -!- FUNCTION: THE 120 kDa SURFACE-EXPOSED PROTEIN IS A MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.

CC -!- FUNCTION: THE 32 kDa BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.

CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-LAYER WITH HEXAGONAL SYMMETRY.

CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP8 FAMILY.

CC -----

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CC -----

DR EMBL; L04661; ABA48987.1; -

DR InterPro; IPR003858; rOMP8\_rOMP8.

DR Pfam; PF02708; rOMP8\_rOMP8; 1.

KW Antigen; S-layer; Transmembrane; Cell wall.

FT CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.

FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.

FT TRANSMEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).

FT CONFLICT 657 657 H -> N (IN REF. 2).

FT CONFLICT 842 842 V -> I (IN REF. 2).

FT CONFLICT 1071 1071 G -> A (IN REF. 2).

FT CONFLICT 1306 1306 G -> S (IN REF. 2).

SQ SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;

Query Match 6.0%; Score 180.5; DB 1; Length 1645;  
Best Local Similarity 21.1%; Pred. No. 0.097;  
Matches 145; Conservative 90; Mismatches 265; Indels 187; Gaps 35;

QY 28 KRASATVATAVLATLLFA-----TVQANATDDDDLYLE-----PVQRT 65  
DB 10 KIISAGLVTAATATVAGFSGVAMGVMQYRNTTAAATVVDGAGFDQTGAGVNLPVATN 69  
QY 66 AVVLSFRSKEGTEGEKTEDSNWAYFDEKRVLKAGAITLKAGDNLKIKQNTNENINDS 125  
DB 70 SVITANSNNAITFNPNGNLNS---LFLDTANTL---AVTINENTTLTGFVTNVTQGNFF 123  
QY 126 SFTYSLSKDLT---DLTSTVETEKLSFGAN-GNKVNT-----TSDTKGLNFAKETAGTNG 175  
DB 124 NFIGAGKSLTITGHGITAQAATTKSAQNVSVKVNAGAINNDNLGSGVSDIFTRAAPS- 182  
QY 176 DPTVHLNGIGSTLTLLNTGATNTVND-----NVTDEKKRAASVKVDVNLNAGWNKGV 230  
DB 183 --VLEFNLIPTTQEAPLTLGDNAKIVNGANGILNITNGFEV---VSDKTFAG--IKTI 234  
QY 231 KPGTTASDNVDFVRYDTVEFLSADTKTTTVNVESKD-----NGKKEVVKI---- 276  
DB 235 NIGD--NQGLMFNTTPDAANALNQQGGNTINFNGRGTGKLVLSKNGNATEFNVGTSL 292  
QY 277 GAKTSVIKED---GKLVTKGK-----DENGSS-----STDEG-----EGLVTA 312  
DB 293 GGNLKGVIEFTTAAGKGLIANGAANAVIGTDNAGRAAGFIVSDVNGNAATISGVYA 352  
QY 313 KEVIDAVNKGWRMKTITANGOT-----GQADKFETVSGTNVTVFASGKGTATV 362  
DB 353 KDIV-----IQSANAGQGVTFEHLVDVGLGGTKNFKTADSKVITIENASFGST--- 400  
QY 363 SKDDQGNITVKYDYN-----VGDALNVNOLNSGWNLDKAVAGSSGKVISGNVSP 413  
DB 401 ---DFGNLAVQIVVPNNKILTNFGIDG-----KNGG-NTAGVITFNANGTLVSGNTDP 450  
QY 414 S-----GKRMDETUNI-----NAGNNEITRNGKNIDIAATSMAPQFSVS 453  
DB 451 NIVVTNKAIEVEGAGIVQLSGIHGAELRLGNAGSIFKLA-DGTVINGPVNQPLVNNA 509  
QY 454 LGAGA---DAPTLISVDD--EGALNVGSKDTNKPVRITNPVAPGVKEGDTVNVQAQLKGAQN 508  
DB 510 LAAGSIQLDGSAITIGDIGNAVNAALQD---ITLAN-----DASKILTLSGA--- 554  
QY 509 LNNRIDNVGDNARAGTAQATATAGLQVAYLPKGSMAA-IGDDTYRGAGYAIGVSSISDG 567  
DB 555 -----NIIGANAGGAHFOANGGTIQLTSTQNNILVDFLDVTDQTG-VVDASSLTNN 607  
QY 568 GNWIKGT-----ASGNSRHFSGAS 589  
DB 608 QTLTNGSIGTIGANTKTLGRFNVGSS 634

RESULT 13

ID SLAP\_CAMEE STANDARD; PRT; 933 AA.

AC P35827; 933 AA.

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-OCT-1994 (Rel. 30, Last annotation update)

DE S-layer protein (Surface array protein) (SAP).

GN SAPA.

OS Campylobacter fetus.

OC Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;

OC Campylobacter.

OX NCBI\_TaxID=196;

RN [1]

RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-20.

RC STRAIN=84-32 / 23D;

RA MEDLINE=90354448; PubMed=2387868;

RA Blaser M.J., Gotschlich E.C.;

RT "Surface array protein of Campylobacter fetus. Cloning and gene structure.";

```
RL J. Biol. Chem. 265:14529-14535(1990).
RN [2]
RP ERRATUM.
RX MEDLINE=91035477; PubMed=2229082;
RA Blaser M.J., Gotschlich E.C.;
RL J. Biol. Chem. 265:19372-19372(1990).
CC -1- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY
CC OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. THIS PROTEIN IS
CC CRITICAL FOR VIRULENCE.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -----
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CC -----
DR EMBL; J05577; AAA23032.1; ..
KW Cell wall; S-layer.
SQ SEQUENCE 933 AA; 96757 MW; F88C729B4BA5B1E9 CRC64;

Query Match          5.98; Score 179.5; DB 1; Length 933;
Best Local Similarity 22.98; Pred. No. 0.055;
Matches 149; Conservative 89; Mismatches 251; Indels 163; Gaps 30;

QY 11 SALNA-----WVVSLETRNTRKASATVATVATLFLFATVQANATDDDLYLEPVQRT 65
DB 228 STLSAFDKTRMSVLGRDTLN-----AIFTAI-----TRAALLTDQAEILIITKRRTN 273
QY 66 AVVLSFSDKRGKTG-----EKEG-----TEDSNWAVFDEKRVLKA-----G 102
DB 274 VENINISDLTSGDFVNGEYKGFVNLGDIVSFADDSKSVNVTGTTTATAGTG 333
QY 103 AITLKAG--DNLIKQNTNEN---TND-----SFTYSLK---KDLTDLTSVETEK 145
DB 334 KVDVVAGKISALTADSRTSVNLATNDTITLSANAATSVNLKQKQAKDAT-ITSMQOK 392
QY 146 LSFGANQKV-NIISDTKGLNFAKETAGTGDPTVHLN-GTGSVLTDTL-----L 193
DB 393 ---YNNRRNRIATISATAVENLTVKHA-TN---VALGGMDKLTATVTDNAALTAADI 445
QY 194 NTGATVNTDNDVTDDEK-----KRAASVKDVLNAGWNIKGVKPGCTTASDNVDF 242
DB 446 KSAFTLNLSNVGPKHLYSKRYCKFKRAA-----VKVLNTTA-----487
QY 243 VRTYDTVEFLSADTKTTVNVYKSDNGKKTEVKIGAKTSVIKEDGKLVTKGKDENGSS 302
DB 488 -----ATDQTVTLKANATDNLSEFDSATAKTTSVTASGSGKTLVIKA-----530
QY 303 TDEGEGLVTAKEVIDAVNKAGWRMKTITANGCQTQADKFEFTVSGTNVTFASGKGTTATV 362
DB 531 ---EVETLVN-----IDTTAFNALQSVSGFKTGQGGKF-SVKTGTGDDKTFEFGVTTLTE 580
QY 363 SK--DDOQNTVKYDVNVGDALNVQLNSGWNLDNSKAVAG---SSGKVISGNSVSPSKGK 417
DB 581 GSVIDAFGNDTIAMKSAALTSANTMKNENVAISDAVATADLSSSAFNKSVIITTKEA 640
QY 418 MDEVTVNAGNIEITRNGKNIDIATSMAPQFSSVSLGAGADPTLSVDDREGALNVGSKG 477
DB 641 ADTTLTINKDQVI-----NFTAADAGSVKLITVKLN---DVTALMIVVKVILDAAAKD 690
QY 478 TNKPV-----RITNVAPGVKEGDTVWVAQL---KVAQNLNNDINVDGNARACIAQAI 528
DB 691 TNIALGTAADAKALVIDTIGTIELTSLVTSKATSPETTANTVNAKLTDTSIIDQMQLTL 750
QY 529 ATAGLVQAYLPCKGMAITGGDTYRGEAGYAGYSSISDGGNWIILKGTASGNS 580
DB 751 GHAGTAGTDYSKVSWM-----DASALKAGLFDASAITLGANATIKGGSGADS 798
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RESULT 14
120K_RICRI
ID 120K_RICRI STANDARD; PRT; 1300 AA.
AC P14914;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE 120 kDa surface-exposed protein.
GN P120.
OS Rickettsia rickettsii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=783;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=R;
RC MEDLINE=90136087; PubMed=2515418;
RA Gilmore R.D. Jr., Joste N., McDonald G.A.;
RT "Cloning, expression and sequence analysis of the gene encoding the
RT 120 kD surface-exposed protein of Rickettsia rickettsii.";
RL Mol. Microbiol. 3:1579-1586(1989).
CC -1- FUNCTION: MAJOR STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS
CC RICKETTSIAL VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- MISCELLANEOUS: ITS C-TERMINUS POTENTIALLY MAY BEAR THE EPITOPES
CC CONFERRING ANTIGENICITY TO THE PROTEIN
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
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CC -----
DR EMBL; X16353; CAA34402.1; ..
PIR; S07575; S07575.
DR InterPro: IPR003858; rompa_ompb.
DR Pfam; PF02708; rompa_ompb; 1.
KW Antigen; Glycoprotein; Cell wall; S-layer.
FT CARBOHYD 66 66 N-LINKED (POTENTIAL).
FT CARBOHYD 86 86 N-LINKED (POTENTIAL).
FT CARBOHYD 103 103 N-LINKED (POTENTIAL).
FT CARBOHYD 147 147 N-LINKED (POTENTIAL).
FT CARBOHYD 268 268 N-LINKED (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (POTENTIAL).
FT CARBOHYD 375 375 N-LINKED (POTENTIAL).
FT CARBOHYD 415 415 N-LINKED (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (POTENTIAL).
FT CARBOHYD 430 430 N-LINKED (POTENTIAL).
FT CARBOHYD 436 436 N-LINKED (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (POTENTIAL).
FT CARBOHYD 515 515 N-LINKED (POTENTIAL).
FT CARBOHYD 547 547 N-LINKED (POTENTIAL).
FT CARBOHYD 593 593 N-LINKED (POTENTIAL).
FT CARBOHYD 655 655 N-LINKED (POTENTIAL).
FT CARBOHYD 698 698 N-LINKED (POTENTIAL).
FT CARBOHYD 710 710 N-LINKED (POTENTIAL).
FT CARBOHYD 799 799 N-LINKED (POTENTIAL).
FT CARBOHYD 800 800 N-LINKED (POTENTIAL).
FT CARBOHYD 826 826 N-LINKED (POTENTIAL).
FT CARBOHYD 844 844 N-LINKED (POTENTIAL).
FT CARBOHYD 861 861 N-LINKED (POTENTIAL).
FT CARBOHYD 879 879 N-LINKED (POTENTIAL).
FT CARBOHYD 920 920 N-LINKED (POTENTIAL).
FT CARBOHYD 926 926 N-LINKED (POTENTIAL).
FT CARBOHYD 1116 1116 N-LINKED (POTENTIAL).
FT CARBOHYD 1128 1128 N-LINKED (POTENTIAL).
FT CARBOHYD 1140 1140 N-LINKED (POTENTIAL).
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Db 1208 NEVINYIDTSVINGTYNYKVAVDLSFNRTESNVVTKPDVWPIKVFNFVTPDYTPDA 1267  
QY 50 -----NAT-DDDDLVLEPVQRTAVVLSFRSDEGT-----GEKEGTEDSNNAVY 92  
Db 1268 VNLAGTFPNATWPSAOQMTKIDNNTYSITLTD-EGTQIEYKARGSWDKVEDEYEGNE 1326  
QY 93 FDEKRVLKAGAILKAGDNLKIKONTNENT-NDS-----SFTYSLKKDLTDLTSVET 143  
Db 1327 FASNR-----KVTI-----VNGNNEMTINDVYWRDIPFIYSPSSNMTVDSNIST 1374  
QY 144 EKLSEGA-NGKNVNTSDT-----KGLNFAKETA---CTN-----GDPTVHLNGIGST 187  
Db 1375 MEVKGNTRYKGAKVINGDSFQDKNGVFTKDVSLNYGVNKKIHVEPNDSGVYGN----- 1429  
QY 188 LTDPLLTGATTNTND---NVTDERKKRAASV--KDVLNAGWNIKGKPGCTTASDNV-- 240  
Db 1430 -----DQGRITELTKDIEIDVIRQENNSGCTGNNTSTSGSNSSTGSGTGSTITS 1483  
QY 241 DFVETDVEFLSADTKTTTVNVESKDKKTEVKIGAKTSVIKEKDKLVTGKGDENG 300  
Db 1484 NISNTSNTSNTIGVITKNGNVITLTDAGK-----AKDLIVNSKDKKVVF----- 1528  
QY 301 SSTDEGE-----LVTAKEVIDAVNKAGWRMKTTFANGOTGOADKFEFVTSGTNVTFASGK 356  
Db 1529 DITITIGEGQKQVQISKDILD-----TSAANGKD----- 1557  
QY 357 GTTATVSKDDOGNTTVKYDVNVGDALNVNOLONGWNLDSKAVAGSSGKVISGNVSPSKG 416  
Db 1558 -----IVIKSDNASIAL-----TKDALNQNQION-GVNVSIK-----DNG 1591  
QY 417 KMDFTVINAGNNTIEITRNKNKIDDIATSMAPQFSSVSLGAGADAPTLSDDEGALNVGSK 476  
Db 1592 KPNVTNVVSLSNVVDITISGISGNV-----TLAKPVEVTINISKA 1631  
QY 477 DTNKPVRI-----TNVAPGVEGDVTNVAQLKGAQNANLNRRIDNVDCNA 520  
Db 1632 NDRPKVAVYYNPTTNQWEXYVGKVDASSGTITFNATHFSQY--AAFEYDKTFENDIKDNW 1689  
QY 521 RAGIAQAIATAGLYOA-----YLPKGS-----MMAIGGDTYRGFAGYAGYSS 563  
Db 1690 AKDVIEVLASRHIVEGMDTQYEPNKTVTRAETAMILRLNLINIKDETYSGE-----FSD 1743  
QY 564 ISDGGNW 570  
Db 1744 VK-SGDW 1749

Search completed: July 3, 2002, 08:49:07  
Job time: 713 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:48:10 ; Search time 100.13 seconds  
(without alignments)  
1026.256 Million cell updates/sec

Title: US-09-771-382-9  
Perfect score: 3023  
Sequence: 1 MNKYIRIWNALNAWVVS.....TASGSRGFGASASVGYQW 594

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_19.\*

- 1: sp\_archaea.\*
- 2: sp\_bacteria.\*
- 3: sp\_fungi.\*
- 4: sp\_human.\*
- 5: sp\_invertebrate.\*
- 6: sp\_mammal.\*
- 7: sp\_mhc.\*
- 8: sp\_organelle.\*
- 9: sp\_phage.\*
- 10: sp\_plant.\*
- 11: sp\_rodent.\*
- 12: sp\_virus.\*
- 13: sp\_vertebrate.\*
- 14: sp\_unclassified.\*
- 15: sp\_rvirus.\*
- 16: sp\_bacteriaph.\*
- 17: sp\_archaeap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3023	100.0	594	2 Q9JPH7	Q9JPH7 neisseria m
2	2997	99.1	598	2 Q9JPS9	Q9JPS9 neisseria m
3	2971	98.3	598	2 Q9JPS0	Q9JPS0 neisseria m
4	2957	97.8	598	2 Q9JPT0	Q9JPT0 neisseria m
5	2948	97.5	598	2 Q9JQY5	Q9JQY5 neisseria m
6	2888	95.5	594	2 Q9JPS2	Q9JPS2 neisseria m
7	2884	95.4	594	2 Q9JPI3	Q9JPI3 neisseria m
8	2874	95.1	594	2 Q9JQY4	Q9JQY4 neisseria m
9	2802.5	92.7	599	2 Q9JPS8	Q9JPS8 neisseria m
10	2800	92.6	600	2 Q9JPS6	Q9JPS6 neisseria m
11	2782	92.0	590	2 Q9JPS3	Q9JPS3 neisseria m
12	2740.5	90.7	591	2 Q9JPS7	Q9JPS7 neisseria m
13	2740.5	90.7	591	16 Q9JRI8	Q9JRI8 neisseria m
14	2734.5	90.5	599	2 Q9JPS8	Q9JPS8 neisseria m
15	2733	90.4	592	2 Q9AQF0	Q9AQF0 neisseria m
16	2721.5	90.0	591	2 Q9JQY3	Q9JQY3 neisseria m

17	2715	89.8	598	2 Q9JPR7	Q9JPR7 neisseria m
18	2694	89.1	592	2 Q9JPS9	Q9JPS9 neisseria m
19	2664	88.1	592	2 Q9JQY2	Q9JQY2 neisseria m
20	2661	88.0	600	2 Q9JPS5	Q9JPS5 neisseria m
21	2656.5	87.9	595	2 Q9JPH0	Q9JPH0 neisseria m
22	2584.5	85.5	589	2 Q9JPH0	Q9JPH0 neisseria m
23	2573.5	85.1	589	2 Q9JQY1	Q9JQY1 neisseria m
24	2552	84.4	592	16 Q9JQW4	Q9JQW4 neisseria m
25	2484.5	82.2	526	2 Q9JPS4	Q9JPS4 neisseria m
26	2482.5	82.1	530	2 Q9JPS1	Q9JPS1 neisseria m
27	1330.5	44.0	2353	2 P71401	P71401 haemophilus
28	1050	34.7	1098	2 Q48152	Q48152 haemophilus
29	442	14.6	1299	16 Q9F3X6	Q9F3X6 pasteurella
30	404	13.4	2059	16 Q9PD50	Q9PD50 xyliella fas
31	392.5	13.0	1190	16 Q9PC04	Q9PC04 xyliella fas
32	371	12.3	1107	2 Q9F2D8	Q9F2D8 salmonella
33	363	12.0	2712	16 Q9F3X5	Q9F3X5 pasteurella
34	260	8.6	1004	16 Q9PD63	Q9PD63 xyliella fas
35	253.5	8.4	1291	16 Q92KQ7	Q92KQ7 rhizobium m
36	244.5	8.1	1953	16 Q98HJ2	Q98HJ2 rhizobium l
37	240.5	8.0	2276	2 Q93TY6	Q93TY6 staphylococ
38	240	7.9	1039	2 Q9L6T7	Q9L6T7 escherichia
39	234.5	7.8	1265	2 Q9FDA0	Q9FDA0 xanthomonas
40	232.5	7.7	1039	2 Q9L6T8	Q9L6T8 escherichia
41	230.5	7.6	989	2 Q9XD84	Q9XD84 escherichia
42	228	7.5	1040	2 Q9AL50	Q9AL50 shigella fl
43	226	7.5	3930	16 Q98E20	Q98E20 rhizobium l
44	218.5	7.2	945	2 Q93F03	Q93F03 shigella fl
45	218	7.2	1557	2 Q9RNI2	Q9RNI2 haemophilus

ALIGNMENTS

RESULT 1

Q9JPH7	PRELIMINARY;	PRT;	594 AA.
ID	Q9JPH7		
AC	Q9JPH7		
DT	01-OCT-2000 (Tremblrel. 15, Created)		
DT	01-OCT-2000 (Tremblrel. 15, Last sequence update)		
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)		
DE	OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).		
GN	GNA992 OR NHHA.		
OS	Neisseria meningitidis.		
OC	Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.		
OX	NCBI_TaxID=487;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BZ198, AND 297-0;		
RX	MEDLINE=20175756; PubMed=10710308;		
RA	Pizza M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,		
RA	Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,		
RA	Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,		
RA	Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,		
RA	Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,		
RA	Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,		
RA	Moxon E.R., Grandi G., Rappuoli R.;		
RT	*Identification of Vaccine Candidates Against Serogroup B		
RT	Meningococcus by Whole-Genome Sequencing.*;		
RL	Science 287:1816-1820(2000).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=BZ198;		
RA	Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;		
RT	*Identification and characterization of a gene encoding a novel outer		
RT	membrane protein of Neisseria meningitidis.*;		
RL	Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.		
DR	EMBL: AF226358; AAF42517.1; -		
DR	EMBL: AF226358; AAF42507.1; -		
DR	EMBL: AF157604; AAK68865.1; -		
SQ	SEQUENCE 594 AA; 62361 MW; 436BDEDE68263C5C CRC64;		

Query Match 100.0%; Score 3023; DB 2; Length 594;  
Best Local Similarity 100.0%; Pred. No. 1.1e-118;  
Matches 594; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
DB 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
QY 61 PVQRTAVVLFRSDKTEGEGEDSNWAVYFDEKRVLKAGAITLTKAGDNLKIKQNTNE 120  
DB 61 PVQRTAVVLFRSDKTEGEGEDSNWAVYFDEKRVLKAGAITLTKAGDNLKIKQNTNE 120  
QY 121 NTNDSSTYSLLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180  
DB 121 NTNDSSTYSLLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180  
QY 181 LINGIGSTLTDLTLLNTGATTNTVNDVDDDEKKRAASVKDVLNAGWNKIKGVPCTASDNV 240  
DB 181 LINGIGSTLTDLTLLNTGATTNTVNDVDDDEKKRAASVKDVLNAGWNKIKGVPCTASDNV 240  
QY 241 DFVRTYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVKEKDKGLVTGKGDENG 300  
DB 241 DFVRTYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVKEKDKGLVTGKGDENG 300  
QY 301 SSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFFASGKGTGA 360  
DB 301 SSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFFASGKGTGA 360  
QY 361 TVSKDDGNTITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420  
DB 361 TVSKDDGNTITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGKMD 420  
QY 421 TVNLNAGNTEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDTNK 480  
DB 421 TVNLNAGNTEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDTNK 480  
QY 481 PVRTITNAPVKEGDTVNTVAQLKGAQNLRNDVNDGNARAGIAQAIAATAGLYQVLP 540  
DB 481 PVRTITNAPVKEGDTVNTVAQLKGAQNLRNDVNDGNARAGIAQAIAATAGLYQVLP 540  
QY 541 KSMMAIGDGYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594  
DB 541 KSMMAIGDGYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594

RESULT 2  
QJPRS9 PRELIMINARY; PRT; 598 AA.

ID QJPRS9  
AC QJPRS9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH36;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226382; AAF42531.1; -;  
SQ SEQUENCE 598 AA; 62718 MW; 9095F8E31AD7C76D CRC64;

Query Match 99.1%; Score 2997; DB 2; Length 598;  
Best Local Similarity 99.0%; Pred. No. 1.3e-117;  
Matches 592; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
DB 1 MNKIYRIIWSALNANWVVSSELTRNHTKRASATVATVATLTLFATVOANATDDDDLYLE 60  
QY 61 PVQRTAVVLFRSDKTEGEGEDSNWAVYFDEKRVLKAGAITLTKAGDNLKIKQNTNE 116  
DB 61 PVQRTAVVLFRSDKTEGEGEDSNWAVYFDEKRVLKAGAITLTKAGDNLKIKQNTNE 120  
QY 117 NTNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176  
DB 121 NTNENTNDSSTYSLLKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180  
QY 177 PTVHLNGIGSTLTDLTLLNTGATTNTVNDVDDDEKKRAASVKDVLNAGWNKIKGVPCTGA 236  
DB 181 PTVHLNGIGSTLTDLTLLNTGATTNTVNDVDDDEKKRAASVKDVLNAGWNKIKGVPCTGA 240  
QY 237 SDNVDFVRTYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVKEKDKGLVTGCK 296  
DB 241 SDNVDFVRTYDTVEFLSADTKTTTNNVESKONGKTEVKIGAKTSVKEKDKGLVTGCK 300  
QY 297 DENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFFASGK 356  
DB 301 DENGSSSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTNVTFFASGK 360  
QY 357 GTTATVSKDDGNTITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
DB 361 GTTATVSKDDGNTITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420  
QY 417 KMDETVINAGNTEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSK 476  
DB 421 KMDETVINAGNTEITRNKNIDTATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSK 480  
QY 477 DTNKPVRTITNAPVKEGDTVNTVAQLKGAQNLRNDVNDGNARAGIAQAIAATAGLYQV 536  
DB 481 DTNKPVRTITNAPVKEGDTVNTVAQLKGAQNLRNDVNDGNARAGIAQAIAATAGLYQV 540  
QY 537 YLPKSKMAIGDGYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 594  
DB 541 YLPKSKMAIGDGYRGEAGYAGYSSISDGNWIIKGTASGNSRGHFGASASVGYOW 598

RESULT 3  
QJPRS9 PRELIMINARY; PRT; 598 AA.

ID QJPRS9  
AC QJPRS9;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH15;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).

```

[2]
SEQUENCE FROM N.A.
RA STRAIN=H15;
RC Peak I.R., Srihanta Y., Dieckelman M., Moxon R., Jennings M.P.;
RT "Identification and characterization of a gene encoding a novel outer
  membrane protein of Neisseria meningitidis.";
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF226381; AAF42530.1; -.
DR EMBL; AF157607; AAK68868.1; -.
SQ SEQUENCE 598 AA; 62763 MW; E6C7AEF0B8BA63CB CRC64;

Query Match      98.3%; Score 2971; DB 2; Length 598;
Best Local Similarity 98.0%; Pred. No. 1.6e-116;
Matches 586; Conservative 1; Mismatches 7; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEGTEGDSNWAYVYFDEKRVLKAGAITLKAGDNLKIKQ---- 116
DB 61 PVORTAVVLSFRSDKEGTGEGTEGDSNWAYVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
QY 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
DB 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
QY 177 PTVHLNGIGSTLDTLLTNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236
DB 181 PTVHLNGIGSTLDTLLTNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240
QY 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTGKGK 296
DB 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTGKGK 300
QY 297 DENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEFVTSCTNVTFSAGK 356
DB 301 DENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEFVTSCTNVTFSAGN 360
QY 357 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
DB 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
QY 417 KMDETWINAGNIEITRNKNIDIAATSMAPQFSSVSLGAGADAPTLVSVDDEGALNVGSK 476
DB 421 KMDETWINAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSK 480
QY 477 DTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQA 536
DB 481 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLAQA 540
QY 537 YLPCKSMMAIGGDTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 594
DB 541 YLPCKSMMAIGGDTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 598

RESULT 4
Q9JPT0 PRELIMINARY; PRT; 598 AA.
ID Q9JPT0;
AC Q9JPT0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE OUTER MEMBRANE PROTEIN GNA992.
GN GNA992.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2996;
RX MEDLINE=20175756; PubMed=10710308;
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RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,
RA Broecker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,
RA Moxon E.R., Grandi G., Rappuoli R.;
RT "Identification of Vaccine Candidates Against Serogroup B
  Meningococcus by Whole-Genome Sequencing.";
RL Science 287:1816-1820(2000).
DR EMBL; AF226359; AAF42508.1; -.
SQ SEQUENCE 598 AA; 62763 MW; 63A6A3BD7F0F2EE3 CRC64;

Query Match      97.8%; Score 2957; DB 2; Length 598;
Best Local Similarity 97.5%; Pred. No. 6.2e-116;
Matches 583; Conservative 2; Mismatches 9; Indels 4; Gaps 1;

QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
DB 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDDDDLYLE 60
QY 61 PVORTAVVLSFRSDKEGTGEGTEGDSNWAYVYFDEKRVLKAGAITLKAGDNLKIKQ---- 116
DB 61 PVORTAVVLSFRSDKEGTGEGTEGDSNWAYVYFDEKRVLKAGAITLKAGDNLKIKQNTNE 120
QY 117 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 176
DB 121 NTNENTNDSSFTYSLKKDLTDLTSVETEKLSFGANGKVNITSDTKGLNFAKETAGTNGD 180
QY 177 PTVHLNGIGSTLDTLLTNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 236
DB 181 PTVHLNGIGSTLDTLLTNTGATTNVTNDVTDDEKKRAASVKDVLNAGWNIKGVKPGTTA 240
QY 237 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTGKGK 296
DB 241 SDNVDFVRTYDTVEFLSADTKTTTVNVESKDNKKTEVKIGAKTSVKEKDKGLVTGKGK 300
QY 297 DENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEFVTSCTNVTFSAGK 356
DB 301 DENGSSDDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTQADKFEFVTSCTNVTFSAGN 360
QY 357 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 416
DB 361 GTTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKG 420
QY 417 KMDETWINAGNIEITRNKNIDIAATSMAPQFSSVSLGAGADAPTLVSVDDEGALNVGSK 476
DB 421 KMDETWINAGNIEITRNKNIDIAATSMTPQFSSVSLGAGADAPTLVSVDDEGALNVGSK 480
QY 477 DTNKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQA 536
DB 481 DANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLAQA 540
QY 537 YLPCKSMMAIGGDTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 594
DB 541 YLPCKSMMAIGGDTYRGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYQW 598

RESULT 5
Q93QY5 PRELIMINARY; PRT; 598 AA.
ID Q93QY5;
AC Q93QY5;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NHHA OUTER MEMBRANE PROTEIN.
GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
```



RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226376; AAF42525.1; -;  
DR EMBL: AF226369; AAF42518.1; -;  
SQ SEQUENCE 594 AA; 62086 MW; 1B25E03B90D04B46 CRC64;

Query Match 95.4%; Score 2884; DB 2; Length 594;  
Best Local Similarity 95.8%; Pred. No. 6.7e-113;  
Matches 569; Conservative 4; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAVWVSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60  
DB 1 MNKIYRIIWNLSALNAVWVSELTRNHTKRASATVAVATLTLFATVQASTTDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKGEKTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120  
DB 61 PVORTAVVLSFRSDKGEKTEGKEDSNWGVYFDEKRVLKAGDNLIKQNTNE 120  
QY 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180  
DB 61 PVORTAVVLSFRSDKGEKTEGKEDSNWGVYFDEKRVLKAGDNLIKQNTNE 120  
QY 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180  
DB 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180  
QY 181 LNGIGSTLDTLNTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240  
DB 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180  
QY 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKDENG 300  
DB 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKDENG 300  
QY 301 SSTDEGEGLVTAKEVIDAVNKGAWRKTTTANGOTGOADKFEFVTSCTNVTFSAGKGTGA 360  
DB 301 SSTDEGEGLVTAKEVIDAVNKGAWRKTTTANGOTGOADKFEFVTSCTNVTFSAGKGTGA 360  
QY 361 TVSKDQGNITVYKDVNVGDALNVQNSGWLDSKAVAGSSGKVISGNVSPSKGMDE 420  
DB 361 TVSKDQGNITVYKDVNVGDALNVQNSGWLDSKAVAGSSGKVISGNVSPSKGMDE 420  
QY 421 TVNINAGNIEITRNKNIDDIATSMAPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDTNK 480  
DB 421 TVNINAGNIEITRNKNIDDIATSMAPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDKANK 480  
QY 481 PVRTITVAPGVKEGDVTNVAQLKGVAQNLRNNDVNDGNARAGIAQAIATAGLVQAYLPG 540  
DB 481 PVRTITVAPGVKEGDVTNVAQLKGVAQNLRNNDVNDGNARAGIAQAIATAGLVQAYLPG 540  
QY 541 KSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594  
DB 541 KSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

RESULT 8  
Q930Y4  
ID Q930Y4 PRELIMINARY; PRT; 594 AA.  
AC Q930Y4;  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE NHHA OUTER MEMBRANE PROTEIN.  
GN NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.

RC STRAIN=EG327;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF157605; AAK68866.1; -;  
SQ SEQUENCE 594 AA; 62297 MW; 9DD48B04B3A8EA2 CRC64;

Query Match 95.1%; Score 2874; DB 2; Length 594;  
Best Local Similarity 95.6%; Pred. No. 1.7e-112;  
Matches 568; Conservative 5; Mismatches 21; Indels 0; Gaps 0;

QY 1 MNKIYRIIWNLSALNAVWVSELTRNHTKRASATVAVATLTLFATVQANATDDDDLYLE 60  
DB 1 MNKIYRIIWNLSALNAVWVSELTRNHTKRASATVAVATLTLFATVQASTTDDDDLYLE 60  
QY 61 PVORTAVVLSFRSDKGEKTEGKEDSNWAVYFDEKRVLKAGAITLKAGDNLIKQNTNE 120  
DB 61 PVORTAVVLSFRSDKGEKTEGKEDSNWGVYFDEKRVLKAGDNLIKQNTNE 120  
QY 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180  
DB 121 NTNDSFTYSLKDLTDLTSVETKLSFGANGKVNITSDTKGLNFAKETAGTNGDPTVH 180  
QY 181 LNGIGSTLDTLNTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240  
DB 181 LNGIGSTLDTLNTGATTNVTNDVNTDDEKRAASVKDVLNAGWNIKGVPKGTASDNV 240  
QY 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKDENG 300  
DB 241 DFVRTYDTVEFLSADTKTTTNNVESKDNKKTEVKIGAKTSVKEKDKLVTKGKDENG 300  
QY 301 SSTDEGEGLVTAKEVIDAVNKGAWRKTTTANGOTGOADKFEFVTSCTNVTFSAGKGTGA 360  
DB 301 SSTDEGEGLVTAKEVIDAVNKGAWRKTTTANGOTGOADKFEFVTSCTNVTFSAGKGTGA 360  
QY 361 TVSKDQGNITVYKDVNVGDALNVQNSGWLDSKAVAGSSGKVISGNVSPSKGMDE 420  
DB 361 TVSKDQGNITVYKDVNVGDALNVQNSGWLDSKAVAGSSGKVISGNVSPSKGMDE 420  
QY 421 TVNINAGNIEITRNKNIDDIATSMAPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDTNK 480  
DB 421 TVNINAGNIEITRNKNIDDIATSMAPQFSSVSLGAGADAPTLVSVDDEGALNVGSKDKANK 480  
QY 481 PVRTITVAPGVKEGDVTNVAQLKGVAQNLRNNDVNDGNARAGIAQAIATAGLVQAYLPG 540  
DB 481 PVRTITVAPGVKEGDVTNVAQLKGVAQNLRNNDVNDGNARAGIAQAIATAGLVQAYLPG 540  
QY 541 KSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594  
DB 541 KSMMAIGGDTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYQW 594

RESULT 9  
Q9JPR8  
ID Q9JPR8 PRELIMINARY; PRT; 599 AA.  
AC Q9JPR8;  
DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (NHHA OUTER MEMBRANE PROTEIN).  
GN GNA992 OR NHHA.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGH38;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizzo M., Scarlato V., Maignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,

RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hufnagel E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=H38;  
 RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
 RT "Identification and characterization of a gene encoding a novel outer  
 RT membrane protein of *Neisseria meningitidis*.";  
 RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AP226383; AAF42532.1; -;  
 DR EMBL: AF157608; AAK68869.1; -;  
 SQ SEQUENCE 599 AA; 62844 MW; BBA16EBF53C1970C CRC64;

Query Match 92.7%; Score 2802.5; DB 2; Length 599;  
 Best Local Similarity 92.5%; Pred. No. 1.7e-109;  
 Matches 554; Conservative 12; Mismatches 28; Indels 5; Gaps 2;  
 QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATD-DDDLXL 59  
 DB 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQANATDEDEEL 60  
 QY 60 EPVORTAVLVSFRSDKCTGKTEGSDNNAWYFDEKRVLKAGAITLKAGDNLIKIKO-- 116  
 DB 61 EPVRSALVQFMIDKKGNGENSTGIGWSYIDNNTLHGATVTLKAGDNLIKIKONTN 120  
 QY 117 -NTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG 175  
 DB 121 KNTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGTNG 180  
 QY 176 DPTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGWNKIKVKGPTT 235  
 DB 181 DTTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGWNKIKVKGPTT 240  
 QY 236 ASDNVDFVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG 295  
 DB 241 ASDNVDFVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG 300  
 QY 296 KDENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTITANGQTQADKFETVTSCTNVTFA 355  
 DB 301 KGENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTITANGQTQADKFETVTSCTNVTFA 360  
 QY 356 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 415  
 DB 361 KGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSK 420  
 QY 416 GKMDETVNIAGNNIEITRNKNIDTATSMAPQSSVSLGAGADAPTLSDVDEGALNVGS 475  
 DB 421 GKMDETVNIAGNNIEITRNKNIDTATSMAPQSSVSLGAGADAPTLSDVDEGALNVGS 480  
 QY 476 KDTNKPVRITNVAPGVKRGEDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGLVQ 535  
 DB 481 KDANKPVRITNVAPGVKRGEDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGLVQ 540  
 QY 536 AYLPGKSMMAIGGDYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 594  
 DB 541 AYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYOW 599  
 RESULT 10  
 Q9JPS6 PRELIMINARY; PRT; 600 AA.  
 ID Q9JPS6  
 AC Q9JPS6;  
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)  
 DE OUTER MEMBRANE PROTEIN GNA992.

OS *Neisseria meningitidis*.  
 OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
 OX NCBI\_TaxID=487;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=E26;  
 RX MEDLINE=20175756; PubMed=10710308;  
 RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
 RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
 RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
 RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
 RA Broeker M., Hufnagel E., Knapp B., Blair E., Mason T., Tettelin H.,  
 RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
 RA Moxon E.R., Grandi G., Rappuoli R.;  
 RT "Identification of Vaccine Candidates Against Serogroup B  
 RT Meningococcus by Whole-Genome Sequencing.";  
 RL Science 287:1816-1820(2000).  
 DR EMBL: AF226371; AAF42520.1; -;  
 SQ SEQUENCE 600 AA; 62762 MW; 36256963E0598CD1 CRC64;  
 Query Match 92.6%; Score 2800; DB 2; Length 600;  
 Best Local Similarity 92.7%; Pred. No. 2.1e-109;  
 Matches 557; Conservative 13; Mismatches 23; Indels 8; Gaps 2;  
 QY 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASADNVQASADN 53  
 DB 1 MNKIYRIIWSALNAWVVSSELTRNHTKRASATVATVATLTLFATVQASADNVQASADN 60  
 QY 54 DDLVLEPVORTAVLVSFRSDKCTGKTEGSDNNAWYFDEKRVLKAGAITLKAGDNLIK 113  
 DB 61 EEEYVFPVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG 120  
 QY 114 IKONTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGT 173  
 DB 121 IKONTNENTNDSSFTYSLKKDLTDLTSVETKLSFGANGKNVITSDTKGLNFAKETAGT 180  
 QY 174 NGDPTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGWNKIKVKGPG 233  
 DB 181 NGDPTVHLNGIGSTLTDLLNTGATTNVDNVDDEKRAASVKDVLNAGWNKIKVKGPG 240  
 QY 234 TTASDNVDFVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG 293  
 DB 241 TTASDNVDFVRYDTVEFLSADTKTTNVNVEKDKNGKTEVKIGAKTSVKEKDGKLVTKG 300  
 QY 294 KGKDENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTITANGQTQADKFETVTSCTNVTFA 353  
 DB 301 KGKDENGSSDDEGEGLVTAKEVIDAVNKAQWRMKTITANGQTQADKFETVTSCTNVTFA 360  
 QY 354 SGKGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 413  
 DB 361 SGKGTATVSKDDQGNITVKYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSP 420  
 QY 414 SKGRMDETVNIAGNNIEITRNKNIDTATSMAPQSSVSLGAGADAPTLSDVDEGALNV 473  
 DB 421 SKGRMDETVNIAGNNIEITRNKNIDTATSMAPQSSVSLGAGADAPTLSDVDEGALNV 479  
 QY 474 GSKDTNKPVRITNVAPGVKRGEDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGL 533  
 DB 480 GSKDTNKPVRITNVAPGVKRGEDVTNVAQLKGVAQNLRNIDNVDGNARAGIAQAIAATAGL 539  
 QY 534 VOAYLPGKSMMAIGGDYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYO 593  
 DB 540 VOAYLPGKSMMAIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGASASVGYO 599  
 QY 594 W 594  
 DB 600 W 600  
 RESULT 11  
 Q9JPS3 PRELIMINARY; PRT; 590 AA.  
 ID Q9JPS3

AC Q9JPS3;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-MAR-2001 (TRENBLrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NGE28;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226378; AAF42527.1; -.  
SQ SEQUENCE 590 AA; 61661 MW; 8AA476AC300D80C8 CRC64;

Query Match 92.0%; Score 2782; DB 2; Length 590;  
Best Local Similarity 93.3%; Pred. No. 1.2e-108;  
Matches 556; Conservative 9; Mismatches 23; Indels 8; Gaps 3;  
QY 1 MNKIYRIIWSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATDDDL-L 59  
DB 1 MNKIYRIIWSALNAWVVSSELTNRHTRKASATVATVATLTLFATVQANATDEEDL 60  
QY 60 EPOVQAVVLSRDKGEGTEGEGED-SNWAIFYDEKRVLKAGAITLKAGDNLKIKQT 118  
DB 61 DPVQRTAVVLIIVNSDKGEGTEGEGEDSNWAIFYDEKRVLKAGAITLKAGDNLKIKQ-- 118  
QY 119 NENTNDSSTYSLLKDLTDLTSVETKLSFGANGKYNITSDTKGLNFAKETAGTNGDPT 178  
DB 119 -----NGTNFTYSLKKDLTDLTSVETKLSFGANGKYNITSDTKGLNFAKETAGTNGDPT 174  
QY 179 VHLNGIGSTLTLTNGTATTNTVNDVTDDEKRAASVKDVLNAGWNKGVKPGTASD 238  
DB 175 VHLNGIGSTLTLTNGTATTNTVNDVTDDEKRAASVKDVLNAGWNKGVKPGTASD 234  
QY 239 NVDFVRYTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGKGE 298  
DB 235 NVDFVRYTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGKGE 294  
QY 299 NGSSSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTQADKFEPTVSGTNTVFASGKT 358  
DB 295 NGSSSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTQADKFEPTVSGTNTVFASGKT 354  
QY 359 TATVSKDDQGNITVYDVNVGDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKGM 418  
DB 355 TATVSKDDQGNITVYDVNVGDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKGM 414  
QY 419 DETVNIAGNNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLSVDDGALNVGSKDT 478  
DB 415 DETVNIAGNNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLSVDDGALNVGSKDT 474  
QY 479 NKPVRTNVAPGVKGGDVTVNAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQAYL 538  
DB 475 NKPVRTNVAPGVKGGDVTVNAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQAYL 534  
QY 539 PKGSMAIGGDTYRGAGYAGYSSISDGGNWIIGTASGNSRGRHFGASASVGYOW 594  
DB 535 PKGSMAIGGDTYRGAGYAGYSSISDGGNWIIGTASGNSRGRHFGASASVGYOW 590

RESULT 12

Q9JPS7  
ID Q9JPS7 PRELIMINARY; PRT; 591 AA.  
AC Q9JPS7;  
DT 01-OCT-2000 (TRENBLrel. 15, Created)  
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)  
DT 01-DEC-2001 (TRENBLrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=B2147;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizze M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Broeker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL; AF226366; AAF42515.1; -.  
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Best Local Similarity 92.1%; Pred. No. 6.2e-107;  
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;  
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QY 58 YLEPQRTAVVLSRDKGEGTEGEGED-SNWAIFYDEKRVLKAGAITLKAGDNLKIKQ 116  
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QY 177 PVHLNGIGSTLTLTNGTATTNTVNDVTDDEKRAASVKDVLNAGWNKGVKPGTGA 236  
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QY 237 SDNVDFVRYTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGKGE 296  
DB 235 SDNVDFVRYTYDTVEFLSADTKTTTVNVEKDKNGKTEVKIGAKTSVKEKDKGLVTGKGE 294  
QY 297 DENGSTDEGEGLVTAKEVIDAVNKAQWRMKTITANGOTQADKFEPTVSGTNTVFASGK 356  
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QY 357 GTTATVSKDDQGNITVYDVNVGDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKG 416  
DB 355 GTTATVSKDDQGNITVYDVNVGDALNVQNSGWNLDKAVAGSSGKVISGNVSPSKG 414  
QY 417 KMDETVNIAGNNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLSVDDGALNVGSK 476  
DB 415 KMDETVNIAGNNIEITRNKNIDIAISMATPQFSSVSLGAGADAPTLSVDDGALNVGSK 473  
QY 477 DTKNKPVRTNVAPGVKGGDVTVNAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQ 536  
DB 474 DTKNKPVRTNVAPGVKGGDVTVNAQLKGVAQNLRIDNVGNARAGIAQAIAATAGLVQ 533  
QY 537 YLPKGSMAIGGDTYRGAGYAGYSSISDGGNWIIGTASGNSRGRHFGASASVGYOW 594  
DB 534 YLPKGSMAIGGDTYRGAGYAGYSSISDGGNWIIGTASGNSRGRHFGASASVGYOW 591



RESULT 13  
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AC Q9JR18;  
DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992 (ADHESIN) (NHHA OUTER MEMBRANE  
DE PROTEIN)  
DE GNA992 OR NMB0992 OR NHHA.  
GN  
OS Neisseria meningitidis, and  
OS Neisseria meningitidis (serogroup B).  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487, 491;  
RN [1]  
SEQUENCE FROM N.A.  
RC STRAIN=MC58 / SEROGROUP B, B2169, B283, AND H44/76;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
RN [2]  
SEQUENCE FROM N.A.  
RC STRAIN=MC58 / SEROGROUP B;  
RX MEDLINE=20175755; PubMed=10710307;  
RA Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., Nelson K.E.,  
RA Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.,  
RA Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.K.,  
RA Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dougherty B.A.,  
RA Mason T., Ciecko A., Parksey D.S., Blair E., Ciftone H., Clark E.B.,  
RA Cotton M.D., Uterback T.R., Khouri H., Qin H., Vamathevan J.,  
RA Gill J., Scarlato V., Masignani V., Pizza M., Grandi G., Sun L.,  
RA Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R., Venter J.C.;  
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain  
RT MC58.";  
RL Science 287:1809-1815(2000).  
RN [3]  
SEQUENCE FROM N.A.  
RC SPECIES=N.meningitidis; STRAIN=PMC21;  
RA Peak I.R., Srikantha Y., Dieckelman M., Moxon R., Jennings M.P.;  
RT "Identification and characterization of a gene encoding a novel outer  
RT membrane protein of Neisseria meningitidis.";  
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AF226375; AAF42524.1; -  
DR EMBL: AE002450; AAF41395.1; -  
DR EMBL: AF226367; AAF42516.1; -  
DR EMBL: AF226370; AAF42519.1; -  
DR EMBL: AF226374; AAF42523.1; -  
DR EMBL: AF157611; AAK68872.1; -  
DR TIGR: NMB0992; -  
KW Complete proteome.  
SQ SEQUENCE 591 AA; 62112 MW; 7C22F3CAE7F73EC6 CRC64;

Query Match 90.7%; Score 2740.5; DB 16; Length 591;  
Best Local Similarity 92.1%; Pred. No. 6.2e-107;  
Matches 551; Conservative 11; Mismatches 25; Indels 11; Gaps 4;  
QY 1 MNKYRIWNSALNMAWVVSSELTNRNHTKRASATVATVATLTLFATVQANATD---DDDL 57  
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QY 58 YLEPQRTAVVLSFRSDEKGEKTED-SNNAVYFDEKRVLKAGAITLKAGDNLIKQ 116  
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121 -----NCTNETYSLKKDLTDLTSVETEKLSFGANGKNVITSDTKGLNFAKETAGTNGD 174  
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DT 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE OUTER MEMBRANE PROTEIN GNA992.  
GN GNA992.  
OS Neisseria meningitidis.  
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.  
OX NCBI\_TaxID=487;  
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SEQUENCE FROM N.A.  
RC STRAIN=A22;  
RX MEDLINE=20175756; PubMed=10710308;  
RA Pizza M., Scarlato V., Masignani V., Giuliani M.M., Arico' B.,  
RA Comanducci M., Jennings G.T., Baldi L., Bartolini E., Capecci B.,  
RA Galeotti C.L., Luzzi E., Manetti R., Marchetti E., Mora M., Nuti S.,  
RA Ratti G., Santini L., Savino S., Scarselli M., Storni E., Zuo P.,  
RA Brooker M., Hundt E., Knapp B., Blair E., Mason T., Tettelin H.,  
RA Hood D.W., Jeffries A.C., Saunders N.J., Granoff D.M., Venter C.,  
RA Moxon E.R., Grandi G., Rappuoli R.;  
RT "Identification of Vaccine Candidates Against Serogroup B  
RT Meningococcus by Whole-Genome Sequencing.";  
RL Science 287:1816-1820(2000).  
DR EMBL: AF226364; AAF42513.1; -  
SQ SEQUENCE 599 AA; 62693 MW; 46C2E974AF7F78E9 CRC64;

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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
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GN NHHA.
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58;
RA Peak I.R., Strikbanta Y., Dieckelman M., Moxon E.R., Jennings M.P.;
RT "Identification and characterisation of a gene encoding a novel outer
RL membrane protein of Neisseria meningitidis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF125375; AAK09243.1;
SQ SEQUENCE 592 AA; 62290 MW; 168986A97381EFC5 CRC64;
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Job time: 702 sec
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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:36:25 ; Search time 104.77 seconds

(without alignments)

627.619 Million cell updates/sec

Title: US-09-771-382-10

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Scoring table: BLOSUM62

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Searched: 747574 seqs, 111073796 residues

Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	2779	93.0	592	20 AAY23744	A surface protein
4	2626.5	87.9	592	22 AAU06172	N. meningitidis H4
5	2626.5	87.9	589	20 AAY23745	A surface protein
6	2626.5	87.9	589	22 AAU06173	N. meningitidis P2
7	2587.5	86.6	599	20 AAY23743	A surface protein
8	2587.5	86.6	599	22 AAU06176	N. meningitidis H3
9	2552	85.4	594	20 AAY23739	A surface protein
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11	2533	84.8	594	20 AAY23740	A surface protein

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24	2443	81.8	592	20	RAY23737	A surface protein
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42	600	20.1	116	21	AAU37832	Neisserial conserv
43	398	13.3	1778	22	AAU52677	Escherichia coli p
44	396.5	13.3	2123	22	AAU00701	Moraxella catarrha
45	393.5	13.2	1992	17	AAU04505	Moraxella 200 kda

ALIGNMENTS

RESULT 1

AAU06180  
ID AAU06180 standard; Protein; 592 AA.

XX AAU06180;

XX 24-OCT-2001 (first entry)

XX N. meningitidis 22491 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain 22491.

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FT Region	51..102
FT	/label= V1
FT	/note= "Variable region 1"
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FT Region	115..124
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FT	/note= "Variable region 2"
FT Region	125..188
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FT	/note= "Conserved region 3"
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FT /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
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XX PD 02-AUG-2001.
XX PF 25-JAN-2001; 2001WO-AU00069.
XX PF 25-JAN-2000; 2000US-0177917.
XX (YOU ) UNIV QUEENSLAND.
XX
XX Peak IRA, Jennings MP;
XX PI
XX
XX WPI: 2001-488774/53.
XX N-PSDB; AAS09170.
XX
XX New Nhha surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
XX preventing broad spectrum of Neisseria meningitidis -
XX
XX Claim 9; Fig 1; 91pp; English.
XX
XX The present invention relates to the isolation of novel Neisseria
XX meningitidis mutant polypeptides of the surface antigen Nhha
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
XX characterised by deletions of non-conserved amino acids, particularly
XX the deletion of variable regions. The deletion mutants are useful in
XX diagnostics, therapeutic and prophylactic vaccines against a broader
XX spectrum of N. meningitidis, and in designing and/or screening of
XX medicaments. The mutant proteins when used as a vaccine can effectively
XX immunise against a broader spectrum of N. meningitidis strains than
XX would be expected from a corresponding wild-type surface antigen.
XX The present sequence representing the wild type surface antigen Nhha
XX from N. meningitidis strain 22491 is 1 of 10 Nhha polypeptide sequences
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in
XX the present invention.
XX
XX Sequence 592 AA;

Query Match 100.0%; Score 2988; DB 22; Length 592;
Best Local Similarity 100.0%; Pred. No. 6e-166;
Matches 592; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNKTYRTIWNALNAAVAVSELTRNHTKRASATVKTAVLATLTFATVQANATDEDEEL 60
DB 1 mnklyrtiwnsalnawvavseltrnhckrasatvktavlatlftatvqanatdedeeel 60

QY 61 ESVQSVVGSIQASMEGSGELETISLMTNDSKEFDVPIYIVVTLKAGDNLKIKQNTNENT 120
DB 61 esvqsvvgsiqasmeqsgelstismtndsksfvdyivvtlkgadnlkikqntnent 120

QY 121 NASSFTYSLKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180
DB 121 nassftyslkdlgtglinvtektlsfgangkknvniisdtkglnfaketagngdtttvhl 180

QY 181 GIGSTLTDTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGWNKIKVYKTGSTTGQSENVDF 240
DB 181 gigtltldtlagssashvdagnosthytraasikdvlnagwnkikvyktgsttgqsenvdf 240

QY 241 VRYDYTFEFLSADTKTTVNVEKSDNGKRTEVKIGAKTSVIKEKDGKLVTKGKGENGSS 300
DB 241 vrydytfevlsadtkttvnveskdngkrtevkigaktsvikekdglvtkgkgengss 300

QY 301 TDEGEGLVTAKEVIDAVNKAQRMKTTTANGQTQADKFETVTSGTNVTASCKGKITATV 360
```

```
DB 301 tdegeglvtakevidavnkagwrmtttangtcqgdkkfetvtsgnvtfasqkgtatv 360
QY 361 SKDDQGNITVMYDNYGDALNVNQLQNSGWNLDKAVAGSSGKVIISGNVSPSKGMDETV 420
DB 361 skddqgnitvmydnygdalnvnlqlqnsqwnldskavagssgkvisgnyvpskgkmdetv 420
QY 421 NINAGNNIEISRNKKNIDITATSMAPOFSSVSLGAGADAPTLSVDDDEGALNVGSKDANKPV 480
DB 421 ninagnnieisrنگknidiatsmapqfssvslgagadapltlsvdddegalnvgsdkankpv 480
QY 481 RITNAPGVKEGDVTNVAOLKGVQAOIINRDNVDCGNARAGIAQAATAGLVAQYLPKGS 540
DB 481 ritnavpgvkegdvtnvaqlkgvaqnlrindvngnaragiataglvaylpqks 540
QY 541 MMAIGGGTYRGAGYAGYSSISDGGNWIKGTASGNSRGHFGASASVGYQW 592
DB 541 mmaigggtyrgeagyaigyssisddggnwiikgtasgnsrghfgasasvgyqw 592

RESULT 2
AAY27203
ID AAY27203 standard; Protein; 592 AA.
XX
XX AC AAY27203;
XX
XX DT 24-SEP-1999 (first entry)
XX
XX DE Amino acid sequence of N. meningitidis protein ORF40a.
XX
XX KW Neisseria meningitidis protein; pharmaceutical; vaccine; diagnosis;
XX bacterial infection; treatment.
XX
XX OS Neisseria meningitidis.
XX
XX PN WO9936544-A2.
XX
XX PD 22-JUL-1999.
XX
XX PF 14-JAN-1999; 99WO-IB001103.
XX
XX PR 09-OCT-1998; 98GB-0022143.
XX PR 14-JAN-1998; 98GB-0000760.
XX PR 01-SEP-1998; 98GB-0019015.
XX
XX PA (CHIR-) CHIRON SPA.
XX
XX PI Grandi G, Masignani V, Pizza M, Rappuoli R, Scarlato V;
XX
XX WPI: 1999-444400/37.
XX N-PSDB; AAX99125.
XX
XX PT New protein and its nucleotide sequence, useful in vaccines or
XX diagnostic compositions for treating and/or preventing Neisseria
XX meningitidis infections
XX
XX PS Claim 1; Page 63; 123pp; English.
XX
XX CC The invention provides proteins (AAY27201-245) from Neisseria
XX meningitidis (strains A and B) and nucleic acid sequences (AAX99123-167)
XX encoding the proteins. Compositions comprising the protein, nucleic acid
XX or antibody specific to the protein are useful as pharmaceuticals, e.g. a
XX vaccine composition or a diagnostic composition. The composition is also
XX useful for treating or preventing an infection due to Neisseria
XX bacteria, especially Neisseria meningitidis.
XX
XX SQ Sequence 592 AA;

Query Match 98.5%; Score 2942; DB 20; Length 592;
Best Local Similarity 98.8%; Pred. No. 2.8e-163;
Matches 585; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
```

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
DB 1 mnkiyriiwsalnawavseltrnrhtkrasatvktavlatllfatvqanatede 60  
QY 61 ESVQRSVVGSIOASMEGSELETISLSMTNDSKEFVDPYIVVTLKAGDNLIKQNTNENT 120  
DB 61 esvqrsvvgsioasmegseletislsmtndsksfvdpvivvllkagdnlikqntn 120  
QY 121 NASSFTYSLSKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180  
DB 121 nassftyslskdlgtlinvxteklsgangkkvniisdtckglnfaketagtdttvhl 180  
QY 181 GIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKIKGVKSTGTGQSENVD 240  
DB 181 gigtstltdtlaagssashvdagpnxsthytraasikdvlagnwnikgvkstgtgs 240  
QY 241 VRTYDTVFELSADTQVTVNVESKONGKRTVEVKIGAKTSVKEKDKLVTGKKGENGSS 300  
DB 241 vrttdtveflsadtqvtvnnveskdngkrtvevkiaktsvikekdglvtgkgkeng 300  
QY 301 TDEGELVTAKVIDAVNKAHRMKTITTTANGOTGOADKFETVTSCTNVTFAASKGTATV 360  
DB 301 tdegeglvtakevidavnkagrmkttttangotgoadkfetvtsctnvtfasgkgtat 360  
QY 361 SKDDQGNITVMYDVNVGDALNVQNSGWNLDKXAVAGSSGKVISGNVSPSKGMDETV 420  
DB 361 skddqgnitvmydvngdalnvnqlnsgwnldskavagssgkvlsngnvspskgmdet 420  
QY 421 NINAGNNIEISRNKNIDATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPV 480  
DB 421 ninagnnieisrngnkidiatsmapqfssvslgagadaptlsvddegalnvsgkdank 480  
QY 481 RITNVAPGVKEGDVTVNVAQLKVAQNLRIDNVGNRAGIAQAIAATAGLVQAYLPKGS 540  
DB 481 ritnvapgvkxgdvtnvaxqlkvaqnlrindvngnragiaqaiaataglvqaylpkgs 540  
QY 541 MMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592  
DB 541 mmaigggtyrgeagyaigyssisdgnwliikgtasngsrghfgasasvgyqw 592

RESULT 3

AAU06172  
ID AAU23744 standard; Protein; 592 AA.  
XX  
AC AAU23744;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9311132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI; 1999-418754/35.  
DR N-PSDB; AAX85796.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.

meningitidis infections

PS Claim 1; Page 118-120; 132pp; English.

XX The present sequence represents a surface protein of Neisseria meningitidis which is approximately 62 kDa. The N. meningitidis surface glycoproteins, nucleic acids, the primers and optionally a thermostable polymerase, or antibodies are useful in a kit for the detection or diagnosis of N. meningitidis infection in humans. CC The N. meningitidis surface glycoproteins can also be used to prevent or treat N. meningitidis infection in humans, especially CC in the form of vaccines. The proteins and antibodies can also CC be used to identify immunoreactive peptides.

SQ Sequence 592 AA;

Query Match 93.0%; Score 2779; DB 20; Length 592;  
Best Local Similarity 93.9%; Pred. No. 8.4e-154;  
Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

QY 1 MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
DB 1 mnkiyriiwsalnawavseltrnrhtkrasatvktavlatllfatvqanatede 60  
QY 61 ESVQRSVVGSIOASMEGSELETISLSMTNDSKEFVDPYIVVTLKAGDNLIKQNTNENT 120  
DB 61 esvqrsvvgsioasmegseletislsmtndsksfvdpvivvllkagdnlikqntn 120  
QY 121 NASSFTYSLSKDLTGLINVEETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180  
DB 121 nassftyslskdlgtlinvxteklsgangkkvniisdtckglnfaketagtdttvhl 180  
QY 181 GIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIKGVKSTGTGQSEN 238  
DB 181 gigtstltdmlntgattntvndvtddekkraasvkdvlagnwnikgvkpgtta--sdnv 238  
QY 239 DFRVRYDTVFELSADTQVTVNVESKONGKRTVEVKIGAKTSVKEKDKLVTGKKGENG 298  
DB 239 dfrvrydtveflsadtqvtvnnveskdngkrtvevkiaktsvikekdglvtgkgkeng 298  
QY 299 SSTDEGELVTAKVIDAVNKAHRMKTITTTANGOTGOADKFETVTSCTNVTFAASKGT 358  
DB 299 sstdegeglvtakevidavnkagrmkttttangotgoadkfetvtsctnvtfasgngtta 358  
QY 359 TVSKDDQGNITVMYDVNVGDALNVQNSGWNLDKXAVAGSSGKVISGNVSPSKGMD 418  
DB 359 tvskddqgnitvmydvngdalnvnqlnsgwnldskavagssgkvlsngnvspskgmd 418  
QY 419 TVNINAGNNIEISRNKNIDATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 478  
DB 419 tvninagnnieisrngnkidiatsmapqfssvslgagadaptlsvddegalnvsgkdank 478  
QY 479 PVRITNVAPGVKEGDVTVNVAQLKVAQNLRIDNVGNRAGIAQAIAATAGLVQAYLP 538  
DB 479 pvrntnvapgvkxgdvtnvaxqlkvaqnlrindvngnragiaqaiaataglvqaylp 538  
QY 539 KSMMAIGGGTYRGEAGYAIGYSSISDGNWIIKGTASGNSRGHFGASASVGYQW 592  
DB 539 ksmmaigggtylgeagyaigyssisaggnwliikgtasngsrghfgasasvgyqw 592

RESULT 4

AAU06172  
ID AAU06172 standard; Protein; 592 AA.  
XX  
AC AAU06172;  
XX  
DT 24-OCT-2001 (first entry)  
XX  
DE N. meningitidis H41 surface antigen NhhA polypeptide sequence.  
XX  
KW Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain H41.  
XX FH Location/Qualifiers  
FT Peptide 1..51  
FT Region /label= Signal\_peptide  
FT 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..102  
FT /label= V1  
FT /note= "Variable region 1"  
FT 52..592  
FT Protein /label= Mature\_Nhha  
FT /note= "Predicted mature protein, specifically  
FT claimed in claim 12"  
FT Region 103..114  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 115..124  
FT Region /label= V2  
FT /note= "Variable region 2"  
FT 125..188  
FT Region /label= C3  
FT /note= "Conserved region 3"  
FT 189..210  
FT /label= V3  
FT /note= "Variable region 3"  
FT 211..229  
FT Region /label= C4  
FT /note= "Conserved region 4"  
FT 230..236  
FT Region /label= V4  
FT /note= "Variable region 4"  
FT 237..592  
FT Region /label= C5  
FT /note= "Conserved region 5"  
XX WO200155182-A1.  
XX 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-AU00069.  
XX 25-JAN-2000; 2000US-0177917.  
XX (UYQU ) UNIV QUEENSLAND.  
XX Peak IRA, Jennings MP;  
XX WPI; 2001-488774/53.  
XX N-PSDB; AAS09162.  
XX New Nhha surface antigen polypeptides and polynucleotides from  
XX Neisseria meningitidis, useful in producing vaccines for treating or  
XX preventing broad spectrum of Neisseria meningitidis -  
XX Claim 9; Fig 1; 91pp; English.  
XX The present invention relates to the isolation of novel Neisseria  
XX meningitidis mutant polypeptides of the surface antigen Nhha  
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
XX characterised by deletions of non-conserved amino acids, particularly  
XX the deletion of variable regions. The deletion mutants are useful in  
XX diagnostics, therapeutic and prophylactic vaccines against a broader  
XX spectrum of N. meningitidis, and in designing and/or screening of  
XX immunisants. The mutant proteins when used as a vaccine can effectively  
XX immunise against a broader spectrum of N. meningitidis strains than  
XX would be expected from a corresponding wild-type surface antigen.  
XX The present sequence representing the wild type surface antigen Nhha  
XX from N. meningitidis strain H41 is 1 of 10 Nhha polypeptide sequences  
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
XX the present invention.

XX SQ Sequence 592 AA;  
Query Match 93.0%; Score 2779; DB 22; Length 592;  
Best Local Similarity 93.9%; Pred. No. 8.4e-154;  
Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVALTLATLFAVQANATDEDEEEL 60  
DB 1 mnkiyriiwnlsalnwavavseltrnhtkrasatvktavlatlifatvqanatedeeseel 60  
QY 61 ESVQSVVSGSIQASMEGSGELETFISLMTNDSKEFVDPPIYIVVTLKAGDNLKIQNTNENT 120  
DB 61 esvqsvvsgsiqasmevsgseletisismntndsksfvdpvivyvtlkagdnlikikntnnt 120  
QY 121 NASSTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180  
DB 121 nasstyslkkdltglinveteKlsfgangkkvniisdtkglnfaketagtngdtvtvhlN 180  
QY 181 GIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIKGVKVTGTGSENV 238  
DB 181 gigstltDmlntgattnvtndnvtddkkrasvkdvlnagwnikgvkpgtta--sdnv 238  
QY 239 DFVRTYDTVEFLSADTKTTTVNVVESKDNKRTEVKIGAKTSVIKEKDGKLVTKGKGENG 298  
DB 239 dfvrtYdtvEflsadtktttvnveskdngkktevkiGaktsvikekdgklvtgkgeng 298  
QY 299 SSTDEGEGLVTAKEVIDAVNKGWRMKTTFANGOTGOADKFETVTSNTVTFASGKGTTA 358  
DB 299 sstdegeglvtakevIdavnkgwrMktttfAngotGoAdkfETvtsntvtfasgkgTTA 358  
QY 359 TVSKDDQGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGMDE 418  
DB 359 tvskddqgnitvkydvnvvgdalnvnlqnsGwnldskavagsgkvisgnvspskgmde 418  
QY 419 TVNINAGNTEISRCKNIDIIATSMAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANK 478  
DB 419 tvninagnnieitrngknidiatmtpfssvslgagadapTLsvddegalnvvgskdank 478  
QY 479 PVRITNVAPGVKEGDDVTNVAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLPG 538  
DB 479 pvrItnvapgvkegdvtnvaqlkgvaqnlrnidnvgnaragIaQaiataglvqaylpg 538  
QY 539 KSMMAIGGGTYRGEAGYAIIGYSSISDGGNWIIRKGTASGNSRGRHFGASASYGYOW 592  
DB 539 ksmmaigggtYlgeagyaigYssisaggwniirKgtasgnsrgrhfgasasygyow 592  
RESULT 5  
AAY23745  
ID AAY23745 standard; Protein; 589 AA.  
XX  
AC AAY23745;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
KW Immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.

PA (UYQU ) UNIV QUEENSLAND.

XX Jennings MP, Moxon ER, Peak IRA;

XX WPI: 1999-418754/35.

DR N-PSDB; AAX85797.

XX Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections

XX Claim 1; Page 122-124; 132pp; English.

XX The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX Sequence 589 AA;

Query Match 87.9%; Score 2626.5; DB 20; Length 589;  
Best Local Similarity 89.1%; Pred. No. 6.1e-145;  
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;

QY 1 MNKIYRIINWALNAWVSELTNRHTKRASATVKTAVLATLFLFATVQANATDEDEEEL 60

Db 1 mnkiyriinwalsalnawvsseltlrhtkrasatvatvlatlflsatvqanatdedeel 60

QY 61 ESQRS-VVGSIQASMEGSELET---ISLSMTNDSKEFVDPIYVTLKAGDNLKIQTNT 116

Db 61 esvarsalvlqfmidkegnesteigswiyddhmtlgh-atvtlkgadnlkik-- 117

QY 117 NENTNASSFTYSLKDLDTGLINVEKELSFAGKNGKVNIIISDTKGLNFAKETAGTNGDIT 176

Db 118 ----sgkdfstyslkkeldtsveteklsfgangknvntsdckglnfaketagtngdpt 173

QY 177 VHLNGTGSLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKIKYKGTGSGTQGE 236

Db 174 vhlngigtltldtlagssashvdagngqsthytraasikdvlhagwnikgvtgtstgqse 233

QY 237 NVDFVRYTYTVEFLSADTKTTTVNVESKNGKRTVEKIGAKTSVKEKCKLVGKKGKE 296

Db 234 nvdfvrytytveflsadtktttvnveskdngkrtevkigaktsvikekdglvkgkge 293

QY 297 NGSSSTDEGEGLYTAKEVIDAVNKGWRMKTTTTANGOTGOADKFPETVTSCTNVTFASSKGT 356

Db 294 ngssstdegeglvtakevidavngkgrwmkttttangotgqadkfetvtsctkvtfasngt 353

QY 357 TATVSKDDGNTVMYDVNVGDALNVLQNSGWNLDKAVAGSSGKVISGNVSPSKGRM 416

Db 354 tatvskddgntvmkydvngdalnvnqlqnsqwnldskavagssgkvlsnvspksgrm 413

QY 417 DETVNNAGNNIEISRNKGNIDATSMAPQFSVSLGACADAPTLSDDEGALNVGSKDA 476

Db 414 detvnnagnnieitrngnkniatsmtpqfssvslgagadaptlsvddegalnvsgkda 473

QY 477 NKPVRTNVPAGVKEGDVTNVAQLKGAONLNNRINDVGNARAGTAQATAGLVQAYL 536

Db 474 nkpvrntnvpagvkegdvtnvqkgaonlnrindvngnaraglaqataglaqayl 533

QY 537 PGKSMMAIGGGYRGAGYAIGYSSISDGNWIKIGTASGNSRGRHFGASASVGQYQW 592

Db 534 pgksmmaigggtylgeagyaigysissidgnwviktasgnsrgrhfgtsasvgqyq 589

RESULT 6

AAU06173

ID AAU06173 standard; Protein; 589 AA.

XX AAU06173;

XX 24-OCT-2001 (first entry)

XX N. meningitidis P20 surface antigen Nhha polypeptide sequence.

XX Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX Neisseria meningitidis strain P20.

XX Key Location/Qualifiers

XX Region 1..50 /label= C1

XX Region 51..105 /note= "Conserved region 1"

XX Region 106..117 /label= V1

XX Region 118..121 /note= "Variable region 1"

XX Region 122..185 /label= C2

XX Region 186..205 /note= "Conserved region 2"

XX Region 206..224 /label= V2

XX Region 225..233 /note= "Variable region 2"

XX Region 234..589 /label= C3

XX Region 235..239 /note= "Conserved region 3"

XX Region 240..244 /label= C4

XX Region 245..253 /note= "Variable region 4"

XX Region 254..589 /label= V4

XX Region 589..593 /note= "Conserved region 5"

XX WO200155182-A1.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYQU ) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

XX WPI: 2001-488774/53.

XX N-PSDB; AAS09163.

XX New Nhha surface antigen polypeptides and polynucleotides from  
XX Neisseria meningitidis, useful in producing vaccines for treating or  
XX preventing broad spectrum of Neisseria meningitidis -  
XX Claim 9; Fig 1; 91pp; English.

XX The present invention relates to the isolation of novel Neisseria  
XX meningitidis mutant polypeptides of the surface antigen Nhha  
XX (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are  
XX characterised by deletions of non-conserved amino acids, particularly  
XX the deletion of variable regions. The deletion mutants are useful in  
XX diagnostics, therapeutic and prophylactic vaccines against a broader  
XX spectrum of N. meningitidis, and in designing and/or screening of  
XX medicaments. The mutant proteins when used as a vaccine can effectively  
XX immunise against a broader spectrum of N. meningitidis strains than  
XX would be expected from a corresponding wild-type surface antigen.  
XX The present sequence representing the wild type surface antigen Nhha  
XX from N. meningitidis strain P20 is 1 of 10 Nhha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.

XX  
SQ Sequence 589 AA;

Query Match 87.9%; Score 2626.5; DB 22; Length 589;  
Best Local Similarity 89.1%; Pred. No. 6.1e-145;  
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;

```
QY 1 MNKIYRIIWSALNANWAVASELNRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
   |||||
Db 1 mnkiyriiwsalnawvvseltrnhtkrasatvatvatllisatvqanatdedeel 60
   |||||

QY 61 ESQVRS--VWGSIOASMEGSGELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQNT 116
   |||||
Db 61 esvarsalvlqfmidkegnestdgiswyddhntlhg-atvclkgadnlkikq-- 117

QY 117 NENTNASSFTYSLKDLTGLINVEKLSFGANGKKVNIISDTKGLNFAKETAGTGDTT 176
   : |||||
Db 118 ----sgkdfyslkkeldltsveteklsfgangknvitsdtkglnfaketagtgndpt 173

QY 177 VHLNGTSTLDTLGLAGSSASHVDAGNOSTHYTRAASIKDVLNAGWNKIGVKTGSTTCQSE 236
   |||||
Db 174 vhlngtstltdtlagssashvdagnsthytraasikdvlnagwnikgvktgsttgse 233

QY 237 NVDFVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIREKDKGLVTGKGKE 296
   |||||
Db 234 nvdvrltydtveflsadtktttvnveskdngkrtvekgigaktsvirekdkglvtgkgke 293

QY 297 NGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSGTNVTFSAGKGT 356
   |||||
Db 294 ngsstdegeglvtakevidavnkagwrmtttangqtqgqadkfetvtsgtkvtfasngt 353

QY 357 TATVSKDDQGNITVWVDVNGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 416
   |||||
Db 354 tatvskddqgnitvkdyvngvda.lnvnlqnsqwnldskavagssgkvvisgnvspkghm 413

QY 417 DETVNIAGNNIEISRNGKNIDIAATSMAPQSSVSLGAGADAPTLSVDDGALNVGSKDA 476
   |||||
Db 414 detvniagnnieitrngknidiatstmpqfssvslgagadapltlsvddgalnvsgkda 473

QY 477 NKPVRITNAPGVKEGVDVTNVAQLKGVQANLNRRIDNVGDNARAGIAQAIATAGLVAYL 536
   |||||
Db 474 nkpvrinavpgvkegdvtnvaqlkgvaqnlrridnvngdnaragiaqaiataglaqyl 533

QY 537 PGKSMMAIGGTYRGEAGYAIYSSISDGGNWIITKGTSNRSRGRHFGASASVGYQW 592
   |||||
Db 534 pgksmmaigggtylgeagyaigyssisdggnwniikgtasgnsrgrhfgtsasvgyqw 589
```

## RESULT 7

AAU23743  
ID AAY23743 standard; Protein; 599 AA.

XX  
AC AAY23743;

XX  
DT 08-SEP-1999 (first entry)

XX  
DE A surface protein of Neisseria meningitidis.

XX  
KW Surface protein; surface glycoprotein; infection; vaccine;  
immunoreactive peptide.

XX  
OS Neisseria meningitidis.

XX  
PN W09931132-A1.

XX  
PD 24-JUN-1999.

XX  
PF 14-DEC-1998; 98WO-AU01031.

XX  
PR 12-DEC-1997; 97GB-0026398.

XX  
PA (ISIS-) ISIS INNOVATION LTD.  
N-PSDB; AAX85795.

XX  
PI Jennings MP, Moxon ER, Peak IRA;

XX  
WPI; 1999-418754/35.

DR N-PSDB; AAX85795.

XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
meningitidis infections

XX  
PS Claim 1; Page 114-115; 132pp; English.

XX  
CC The present sequence represents a surface protein of Neisseria  
meningitidis which is approximately 62 kDa. The N. meningitidis  
surface glycoproteins, nucleic acids, the primers and optionally  
a thermostable polymerase, or antibodies are useful in a kit for  
the detection or diagnosis of N. meningitidis infection in humans.  
The N. meningitidis surface glycoproteins can also be used to  
prevent or treat N. meningitidis infection in humans, especially  
in the form of vaccines. The proteins and antibodies can also  
be used to identify immunoreactive peptides.

XX  
SQ Sequence 599 AA;

Query Match 86.6%; Score 2587.5; DB 20; Length 599;  
Best Local Similarity 88.0%; Pred. No. 1.2e-142;  
Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;

```
QY 1 MNKIYRIIWSALNANWAVASELNRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60
   |||||
Db 1 mnkiyriiwsalnawvvseltrnhtkrasatvktavlatllfatvqanatedeheel 60

QY 61 ESQVRS--VWGSIOASMEGSGELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQ-- 114
   |||||
Db 61 epvvralsvlqfmidkegnestdgiswyddhntlhg-atvclkgadnlkikqnt 119

QY 115 --NTNENTNASSFTYSLKDLTGLINVEKLSFGANGKKVNIISDTKGLNFAKETAGTN 172
   |||||
Db 120 nktntentndssfyisllkldltsveteklsfgangknvitsdtkglnfaketagn 179

QY 173 GDTTVHLNGTSTLDTLGLAGSSASHVDAGNOST---HYTRAASIKDVLNAGWNKIGVKTGS 230
   |||||
Db 180 gdttvhlngtstltdtllntgattntvndtdkdkkrraasvkdvnagwnikgvkpgt 239

QY 231 TTGQSENVDVVRTYDTVEFLSADTKTTTVNVESKDNGKRTVEKIGAKTSVIREKDKGLVT 290
   |||||
Db 240 ta--sdhndvrtvtydtveflsadtktttvnveskdngkrtvekgigaktsvirekdkglvt 297

QY 291 GKGKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGQTQADKFETVTSGTNVT 350
   |||||
Db 298 gkgkgengstdegeglvtakevidavnkagwrmtttangqtqadkfetvtsgtntvf 357

QY 351 ASGKGTATVSKDDQGNITVWVDVNGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410
   |||||
Db 358 asgkgtatvskddqgnitvkdyvngvda.lnvnlqnsqwnldskavagssgkvvisgnvs 417

QY 411 PSKGMDETVINAGNNIEISRNGKNIDIAATSMAPQSSVSLGAGADAPTLSVDDGALN 470
   |||||
Db 418 pskgmdetvniagnnieitrngknidiatstmpqfssvslgagadapltlsvddkgaln 477

QY 471 VGSKDANKPVRITNAPGVKEGVDVTNVAQLKGVQANLNRRIDNVGDNARAGIAQAIATAG 530
   |||||
Db 478 vgskdankpvrinavpgvkegdvtnvaqlkgvaqnlrridnvngdnaragiaqaiatag 537

QY 531 LVQAYLPKGSMMMAITGGTYRGEAGYAIYSSISDGGNWIITKGTSNRSRGRHFGASASVGY 590
   |||||
Db 538 lvqaylpkgsmmaigggtyrgeagyaigyssisdggnwiikgtasgnsrgrhfgasasvgy 597

QY 591 QW 592
   ||
```



Db 598 qw 599

RESULT 8

AAU06176

ID AAU06176 standard; Protein: 599 AA.

XX AC AAU06176;

XX DT 24-OCT-2001 (first entry)

XX DE N. meningitidis H38 surface antigen Nhha polypeptide sequence.

XX KW Surface antigen Nhha; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain H38.

XX FH Key Location/Qualifiers

FT Region 1..50

FT /label= C1

FT /note= "Conserved region 1"

FT Region 51..105

FT /label= V1

FT /note= "Variable region 1"

FT Region 106..117

FT /label= C2

FT /note= "Conserved region 2"

FT Region 118..131

FT /label= V2

FT /note= "Variable region 2"

FT Region 132..195

FT /label= C3

FT /note= "Conserved region 3"

FT Region 196..217

FT /label= V3

FT /note= "Variable region 3"

FT Region 218..236

FT /label= C4

FT /note= "Conserved region 4"

FT Region 237..243

FT /label= V4

FT /note= "Variable region 4"

FT Region 244..599

FT /label= C5

FT /note= "Conserved region 5"

PN WO200155182-A1.

XX 02-AUG-2001.

XX 25-JAN-2001; 2001WO-AU00069.

XX 25-JAN-2000; 2000US-0177917.

XX (UYQU ) UNIV QUEENSLAND.

XX Peak IRA, Jennings MP;

XX WPI; 2001-488774/53.

XX N-PSDB; AAS09166.

XX New Nhha surface antigen polypeptides and polynucleotides from

PT Neisseria meningitidis, useful in producing vaccines for treating or

PT preventing broad spectrum of Neisseria meningitidis -

XX Claim 9; Fig 1; 9lpp; English.

XX The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Nhha

CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broad

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Nhha

CC from N. meningitidis strain H38 is 1 of 10 Nhha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

CC the present invention.

XX SQ Sequence 599 AA;

Query Match 86.6%; Score 2587.5; DB 22; Length 599;

Best Local Similarity 88.0%; Pred. No. 1.2e-142;

Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;

Qy 1 MNKYRIIWSALNNAWAVSELTRNHTKRASATVTVAVLATLLFATVQANATDEDEEEL 60

Db 1 mnkyriiwsalnawavseltrnhtkrasatvktavlatllfatvqanatdedeeel 60

Qy 61 ESVQRS-VVGSIQASMEGSGELET---ISLSMTNDSKEFVDPIYIVVTLKAGNLIKQ-- 114

Db 61 epvrsalvlqfmidkegnesestgnlgwsllydnhtihg-atvtlkagdnllkiknt 119

Qy 115 --NTNENTNASFTYSLKKDLTGLINVETEKLSFGANGKKVNIISDTKGLNFAKETAGTN 172

Db 120 nkntnentndssftysllkldltltsveteklsfgangknvntsdtkglnfaketagn 179

Qy 173 GDTVHLNGIGSTLDTLAGSASHVDAGNQST--HYTRAASIKOVLNAGWIKGVKQGS 230

Db 180 gdtvhlngigstltdtllntgattntndnvtddkkrasvkvdlvnagwnikgvkpgt 239

Qy 231 TTGOSENVDFVRYDTVEFLSADTKTTVNVESKDKGRTEVKIGAKTSVKEKGKLV 290

Db 240 ta--sdnvdvhtydtveflsadtkttvnveskdkgrtevkigaktsvikekgklvt 297

Qy 291 GKKGSGSSTDEGEGLVTAKEVIDAVNAKAGWRMKT---ANGOTGOADKFPETVTSNTVF 350

Db 298 gkgksgsstdegeglvtakevidavnaagwrmktttangtgqadkfetvtsntvf 357

Qy 351 ASGKTTATVSKDDGNITVMYDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVISGNVS 410

Db 358 asgkttatvskddgnitvkydvnvgdalnvqnqlnsgwnldskavagssgkvisgnvs 417

Qy 411 PSKGMDETVNINAGNNTIEISRNKKNIDITATSMAPQSSVSGAGADAPTLSVDDGALN 470

Db 418 pskgmde tvn inag nntie i s r n k k n i d i t a t s m a p q s s v s g a g a d a p t l s v d d g a l n 477

Qy 471 VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLNNRIDNVDCNARAGIAQAIATAG 530

Db 478 vgskdankpvr itnvapgvkegdvtnvaqlkgvaqnl n r i d n v d c n a r a g i a q a i a t a g 537

Qy 531 LVQAYLPKSKMMAIGGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHGASVGY 590

Db 538 lvqaylpksgmmaigggtyrgeagyaigyssisdgnwii k g t a s g n s r g h g a s v g y 597

Qy 591 QW 592

Db 598 qw 599

RESULT 9

RAY23739

ID AAY23739 standard; Protein: 594 AA.

XX AC AAY23739;

XX DT 08-SEP-1999 (first entry)

XX DE A surface protein of Neisseria meningitidis.

XX KW Surface protein; surface glycoprotein; infection; vaccine;

KW immunoreactive peptide.

```
XX  Neisseria meningitidis.
OS  W09931132-A1.
PN  XX
XX  24-JUN-1999.
PD  XX
XX  14-DEC-1998; 98WO-AU01031.
PF  XX
XX  12-DEC-1997; 97GB-0026398.
PR  XX
XX  (ISIS-) ISIS INNOVATION LTD.
PA  (UYQU ) UNIV QUEENSLAND.
XX  XX
XX  Jennings MP, Moxon ER, Peak IRA;
PI  WPI; 1999-418754/35.
XX  N-PSDB; AAX85791.
DR  XX
XX  Neisseria meningitidis surface proteins useful for treating N.
PT  meningitidis infections
PS  Claim 1; Page 95-97; 132pp; English.
XX  The present sequence represents a surface protein of Neisseria
CC  meningitidis which is approximately 62 kDa. The N. meningitidis
CC  surface glycoproteins, nucleic acids, the primers and optionally
CC  a thermostable polymerase, or antibodies are useful in a kit for
CC  the detection or diagnosis of N. meningitidis infection in humans.
CC  The N. meningitidis surface glycoproteins can also be used to
CC  prevent or treat N. meningitidis infection in humans, especially
CC  in the form of vaccines. The proteins and antibodies can also
CC  be used to identify immunoreactive peptides.
XX  XX
SQ  Sequence 594 AA;

Query Match 85.4%; Score 2552; DB 20; Length 594;
Best Local Similarity 86.8%; Pred. No. 1.3e-140;
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;

QY 1 MNKIYRIWNSALNANVAVSELFRNHTKRASATKAVLATLFTATVQANATDEDEEEL 60
DB 1 mnkiyriwnsalnawvvsellrnhthkrasatvatavlatlftatvqanatd-dddlyl 59
QY 61 ESYQR-SWVGSIOASMEGSELETISLSMTNDSKEFVDPVI-----VVTLKAGDNL 110
DB 60 epvqrtavlvlsfrsdkegtgekeg-----tedsnwav--yfdkrrvlkagaitikagdnl 112
QY 111 KIKONTNENTNASSFTYSLKKDLTGLINVETELKSLFGANGKKNIIISDTKGLNFAKETAG 170
DB 113 kikontnentndsfyslkkdltdltsveteklsfgangkkniiisdtkglnfaketag 172
QY 171 TNGDTTVHLNGIGSTLDTLTLGSSASHVDAGNOST--HYTRAASIKDVLNAGWNIKGVKT 228
DB 173 tngdptvhlngigtldtlltngattvndnvtdekkraasvkdvlnaagwnikgvkp 232
QY 229 GSTTGOSENVDVFTYDTVEFLSADTKTTTVNVEDKNGKRTVEKTCARTSVIKEKDGKL 288
DB 233 gttc--sdnvdfvrtvotveflsadtkttvvnvesdngkktvekgaktsvikekdgl 290
QY 289 VTGKGKENGSSSTDEGEGLVTAKEVIDAVNKGWRMKTITANGTGTQADRFETVTSCTNV 348
DB 291 vtgkgkdengsstdegeglvtakevidavnnkagwrmtttangtgtgqadkfetvtsctnv 350
QY 349 TFASGKGTATVSKDDOGNTVMYDWNVGDALNVQNLQNSGWNLDSKAVAGSSGKVIISGN 408
DB 351 tfasgkgtatvskddognitvdyvnnvgdnlvngqlnsgwnldskavagssgkvlisgn 410
QY 409 VSPSKGMDFTVINAGNNTEISRNGKNIDIAATSMAPQFSSVSIAGACADPTLSVDDEGA 468
DB 411 vspskgmdftvinagnnleitrngknidiatmapqfssvsiagacaptlsvddega 470
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QY 469 LNVGSKDANKPVRIITNVAPGVKEGVDVTNVAOLKGVQANLNRRIDNVGNARAGIAQAIAT 528
DB 471 lnvgskdtnkpvritnvpagvkegdvtnvaqlkgvaqlnnrldnvdgnaraglaqaiat 530
QY 529 AGLVQAYLPCKSNMAIGGGTYRGAGYAGYSSYSDGNNWIIKGTASGSRGHFGASASV 588
DB 531 aglvqaylpqksmma19gdtyrgeagyagyslsdggnnwllkgtasgnsrghfgasav 590
QY 589 GYQW 592
DB 591 gyqw 594

RESULT 10.
AAU06179
ID AAU06179 standard; Protein; 594 AA.
XX AC AAU06179;
XX 24-OCT-2001 (first entry)
XX N. meningitidis BZ198 surface antigen NhhA polypeptide sequence.
XX Surface antigen NhhA; meningococcal disease; meningitis vaccine.
XX Neisseria meningitidis strain BZ198.
XX Key Location/Qualifiers
FT Region 1..50 /label= C1
FT /note= "Conserved region 1"
FT Region 51..104 /label= V1
FT /note= "Variable region 1"
FT Region 105..116 /label= C2
FT /note= "Conserved region 2"
FT Region 117..126 /label= V2
FT /note= "Variable region 2"
FT Region 127..190 /label= C3
FT /note= "Conserved region 3"
FT Region 191..212 /label= V3
FT /note= "Variable region 3"
FT Region 213..231 /label= C4
FT /note= "Conserved region 4"
FT Region 232..238 /label= V4
FT /note= "Variable region 4"
FT Region 239..594 /label= C5
FT /note= "Conserved region 5"
XX WO200155182-A1.
XX 02-AUG-2001.
XX 25-JAN-2001; 2001WO-AU00069.
XX 25-JAN-2000; 2000US-0177917.
XX (UYQU ) UNIV QUEENSLAND.
XX Peak IRA, Jennings MP;
PI WPI; 2001-488774/53.
XX N-PSDB; AAS09169.
DR New NhhA surface antigen polypeptides and polynucleotides from
XX Neisseria meningitidis, useful in producing vaccines for treating or
PT
```

PT preventing broad spectrum of Neisseria meningitidis -

PS Claim 9; Fig 1; 9lpp; English.

XX The present invention relates to the isolation of novel Neisseria

CC meningitidis mutant polypeptides of the surface antigen Nhha

CC (AAU06182-AAU06186). The modified or mutant Nhha polypeptides are

CC characterised by deletions of non-conserved amino acids, particularly

CC the deletion of variable regions. The deletion mutants are useful in

CC diagnostics, therapeutic and prophylactic vaccines against a broader

CC spectrum of N. meningitidis, and in designing and/or screening of

CC medicaments. The mutant proteins when used as a vaccine can effectively

CC immunise against a broader spectrum of N. meningitidis strains than

CC would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Nhha

CC from N. meningitidis strain B2198 is 1 of 10 Nhha polypeptide sequences

CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in

CC the present invention.

XX

SQ Sequence 594 AA;

Query Match 85.4%; Score 2552; DB 22; Length 594;  
Best Local Similarity 86.8%; Pred. No. 1.3e-140;  
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;

Qy 1 MNKIYRIITWNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 mnkiyriiwnsalnawvseltrnhtkrasatvatavlatllfatvqanadtd-dddlyl 59  
Qy 61 ESVQR-SVVGSTQASMEGSELETISLSMTNDSKEFVDPYI-----VVTLAGDNIL 110  
Db 60 epvqrtavvlsfrsdegekeg-----tedsnawv--yfdkvrkagaitlkagdnl 112  
Qy 111 KIKQNTNENTNASSFTYSLKDLTGLINVEFKLSFGANGKKNVNIISDTKGLNFAKETAG 170  
Db 113 kikqntentndssftyslkkdltltsveteklsfgangknvnitsdtkglnfaketag 172  
Qy 171 TNGDPTVHLNGISLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIGVKY 228  
Db 173 tngdptvhlngisltltdlntgattntvndnvtddkkrasvkdvlnagwnkigvkv 232  
Qy 229 GSTTGQSENVDVRYDYTFEFLSADTKTTVNVESKDNGKRTVEKIGAKTSVIREKDGKL 288  
Db 233 gttta--sdnvdfvrydytfeflsadtktttnveskdngkrtvekgaktsvirekdgkl 290  
Qy 289 VTGKKGKNGSSTDGEGLVTAKEVIDAVNKAQWRMKTNTTANGQTGQADKFTETVSGTNV 348  
Db 291 vtgkkgkngsstdgeglvtakevidavnkagwrmtktntangqtgqadkftetvsgtnv 350  
Qy 349 TPASCKGTTATVSKDDQGNITVMYDVNVCDAIYNOLNSGWNLDKAVAGSSGKVISGN 408  
Db 351 tpassckgttatvskddqgnitvmydvnnvgdalinvolnsgwnldskavagssgkvisgn 410  
Qy 409 VSPSGKGMDETNIINAGNIEISRNGKNIIDTATSMAPQFSVSLGAGADAPTLSDVDDGGA 468  
Db 411 vpspgkgmdetvniinagnieitrngknidiatmapqfssvslgagadaptlsvddgga 470  
Qy 469 LNVGSKDANKPVRIINAPGVKEGQVNTVAQLKGVQAQLNNRIDNVDGNARAGIAQAIAT 528  
Db 471 lnvgskdankpvriinavgvkegdvntvaqlkgvaqnlnnridnvdgnaragiaqaiat 530  
Qy 529 AGLVQALPGKSMMAIGGTGVRGEAGYALGYSSISDGGNWIILKGTASGNSRHFQASASV 588  
Db 531 aglvqalpgksmmaiggtgvrgeagyalgyssisdggnwiilkgtasgnsrghfgasasv 590  
Qy 589 GYQW 592  
Db 591 gyqw 594

RESULT 11  
AAU23740

ID AAY23740 standard; Protein: 594 AA.  
XX  
AC AAY23740;  
XX  
DT 08-SEP-1999 (first entry)  
XX  
DE A surface protein of Neisseria meningitidis.  
XX  
KW Surface protein: surface glycoprotein; infection; vaccine;  
immunoreactive peptide.  
XX  
OS Neisseria meningitidis.  
XX  
PN WO9931132-A1.  
XX  
PD 24-JUN-1999.  
XX  
PF 14-DEC-1998; 98WO-AU01031.  
XX  
PR 12-DEC-1997; 97GB-0026398.  
XX  
PA (ISIS-) ISIS INNOVATION LTD.  
PA (UYQU ) UNIV QUEENSLAND.  
XX  
PI Jennings MP, Moxon ER, Peak IRA;  
XX  
DR WPI: 1999-418754/35.  
DR N-PSDB; AAX85792.  
XX  
PT Neisseria meningitidis surface proteins useful for treating N.  
PT meningitidis infections  
XX  
PS Claim 1; Page 100-101; 132pp; English.  
XX  
CC The present sequence represents a surface protein of Neisseria  
CC meningitidis which is approximately 62 kDa. The N. meningitidis  
CC surface glycoproteins, nucleic acids, the primers and optionally  
CC a thermostable polymerase, or antibodies are useful in a kit for  
CC the detection or diagnosis of N. meningitidis infection in humans.  
CC The N. meningitidis surface glycoproteins can also be used to  
CC prevent or treat N. meningitidis infection in humans, especially  
CC in the form of vaccines. The proteins and antibodies can also  
CC be used to identify immunoreactive peptides.

XX

SQ Sequence 594 AA;

Query Match 84.8%; Score 2533; DB 20; Length 594;  
Best Local Similarity 86.4%; Pred. No. 1.7e-139;  
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;

Qy 1 MNKIYRIITWNSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 mnkiyriiwnsalnawvseltrnhtkrasatvatavlatllfatvqasttd-dddlyl 59  
Qy 61 ESVQR-SVVGSTQASMEGSELETISLSMTNDS-----KEFVDPYIIVVTLKAGDNLI 112  
Db 60 epvqrtavvlsfrsdegekeg-----vtedsnwgyvfdkkgvitagtitlkagdnli 114  
Qy 113 KONTNENTNASSFTYSLKDLTGLINVEFKLSFGANGKKNVNIISDTKGLNFAKETAGTN 172  
Db 115 kqntentnassftyslkkdltltsvgteklsfsansknvnitsdtkglnfakktatn 174  
Qy 173 GDTTVHLNGISLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIGVKY 230  
Db 175 gdtvhlngisltltdlntgattntvndnvtddkkrasvkdvlnagwnkigvkvpt 234  
Qy 231 TTGQSENVDVRYDYTFEFLSADTKTTVNVESKDNGKRTVEKIGAKTSVIREKDGKLV 290  
Db 235 ta--sdnvdfvrydytfeflsadtktttnveskdngkrtvekgaktsvirekdgkvl 292  
Qy 291 GKGKNGSSTDGEGLVTAKEVIDAVNKAQWRMKTNTTANGQTGQADKFTETVSGTNVTF 350  
XX

Db	293	gkdkgendsdtkgeglvtakevidavnkagwrmktttangtqgqadkfetvtsqntvtf	352
Qy	351	ASGKGTATVSKDDOGNITVMYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVS	410
Db	353	asgkgtatvskddqgnitvmYdvNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVS	412
Qy	411	PSKGMDETVMNINAGNNIEISRNKGNIDITATSMAPQSSVSLGAGADAPTLSVDDGALN	470
Db	413	pskgmdetvnnagnnieitrngnkndiatstmpqfssvslgagadapltlsvddgaln	472
Qy	471	VGSKDANKPVRITNVAPGVKEGDTNVQAQLKGYAQNLRIDNVGNARAGIAQAATAG	530
Db	473	vgskdankpvriltvnapgvkegdvtnvaqlkgvaqnlhndvgnaraglaqatag	532
Qy	531	LVQAYLPKGSMAIGGTYRGAGYAIGYSSISDGGNWIIGKTASNSRGHFGASASVGY	590
Db	533	lvqaylpkgmmaiggytyrgeagyaigyssisdggnwliikgtasnsrghfgasasvgy	592
Qy	591	QW 592	
Db	593	qw 594	
RESULT 12			
AAV57044			
ID	AAV57044 standard; Protein; 594 AA.		
AC	AAV57044;		
XX			
DT	21-FEB-2000 (first entry)		
DE	BASB029 amino acid sequence from N. meningitidis strain ATCC13090.		
KW	BASB029; Neisseria meningitidis; surface fibril protein; HSF; diagnosis;		
KW	infection; treatment; prevent; antibacterial drug.		
OS	Neisseria meningitidis.		
Key	Location/Qualifiers		
FT	Misc-difference 104		
FT	/note= "Encoded by AATC"		
XX	WO9958683-A2.		
PN	18-NOV-1999.		
PD	07-MAY-1999; 99WO-EP03255.		
PF	13-MAY-1998; 98GB-0010276.		
PR	(SMIK ) SMITHKLINE BEECHAM BIOLOGICALS.		
PA	Ruelle J;		
PI	WPI; 2000-053103/04.		
XX	N-PSDB; AA239864.		
DR	New polypeptide from neisseria meningitidis useful for diagnosis,		
XX	treatment or prevention of bacterial infections in mammal		
PT	Claim 4; Fig 2; 74pp; English.		
PS	This is the Neisseria meningitidis BASB029 amino acid sequence from		
CC	serogroup B strain ATCC13090. The BASB029 protein is homologous to the		
CC	Haemophilus influenzae surface fibril (HSF) protein. The invention		
CC	relates to BASB029 polynucleotide sequences (AA239864-239865) and		
CC	polypeptide sequences (AAV57044-Y57045) and their immunogenic fragments.		
CC	BASB029 polypeptides are useful in a method of diagnosing a Neisseria		
CC	meningitidis infection in a mammal. Compositions containing BASB029		
CC	polynucleotides and polypeptides are useful for generating an immune		
CC	response in an animal. A therapeutic composition comprising an antibody		
CC	directed against BASB029 is useful in treating humans with Neisseria		
CC	meningitidis disease. The polynucleotide is useful in the diagnosis of		

CC	the stage of infection, type of infection, susceptibility to an
CC	infection which results from increased or decreased expression of the
CC	polynucleotide, and for therapeutic or prophylactic purposes,
CC	particularly genetic immunisation. Antibodies against BASB029
CC	polynucleotides and polypeptides are also useful for treating infections
CC	particularly bacterial infections. The protein is useful in the
CC	screening and development of antibacterial drugs. Fused recombinant
CC	protein is useful for the stimulation of the immune system of an organism
CC	receiving the protein.
XX	
SQ	Sequence 594 AA;
Query Match 84.8%; Score 2533; DB 21; Length 594;	
Best Local Similarity 86.4%; Pred. No. 1.7e-139;	
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;	
Qy	1 MNKIYRIIWNALNARVAVSELTNRHTRKASATVKTAVLATILLFATVOANATDEDEEEL 60
Db	1 mnkiyriiwnsalnawavseiltnrhtkrasatvatavlatilfatvqastld-dddlyl 59
Qy	61 ESVQR-SVVGSIQASMEGSGELETISLSMTNDS-----KEFVDPIYIVVTLKAGDNLKI 112
Db	60 epvqrtavvlsvfrskdkgteke-----vtedsnvgvyfdkkgvltagtitlkagdnlki 114
Qy	113 KONTNENTNASSFTYSLKKDLTLGLINVEYTEKLSFGANGKKVNIISDTKGLNFAKETAGTN 172
Db	115 kqntnentnassftysslkldltlsvgteklfsfsansknvitsdtkglnfakktactn 174
Qy	173 GDTTVHLNGIGSTLTDLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIGVKVTS 230
Db	175 gdttvhlngigstltdlntgattntvndvtddekkraasvkdvlngwnikgvkpgt 234
Qy	231 TTGQSENVDVFTYDVEFLSADTKTTTVNVEKDKNGKRETKIGAKTSVIKEKDGKLYT 290
Db	235 ta--sdnvdfvtydteflsadtktttvnveskdngkrtvkgigaktsvikekdglvt 292
Qy	291 GKGKGENSGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGTGQADKFPETVTSQTNVTF 350
Db	293 gkdkgendsdtkgeglvtakevidavnkagwrmktttangtqgqadkfetvtsqntvtf 352
Qy	351 ASGKGTATVSKDDOGNITVMYDVNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVS 410
Db	353 asgkgtatvskddgdnitvmYdvNVGDALNVNQLNSGNWLDKAVAGSSGKVISGNVS 412
Qy	411 PSKGMDETVMNINAGNNIEISRNKGNIDITATSMAPQSSVSLGAGADAPTLSVDDGALN 470
Db	413 pskgmdetvnnagnnieitrngnkndiatstmpqfssvslgagadapltlsvddgaln 472
Qy	471 VGSKDANKPVRITNVAPGVKEGDTNVQAQLKGYAQNLRIDNVGNARAGIAQAATAG 530
Db	473 vgskdankpvriltvnapgvkegdvtnvaqlkgvaqnlhndvgnaraglaqatag 532
Qy	531 LVQAYLPKGSMAIGGTYRGAGYAIGYSSISDGGNWIIGKTASNSRGHFGASASVGY 590
Db	533 lvqaylpkgmmaiggytyrgeagyaigyssisdggnwliikgtasnsrghfgasasvgy 592
Qy	591 QW 592
Db	593 qw 594
RESULT 13	
AAU06174	
ID	AAU06174 standard; Protein; 594 AA.
XX	
AC	AAU06174;
XX	
DT	24-OCT-2001 (first entry)
XX	N. meningitidis EG327 surface antigen NhhA polypeptide sequence.
XX	Surface antigen NhhA; meningococcal disease; meningitis vaccine.

XX OS Neisseria meningitidis strain EG327.  
XX PH Key Location/Qualifiers  
FT Region 1..50  
FT /label= C1  
FT /note= "Conserved region 1"  
FT 51..104  
FT /label= V1  
FT /note= "Variable region 1"  
FT 105..116  
FT /label= C2  
FT /note= "Conserved region 2"  
FT 117..126  
FT /label= V2  
FT /note= "Variable region 2"  
FT 127..190  
FT /label= C3  
FT /note= "Conserved region 3"  
FT 191..212  
FT /label= V3  
FT /note= "Variable region 3"  
FT 213..231  
FT /label= C4  
FT /note= "Conserved region 4"  
FT 232..238  
FT /label= V4  
FT /note= "Variable region 4"  
FT 239..594  
FT /label= C5  
FT /note= "Conserved region 5"  
XX WO200155182-A1.  
XX 02-AUG-2001.  
XX 25-JAN-2001; 2001WO-AU00069.  
XX 25-JAN-2000; 2000US-0177917.  
XX (UYQU ) UNIV QUEENSLAND.  
XX Peak IRA, Jennings MP;  
XX WPI; 2001-488774/53.  
XX N-PSDB; AAS09164.  
XX  
XX New Nhba surface antigen polypeptides and polynucleotides from  
XX Neisseria meningitidis, useful in producing vaccines for treating or  
XX preventing broad spectrum of Neisseria meningitidis -  
XX Claim 9; Fig 1; 9lpp; English.  
XX  
XX The present invention relates to the isolation of novel Neisseria  
XX meningitidis mutant polypeptides of the surface antigen Nhba  
XX (AAU06182-AAU06186). The modified or mutant Nhba polypeptides are  
XX characterised by deletions of non-conserved amino acids, particularly  
XX the deletion of variable regions. The deletion mutants are useful in  
XX diagnostics, therapeutic and prophylactic vaccines against a broader  
XX spectrum of N. meningitidis, and in designing and/or screening of  
XX medicaments. The mutant proteins when used as a vaccine can effectively  
XX immunise against a broader spectrum of N. meningitidis strains than  
XX would be expected from a corresponding wild-type surface antigen.  
XX The present sequence representing the wild type surface antigen Nhba  
XX from N. meningitidis strain EG327 is 1 of 10 Nhba polypeptide sequences  
XX (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
XX the present invention.  
XX  
XX Sequence 594 AA;  
XX  
XX Query Match 84.8%; Score 2533; DB 22; Length 594;  
XX Best Local Similarity 86.4%; Pred. No. 1.7e-139;

Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;  
QY 1 MNKIYRIIWNLSALNAWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
DB 1 mnkiyriiwnlsalnawavseltrnhtkrasatvatlatllfatvqastdd-dddlyl 59  
QY 61 ESVQR-SVVGSIQASMEGSELETISLMTNDS-----KEFVDPYIYVIVTKAGDNLKI 112  
DB 60 epvqrtavvlsfrskdkegtgeke-----vtedsnwgvvyfdkkgvltagtitikagdnlki 114  
QY 113 KONTNNTNASSFTYSLKDLTGLINVEKTEKLSFGANGKKVNIISDTKGLNFAKETAGTN 172  
DB 115 kqntnntnassftysllkldltltsvgteklsfsansknvntsdtkglnfakktactn 174  
QY 173 GDTTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWTKGVKTCG 230  
DB 175 gdttvhlngigstltdtlntgatntvndvtddekkraasvkdvinagwnikgvkpgt 234  
QY 231 TTGQSENVDFVRYDTVEFLSADTKTTTVNVESKONGKRTVEKIGAKTSVIKEKDGKLYT 290  
DB 235 ta--sdnvdfvrydtveflsadtktttvneskdngkrtevkigaktsvikekdglvt 292  
QY 291 GKKGKNGSSSTDEGGLVTAKEVIDAVNAGWRMKTTTANGOTGQADKFETVTSNTVTF 350  
DB 293 gkdkgendsstdkgeglvtakevidavnkagwrmttttangtggadkfetvtsgtnvtf 352  
QY 351 ASGKGTATTATVSKDDOGNITVMYDVNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVS 410  
DB 353 asgkgtattatvskddognitvmydvnvgdalnvqnqsgwnldskavagssgkvisgnvs 412  
QY 411 PSKGMDETVNINAGNNIEISRNKGNIDTIATSMAPOFSSVSLGAGADAPTLSDYDEGALN 470  
DB 413 pskgmdetvnnagnnieitrngknidiatsmtpfssvslgagadaptlsvddegaln 472  
QY 471 VGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAQNLRIDNVGNARAGIAQAIAATAG 530  
DB 473 vgskdankpvrntnvapgvkegdvtnvaqlkgvaqnlrnhidnvdgnaragialatag 532  
QY 531 LVQAVLPKSKMMAIGGCTYRGEAGYAGYSSISDGGNWLIIKGTASGNSRHCFCASASVGY 590  
DB 533 lvqaylpkksmmaigggtyrgeagyalgysissdggwnliikgtasgnsrghifgasasvy 592  
QY 591 QW 592  
DB 593 qw 594  
RESULT 14  
AA23742  
ID AA23742 standard; Protein; 598 AA.  
XX AC AA23742;  
XX  
XX 08-SEP-1999 (first entry)  
XX DE A surface protein of Neisseria meningitidis.  
XX KW Surface protein; surface glycoprotein; infection; vaccine;  
XX NW immunoreactive peptide.  
XX OS Neisseria meningitidis.  
XX PN WO9931132-A1.  
XX XX  
XX PD 24-JUN-1999.  
XX XX  
XX PF 14-DEC-1998; 98WO-AU01031.  
XX PR 12-DEC-1997; 97GB-0026398.  
XX PA (ISIS-) ISIS INNOVATION LTD.  
XX PA (UYQU ) UNIV QUEENSLAND.  
XX XX

PI	Jennings MP, Moxon ER, Peak IRA;	
XX	WPI; 1999-418754/35.	
DR	N-PSDB; AAX85794.	
XX		
XX	Neisseria meningitidis surface proteins useful for treating N.	
PT	meningitidis infections	
XX		
PS	Claim 1; Page 108-110; 132pp; English.	
XX		
CC	The present sequence represents a surface protein of Neisseria	
CC	meningitidis which is approximately 62 kDa. The N. meningitidis	
CC	surface glycoproteins, nucleic acids, the primers and optionally	
CC	a thermostable polymerase, or antibodies are useful in a kit for	
CC	the detection or diagnosis of N. meningitidis infection in humans.	
CC	The N. meningitidis surface glycoproteins can also be used to	
CC	prevent or treat N. meningitidis infection in humans, especially	
CC	in the form of vaccines. The proteins and antibodies can also	
CC	be used to identify immunoreactive peptides.	
XX		
SQ	Sequence 598 AA;	
	Query Match 84.5%; Score 2524; DB 20; Length 598;	
	Best Local Similarity 85.5%; Pred. No. 5.7e-139;	
	Matches 520; Conservative 17; Mismatches 45; Indels 26; Gaps 8;	
QY	1 MNKYRIWNSALNAWAVASELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60	
Db	1 mnklyriwnsalnawvavseltrnhtrkrasatvatavlatllfatvqanatd-dddlyl 59	
QY	61 ESVOR-SVVGSIQASMEGSGELETISLMTNDSKEFVDPIY-----VVTLKAGDNL 110	
Db	60 epvqrtavvlfsfkdsgtgekeg-----tedsnwv--yfdekrvlkagaitlkagdnl 112	
QY	111 KIKQNTNENTNA-----SSFYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAK 166	
Db	113 kikqntnentndntdssfyslkkdltdtsveteklsfgangknvniitsdtkglnfak 172	
QY	167 ETAGTNGDTTVHNLGIGSTLTDLAGSSASHVDAGNOST--HYTRAASIKDVLNAGWNK 224	
Db	173 etagngdptvhngigstltdtlntgatntvndntddekkrasvkdvinagwnik 232	
QY	225 GVKTGTGSGSENVDVRYTDTVEFLSADTKTTTVNVESKDNKRTEVKIGAKTSVIKEK 284	
Db	233 gvkpgtta--sdnvdfvrytdtveflsadtktttvneskdngkktvkgaktsvikek 290	
QY	285 DGKLVTKGKGENGSSDTEGEGLVTAKEVIDAVNKAGWRMKTITTANGQTQADKFETVTS 344	
Db	291 dgkltvgkgkdengsstdegeglvtakevidavnkagwrmttttangtggadkfetvts 350	
QY	345 GTNVTAFASGKGTATVSKDQGNITVMYDYNVDALNVNOLQSGWNLDKAVAGSSGKV 404	
Db	351 gtkvtfasngtlatvskddqgnitvkydvnvdalnvnlqsgwnldskavagssgkv 410	
QY	405 ISGNVSPSKGMDETVINAGNIEISRNGKNIDIATSMAPQSFSSVSLGAGADAPTLISVD 464	
Db	411 isgnvpskkgmdetvinagnnieitrngknidiatsmtpqfssvslgagadaptilsvd 470	
QY	465 DEGALNVGSDANKPVRITWVAPGVKEGDTVNVQAQLKGVAQNLRINDVDGNARAGIAQ 524	
Db	471 degalnvgsdankpvrirtwvapgvgkgdvtvnaqlkgvaqnlrindvndgnaraglaq 530	
QY	525 AIATAGLVQAVLPCKSMATGGGTGRCEAGYAIGYSSISDPGGNWIKGTASGNSRHFGA 584	
Db	531 aiataglaqavlpqksmma199gtyrgeadyaigysissdtdgnwllkgtasgnsrghfga 590	
QY	585 SASGYQW 592	
Db	591 sasgyqw 598	
	RESULT 15	

AAU06177	
ID	AAU06177 standard; Protein; 598 AA.
XX	
AC	AAU06177;
XX	
DT	24-OCT-2001 (first entry)
XX	
DE	N. meningitidis H15 surface antigen Nhha polypeptide sequence.
XX	
KW	Surface antigen Nhha; meningococcal disease; meningitis vaccine.
XX	
OS	Neisseria meningitidis strain H15.
XX	
FH	Key Location/Qualifiers
FT	Region 1..50 /label= C1
FT	/note= "Conserved region 1"
FT	Region 51..104 /label= V1
FT	/note= "Variable region 1"
FT	Region 105..116 /label= C2
FT	/note= "Conserved region 2"
FT	Region 117..130 /label= V2
FT	/note= "Variable region 2"
FT	Region 131..194 /label= C3
FT	/note= "Conserved region 3"
FT	Region 195..216 /label= V3
FT	/note= "Variable region 3"
FT	Region 217..235 /label= C4
FT	/note= "Conserved region 4"
FT	Region 236..242 /label= V4
FT	/note= "Variable region 4"
FT	Region 243..598 /label= C5
FT	/note= "Conserved region 5"
XX	
PN	W0200155182-A1.
XX	
PD	02-AUG-2001.
XX	
XX	25-JAN-2001; 2001WO-AU000069.
XX	
XX	25-JAN-2000; 2000US-0177917.
PR	
XX	(UYQU ) UNIV QUEENSLAND.
PA	
XX	Peak IRA, Jennings MP;
PI	
XX	WPI; 2001-488774/53.
DR	N-PSDB; AAS09167.
XX	
PT	New Nhha surface antigen polypeptides and polynucleotides from
PT	Neisseria meningitidis, useful in producing vaccines for treating or
PT	preventing broad spectrum of Neisseria meningitidis -
XX	
PS	Claim 9; Fig 1; 91pp; English.
XX	
CC	The present invention relates to the isolation of novel Neisseria
CC	meningitidis mutant polypeptides of the surface antigen Nhha
CC	(AAU06182-AAU06186). The modified or mutant Nhha polypeptides are
CC	characterised by deletions of non-conserved amino acids, particularly
CC	the deletion of variable regions. The deletion mutants are useful in
CC	diagnostics, therapeutic and prophylactic vaccines against a broader
CC	spectrum of N. meningitidis, and in designing and/or screening of
CC	medicaments. The mutant proteins when used as a vaccine can effectively
CC	immunise against a broader spectrum of N. meningitidis strains than
CC	would be expected from a corresponding wild-type surface antigen.

CC The present sequence representing the wild type surface antigen Nhha  
CC from N. meningitidis strain H15 is 1 of 10 Nhha polypeptide sequences  
CC (AAU06171-AAU06180) from 10 different N. meningitidis strains given in  
CC the present invention.  
XX

SQ	Sequence	598	AA;
Query Match			
Best Local Similarity		84.5%;	Score 2524; DB 22; Length 598;
Matches		520; Conservative	17; Mismatches 45; Indels 26; Gaps 8;
Qy	1	MNKYRIIWSALNAWAVSELTRNHRKASATVKTAVLATLLFATVQANATDEDEEEL	60
Db	1	mnkiyriiwnsalnawvvselttrnhtrkrasatvatlatllfatvqanatd-dddlyl	59
Qy	61	ESVQR-SVVGSIQASMEGSELEFISLWNTSDSKFVDPYI-----VVTLRAGDNL	110
Db	60	epvqrtavvlfrsdkegtgekg-----tedsnwav--yfdkrrvlkagaitlkkagdn	112
Qy	111	KIKQNTNENTNA----SSFTYSLKKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAK	166
Db	113	kikqntnntentndsfstysllkdlldlcsveteklsfgangknvnitsdtkglnfak	172
Qy	167	ETAGTNGDTTTHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIK	224
Db	173	etagtngdptvhlngigstltdtllntgattntdntddekkrasvkvlnagwnik	232
Qy	225	GVKGTSTTGQSENVDFTVDTVEPLSADTKTTTVNVESKONGKRTVEVKIGAKTSVIREK	284
Db	233	gvkpgtta--sdnvdfrvtydtveflsadtktttvnveskdngkktevkigaktsvikek	290
Qy	285	DGKLVTKGKGKENGSTDEGEGLVTAKEVIDAVNKAGHRMKTTTTANGOTGOADKEETVTS	344
Db	291	dgklytvgkgdeengsstdegeglvtakevidavnkagwrmkttttangtqgqadkfetvts	350
Qy	345	GTNVTFASGKGTATVSKDDQGNITVMYDVNVGDALNVNQLNSGNLDSKAVAGSSGKV	404
Db	351	gtkvtfasngtattatvskddggnitvkydvnvgdalnvnglqnsqwnldskavagssgv	410
Qy	405	ISGNVSPSKGMDETVNTINAGNNIEISRNKNIDIATSMAPQFSSVSLGAGADAPTLSVD	464
Db	411	lsgnvspskgmdetvnnagnnieitrngknidiatsmtpqfssvslgagadaptsld	470
Qy	465	DEGALNVGSKDANKPVRTNVPAGVKEGVDVNVQALKGVAQNLNRRIDNVDCNARAGIAQ	524
Db	471	degalnvsgskdankpvriltnvapgykegdvtnvaqlkgvaqnlnnrldnvdgnaraglaq	530
Qy	525	AIATAGLVQAYLPGKSMMAIGGGTYRGAGYAIGYSSISDGNWIIKGTASGNSRGHFGA	584
Db	531	aiataglaqaylpqksmmaiaggtyrgeagyaigyssisdtnwnvikgtasgnsrghfga	590
Qy	585	SASVGYQW 592	
Db	591	sasvgyqw 598	

Search completed: July 3, 2002, 08:36:27  
Job time: 323 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 3, 2002, 08:37:11 ; Search time 39.66 seconds  
(without alignments)  
364.598 Million cell updates/sec

Title: US-09-771-382-10

Perfect score: 2988

Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGSRGFGASGVQW 592

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents\_AA.\*

- 1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pap.\*
- 2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pap.\*
- 3: /cgn2\_6/ptodata/2/iaa/6A\_COMB.pap.\*
- 4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pap.\*
- 5: /cgn2\_6/ptodata/2/iaa/PCTUS\_COMB.pap.\*
- 6: /cgn2\_6/ptodata/2/iaa/backfiles1.pap.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
1	2779	93.0	592	4	US-09-377-155-17		Sequence 17, Appl
2	2779	93.0	592	4	US-09-669-974-17		Sequence 17, Appl
3	2626.5	87.9	589	4	US-09-377-155-19		Sequence 19, Appl
4	2626.5	87.9	589	4	US-09-669-974-19		Sequence 19, Appl
5	2587.5	86.6	599	4	US-09-377-155-15		Sequence 15, Appl
6	2587.5	86.6	599	4	US-09-669-974-15		Sequence 15, Appl
7	2552	85.4	594	4	US-09-377-155-7		Sequence 7, Appl
8	2552	85.4	594	4	US-09-669-974-7		Sequence 7, Appl
9	2533	84.8	594	4	US-09-377-155-9		Sequence 9, Appl
10	2533	84.8	594	4	US-09-669-974-9		Sequence 9, Appl
11	2524	84.5	598	4	US-09-377-155-13		Sequence 13, Appl
12	2524	84.5	598	4	US-09-669-974-13		Sequence 13, Appl
13	2521	84.4	598	4	US-09-377-155-5		Sequence 5, Appl
14	2521	84.4	598	4	US-09-669-974-5		Sequence 5, Appl
15	2464.5	82.5	591	4	US-09-377-155-21		Sequence 21, Appl
16	2464.5	82.5	591	4	US-09-669-974-21		Sequence 21, Appl
17	2445.5	81.8	591	4	US-09-377-155-11		Sequence 11, Appl
18	2445.5	81.8	591	4	US-09-669-974-11		Sequence 11, Appl
19	2443	81.8	592	4	US-09-377-155-2		Sequence 2, Appl
20	2443	81.8	592	4	US-09-669-974-2		Sequence 2, Appl
21	1135	38.0	1098	3	US-08-409-995-2		Sequence 2, Appl
22	1135	38.0	1098	3	US-08-685-467-2		Sequence 2, Appl
23	1135	38.0	1098	4	US-09-377-155-32		Sequence 32, Appl
24	1135	38.0	1098	4	US-08-913-942-2		Sequence 2, Appl
25	1135	38.0	1098	4	US-09-669-974-32		Sequence 32, Appl
26	1135	38.0	1098	4	US-09-268-347-44		Sequence 44, Appl
27	1132.5	37.9	2353	4	US-09-377-155-33		Sequence 33, Appl

28	1132.5	37.9	2353	4	US-08-913-942-4		Sequence 4, Appl
29	1132.5	37.9	2353	4	US-09-669-974-33		Sequence 33, Appl
30	1131.5	37.9	2354	4	US-09-268-347-47		Sequence 47, Appl
31	1121	37.5	658	1	US-08-409-995-5		Sequence 5, Appl
32	1121	37.5	658	3	US-08-685-467-5		Sequence 5, Appl
33	1121	37.5	658	4	US-08-913-942-5		Sequence 36, Appl
34	1102.5	36.9	2411	4	US-09-268-347-36		Sequence 6, Appl
35	1061	35.5	607	1	US-08-409-995-6		Sequence 6, Appl
36	1061	35.5	607	3	US-08-685-467-6		Sequence 6, Appl
37	1061	35.5	607	4	US-08-913-942-6		Sequence 6, Appl
38	1061	35.5	1912	1	US-08-409-995-4		Sequence 4, Appl
39	1061	35.5	1912	3	US-08-685-467-4		Sequence 4, Appl
40	1000.5	33.5	679	4	US-08-913-942-15		Sequence 15, Appl
41	1000.5	33.5	679	4	US-09-268-347-26		Sequence 26, Appl
42	975	32.6	1094	4	US-09-268-347-32		Sequence 32, Appl
43	730	24.4	1002	4	US-09-268-347-24		Sequence 24, Appl
44	721	24.1	1004	4	US-09-268-347-30		Sequence 30, Appl
45	666	22.3	1104	4	US-09-268-347-28		Sequence 28, Appl

#### ALIGNMENTS

RESULT 1

US-09-377-155-17

; Sequence 17, Application US/09377155

; Patent No. 6197312

; GENERAL INFORMATION:

; APPLICANT: PEAK, Ian Richard Anselm

; APPLICANT: JENNINGS, Michael Paul

; APPLICANT: MOXON, E. Richard

; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN

; FILE REFERENCE: 065064/0128

; CURRENT APPLICATION NUMBER: US/09/377,155

; PRIOR FILING DATE: 1999-08-19

; PRIOR APPLICATION NUMBER: PCT/AU98/01031

; PRIOR FILING DATE: 1998-12-14

; PRIOR APPLICATION NUMBER: GB 9726398.2

; PRIOR FILING DATE: 1997-12-12

; NUMBER OF SEQ ID NOS: 33

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 17

; LENGTH: 592

; TYPE: PRT

; ORGANISM: Neisseria meningitidis

; US-09-377-155-17

Query Match 93.0%; Score 2779; DB 4; Length 592;

Best Local Similarity 93.9%; Pred No. 2.4e-207;

Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;

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Db 61 ESQVRSVGSIOASMEGSELETISLSMTNDSKEFVDPYIVVTLRAGDNLTQNTNENT 120

||||| : : : : : ||||| : : : : : ||||| : : : : : |||||

QY 121 NASSTYSLKDLTGILINVTETKLSFGANGKVNISDTKGLNFAKETAGTNGDTTVHLN 180

||||| : : : : : ||||| : : : : : ||||| : : : : : |||||

Db 121 NASSTYSLKDLTGILINVTETKLSFGANGKVNISDTKGLNFAKETAGTNGDTTVHLN 180

||||| : : : : : ||||| : : : : : ||||| : : : : : |||||

QY 181 GIGSTLTDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNNTKGVKTGSTTGOSENV 238

||||| : : : : : ||||| : : : : : ||||| : : : : : |||||

Db 181 GIGSTLTDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNNTKGVKTGSTTGOSENV 238

||||| : : : : : ||||| : : : : : ||||| : : : : : |||||

QY 239 DFRVRYDVEFLSADTKTTTVNVESKDNGKREVKIGAKTSVIKEDGKLVTKGKGENG 298

||||| : : : : : ||||| : : : : : ||||| : : : : : |||||

Db 239 DFRVRYDVEFLSADTKTTTVNVESKDNGKREVKIGAKTSVIKEDGKLVTKGKGENG 298

||||| : : : : : ||||| : : : : : ||||| : : : : : |||||

QY 299 SSTDEGEGLVTAKEVIDAVNKAGWRMKTITANGQTQADKFEFTVTSGTNVTTFASGKGTTA 358

Db 299 SSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTKVTAFSGNGTTA 358  
QY 359 TVSKDDQGNITVYDYNVNGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKMD 418  
Db 359 TVSKDDQGNITVYDYNVNGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKMD 418  
QY 419 TVNINAGNIEISRNGKNIDIAATSMAPQFSSVSLGAGADAPTILSVDDDEGALNVGSKDKANK 478  
Db 419 TVNINAGNIEISRNGKNIDIAATSMAPQFSSVSLGAGADAPTILSVDDDEGALNVGSKDKANK 478  
QY 479 PVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVNNGNARAGIAQAIAATAGLVQAYLPG 538  
Db 479 PVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVNNGNARAGIAQAIAATAGLVQAYLPG 538  
QY 539 KSMAIIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYOW 592  
Db 539 KSMAIIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYOW 592

RESULT 2  
US-09-669-974-17  
; Sequence 17, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 17  
; LENGTH: 592  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-17

Query Match 93.0%; Score 2779; DB 4; Length 592;  
Best Local Similarity 93.9%; Pred. No. 2.4e-207;  
Matches 558; Conservative 9; Mismatches 23; Indels 4; Gaps 2;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
QY 61 ESVORSVVGSIQASMEGSGELETISLMTNDSKEFVDPYIIVTLKAGDNLKIKONTNENT 120  
Db 61 ESVORSVVGSIQASMEGSGELETISLMTNDSKEFVDPYIIVTLKAGDNLKIKONTNENT 120  
QY 121 NASFTYSLKKDLTGLINVETELKSFANGKKNYIISDTKGLNFAKETAGTNGDVTTLN 180  
Db 121 NASFTYSLKKDLTGLINVETELKSFANGKKNYIISDTKGLNFAKETAGTNGDVTTLN 180  
QY 181 GIGSTLDTLAGSSASHVDAGNOST--HYTRAASIKDVLNAGNWKIKVKTGSTTQSENV 238  
Db 181 GIGSTLDMLNLTGATNTVDNNTDDEKRAASVSKDVLNAGNWKIKVKGPTTA--SDNV 238  
QY 239 DFVRTYDVEFLSADTKTTVNVESKDKRTEVKIGAKTSVIKEDGKLVTKGKGENG 298  
Db 239 DFVRTYDVEFLSADTKTTVNVESKDKRTEVKIGAKTSVIKEDGKLVTKGKGENG 298  
QY 299 SSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTKVTAFSGNGTTA 358

Db 299 SSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTKVTAFSGNGTTA 358  
QY 359 TVSKDDQGNITVYDYNVNGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKMD 418  
Db 359 TVSKDDQGNITVYDYNVNGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKMD 418  
QY 419 TVNINAGNIEISRNGKNIDIAATSMAPQFSSVSLGAGADAPTILSVDDDEGALNVGSKDKANK 478  
Db 419 TVNINAGNIEISRNGKNIDIAATSMAPQFSSVSLGAGADAPTILSVDDDEGALNVGSKDKANK 478  
QY 479 PVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVNNGNARAGIAQAIAATAGLVQAYLPG 538  
Db 479 PVRITNVAPGVKGGDVTNVAQLKGVAQNLRNIDNVNNGNARAGIAQAIAATAGLVQAYLPG 538  
QY 539 KSMAIIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYOW 592  
Db 539 KSMAIIGGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGRHFGASASVGYOW 592

Query Match 87.9%; Score 2626.5; DB 4; Length 589;  
Best Local Similarity 89.1%; Pred. No. 1.6e-195;  
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;  
QY 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
QY 61 ESVORSVVGSIQASMEGSGELET--ISLMTNDSKEFVDPYIIVTLKAGDNLKIKONT 116  
Db 61 ESVARSALVQLFMIDKEGNEIESTGDIWSIYDDHNTLHG--ATVTLKAGDNLKIKQ-- 117  
QY 117 NENTNASSFTYSLKKDLTGLINVETELKSFANGKKNYIISDTKGLNFAKETAGTNGDVT 176  
Db 118 ----SKDFTYSLKKDLTGLINVETELKSFANGKKNYIISDTKGLNFAKETAGTNGDPT 173  
QY 177 VHLNGIGSTLDTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGNWKIKVKTGSTTQOSE 236  
Db 174 VHLNGIGSTLDTLAGSSASHVDAGNOSTHYTRAASIKDVLNAGNWKIKVKTGSTTQOSE 233  
QY 237 NVDFVRTYDVEFLSADTKTTVNVESKDKRTEVKIGAKTSVIKEDGKLVTKGKGKE 296  
Db 234 NVDFVRTYDVEFLSADTKTTVNVESKDKRTEVKIGAKTSVIKEDGKLVTKGKGKE 293  
QY 297 NGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTKVTAFSGNGT 356  
Db 294 NGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGOTGOADKFETVTSCTKVTAFSGNGT 353  
QY 357 TATVSKDDQGNITVYDYNVNGDALNVNOLNSGWNLDKAVAGSSGKVTISGNVSPSKGKM 416

Db 354 TATVSKDQGNITVYKVDNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 413  
Qy 417 DETVINAGNNEISRNGKNIDIIATSMAPQSFSSVSLGAGADAPTLSVDDGALNVGSKDA 476  
Db 414 DETVINAGNNEIIRNGKNIDIIATSMTPQSFSSVSLGAGADAPTLSVDDGALNVGSKDA 473  
Qy 477 NKPRVITNVAPGVKGGDVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAQYL 536  
Db 474 NKPRVITNVAPGVKGGDVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAQYL 533  
Qy 537 PKGSMMAIGGGTYLGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYOW 592  
Db 534 PKGSMMAIGGGTYLGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGTSASVGYOW 589

## RESULT 4

US-09-669-974-19  
; Sequence 19, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 19  
; LENGTH: 589  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-19

Query Match 87.9%; Score 2626.5; DB 4; Length 589;  
Best Local Similarity 89.1%; Pred. No. 1.6e-195;  
Matches 531; Conservative 13; Mismatches 41; Indels 11; Gaps 4;  
Qy 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEL 60  
Qy 61 ESVQRS-VVGSIQASMEGSELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQ-- 116  
Db 61 ESVARSALVLPQMDIKEGNESTGNGWSTYYDDHNTLHG-ATVTLKAGDNLKIKQ-- 117  
Qy 117 NENTNASSFTYSLKKDLTGLINVEPEKLSFGANGKKNVLIISDTKGLNFAKETAGTNDTT 176  
Db 118 ----SKDFTYSLKKDLTGLINVEPEKLSFGANGKKNVLIISDTKGLNFAKETAGTNDTT 173  
Qy 177 VHLNGTGSTLTDLTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKIKVKTGSTTGOSE 236  
Db 174 VHLNGTGSTLTDLTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKIKVKTGSTTGOSE 233  
Qy 237 NVDFVRYTYDVEFLSADTKTTTVNVEKDNKRTEVKIGAKTSVIKEKDKLVTKGKGE 296  
Db 234 NVDFVRYTYDVEFLSADTKTTTVNVEKDNKRTEVKIGAKTSVIKEKDKLVTKGKGE 293  
Qy 297 NCGSSDDEGELVTAKEVIDAVNKAAGRMTTTTANGQTGOADKFEVTSNTVTFASGKT 356  
Db 294 NCGSSDDEGELVTAKEVIDAVNKAAGRMTTTTANGQTGOADKFEVTSNTVTFASGKT 353  
Qy 357 TATVSKDQGNITVYKVDNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 416

Db 354 TATVSKDQGNITVYKVDNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNVSPSKGM 413  
Qy 417 DETVINAGNNEISRNGKNIDIIATSMAPQSFSSVSLGAGADAPTLSVDDGALNVGSKDA 476  
Db 414 DETVINAGNNEIIRNGKNIDIIATSMTPQSFSSVSLGAGADAPTLSVDDGALNVGSKDA 473  
Qy 477 NKPRVITNVAPGVKGGDVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAQYL 536  
Db 474 NKPRVITNVAPGVKGGDVNTVAQLKGVAQNLNRRIDNVGNARAGIAQAIATAGLVAQYL 533  
Qy 537 PKGSMMAIGGGTYLGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGASASVGYOW 592  
Db 534 PKGSMMAIGGGTYLGEAGYAGYSSISDGNWIIKGTASGNSRGRHFGTSASVGYOW 589

## RESULT 5

US-09-377-155-15  
; Sequence 15, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-15

Query Match 86.6%; Score 2587.5; DB 4; Length 599;  
Best Local Similarity 88.0%; Pred. No. 1.7e-192;  
Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;  
Qy 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWNLSALNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Qy 61 ESVQRS-VVGSIQASMEGSELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIKQ-- 114  
Db 61 EPVRSALVLPQMDIKEGNESTGNGWSTYYDDHNTLHG-ATVTLKAGDNLKIKQNT 119  
Qy 115 --NTNENTNASSFTYSLKKDLTGLINVEPEKLSFGANGKKNVLIISDTKGLNFAKETAGTN 172  
Db 120 NKTNTNENTNDSFTYSLKKDLTGLINVEPEKLSFGANGKKNVLIISDTKGLNFAKETAGTN 179  
Qy 173 GDTTVHLNGIGSTLTDLTLAGSSASHVDAGNQST--HYTRAASIKOVNLNAGWNKIKVKTGS 230  
Db 180 GDTTVHLNGIGSTLTDLTLAGSSASHVDAGNQST--HYTRAASIKOVNLNAGWNKIKVKTGS 239  
Qy 231 TVGQSENVDFVRYTYDVEFLSADTKTTTVNVEKDNKRTEVKIGAKTSVIKEKDKLV 290  
Db 240 TA--SDNVDFVRYTYDVEFLSADTKTTTVNVEKDNKRTEVKIGAKTSVIKEKDKLV 297  
Qy 291 GKKGKNGSSDDEGELVTAKEVIDAVNKAAGRMTTTTANGQTGOADKFEVTSNTVTF 350  
Db 298 GKKGKNGSSDDEGELVTAKEVIDAVNKAAGRMTTTTANGQTGOADKFEVTSNTVTF 357  
Qy 351 ASGKGTATVSKDDQGNITVYKVDNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNV 410  
Db 358 ASGKGTATVSKDDQGNITVYKVDNVGDALNVNQLNSGWNLDKAVAGSSGKVISGNV 417  
Qy 411 PSKGRMDETVNINAGNNIEISRNGKNIDIIATSMAPQSFSSVSLGAGADAPTLSVDDGALN 470

Db 418 PSKGMDETVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTSLVDDRGALN 477  
QY 471 VGSKDANKPVRITNVAPGKGEQDVTNVAOLKGYAQNLRNDRIDNVNAGNAGIAQAATAG 530  
Db 478 VGSKDANKPVRITNVAPGKGEQDVTNVAOLKGYAQNLRNDRIDNVNAGNAGIAQAATAG 537  
QY 531 LVQAYLPKGSMAIGAAGGTGTYRGEAGYAGYSSISDGGNWIIGTASGNSRHFAGSASVGY 590  
Db 538 LVQAYLPKGSMAIGAAGGTGTYRGEAGYAGYSSISDGGNWIIGTASGNSRHFAGSASVGY 597  
QY 591 QW 592  
Db 598 QW 599

RESULT 6  
US-09-669-974-15  
; Sequence 15, Application US/09669974  
; Patent No. 6333173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 15  
; LENGTH: 599  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-15

Query Match 86.6%; Score 2587.5; DB 4; Length 599;  
Best Local Similarity 88.0%; Pred. No. 1.7e-192;  
Matches 530; Conservative 15; Mismatches 44; Indels 13; Gaps 6;

QY 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
QY 61 ESVQRS-VVGSIOASMEGSGELET---ISLSMTNDSKEFVDPYIVVTLKAGDNLKIQ-- 114  
Db 61 EPVVRSLVLOFMIDREGNENSTGNIGHSYIYDHNHTLHG-ATVTLKAGDNLKIQNT 119  
QY 115 --NTNENTNASSFTYSLKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAGTN 172  
Db 120 NKNTNENTNDSFTYSLKDLTGLTDLTSLVETKLSFGANGKVNITSDTKGLNFAKETAGTN 179  
QY 173 GDTTVHLNGIGSLTDLTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIGVKTGS 230  
Db 180 GDTTVHLNGIGSLTDLTLLNTGATNTVNDNVTDDEKRAASVKDVLNAGWNKIGVKTGS 239  
QY 231 TTGQSENVDFVRYTDFEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVKEKDGKLV 290  
Db 240 TA--SDNVDFVRYTDFEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVKEKDGKLV 297  
QY 291 GKKGKENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFTVTSNTV 350  
Db 298 GKKGKENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFTVTSNTV 357  
QY 351 ASGKGTATVSKDDQGNITVMYDYNVGDALNVQNLQNSGNLDSKAVAGSSGKVISGNV 410

Db 358 ASGKGTATVSKDDQGNITVMYDYNVGDALNVQNLQNSGNLDSKAVAGSSGKVISGNV 417  
QY 411 PSKGMDETVNINAGNIEISRNKNIDTATSMAPQFSSVSLGAGADAPTSLVDDRGALN 470  
Db 418 PSKGMDETVNINAGNIEITRNGKNIDTATSMTPQFSSVSLGAGADAPTSLVDDRGALN 477  
QY 471 VGSKDANKPVRITNVAPGKGEQDVTNVAOLKGYAQNLRNDRIDNVNAGNAGIAQAATAG 530  
Db 478 VGSKDANKPVRITNVAPGKGEQDVTNVAOLKGYAQNLRNDRIDNVNAGNAGIAQAATAG 537  
QY 531 LVQAYLPKGSMAIGAAGGTGTYRGEAGYAGYSSISDGGNWIIGTASGNSRHFAGSASVGY 590  
Db 538 LVQAYLPKGSMAIGAAGGTGTYRGEAGYAGYSSISDGGNWIIGTASGNSRHFAGSASVGY 597  
QY 591 QW 592  
Db 598 QW 599

RESULT 7  
US-09-377-155-7  
; Sequence 7, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 7  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-7

Query Match 85.4%; Score 2552; DB 4; Length 594;  
Best Local Similarity 86.8%; Pred. No. 9.5e-190;  
Matches 524; Conservative 16; Mismatches 42; Indels 22; Gaps 7;

QY 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIIWSALNANWAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59  
QY 61 ESVOR-SVVGSIQASMEGSGELETISLSMTNDSKEFVDPYI-----VVTLKAGDNL 110  
Db 60 EPQRTAVVLFSRDEKGEKEG-----TEDSNWAV--YFDEKRVLKAGAITLKAGDNL 112  
QY 111 KIKONTNENTNASSFTYSLKDLTGLINVTETKLSFGANGKKVNIISDTKGLNFAKETAG 170  
Db 113 KIKONTNENTNDSFTYSLKDLTGLTDLTSLVETKLSFGANGKVNITSDTKGLNFAKETAG 172  
QY 171 TNGDPTVHLNGIGSLTDLTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNKIGVKT 228  
Db 173 TNGDPTVHLNGIGSLTDLTLLNTGATNTVNDNVTDDEKRAASVKDVLNAGWNKIGVKT 232  
QY 229 GSTTGOSENVDFVRYTDFEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVKEKDGK 288  
Db 233 GITA--SDNVDFVRYTDFEFLSADTKTTTVNVEKDNKRTVEKIGAKTSVKEKDGK 290  
QY 289 VTGKGKENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFTVTSNTV 348  
Db 291 VTGKGKENGSTDEGEGLVTAKEVIDAVNKAGWRMKTTFANGQTGQADKFTVTSNTV 350  
QY 349 TFASGKGTATVSKDDQGNITVMYDYNVGDALNVQNLQNSGNLDSKAVAGSSGKVISGN 408

Db	291	VTGKGKDENGSSDDEGLVTAKEIDAVNVAKGRMKTTTTANGCTGOADKFETVTSCTNV	350
Qy	349	TFASGKGTTATFVSCKDDQGNITVMYDVNVGDALNYQLONGSWNLDSKAVAGSGKVJISGN	408
Dd	351	TFASGKGTTATFVSCKDDQGNITVKVDNVGDALNYQLONGSWNLDSKAVAGSGKVJISGN	410
Qy	409	VSPSKGKDEFTVNNTNACNNTEISRNGKNIDIATSMAPQFSVSLGACADAPTLLSVDDGA	468
Dd	411	VSPSKGKDEFTVNNTNACNNTEISRNGKNIDIATSMAPQFSVSLGACADAPTLLSVDDGA	470
Qy	469	LNVGSKBANKPVRTTNVAPGVKEGDVTNV AOLKGVAQNLRNRIDNV DGNRAGIAQA IAT	528
Dd	471	LNVGSKDTRNPVRTTNVAPGVKEGDVTNV AOLKGVAQNLRNRIDNV DGNRAGIAQA IAT	530
Qy	529	AGLVQAYILPKGKSMAIAGGGTVRGAGYAIGYSSTSDCGNMIIKTGTASNRSRGHFGASV	588
Dd	531	AGLVQAYILPGKSMAIAGDTVRGAGYAIGYSSTSDCGNMIIKTGTASNRSRGHFGASV	590
Qy	589	GYOW 592	
Dd	591	GYOW 594	

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RESULT          9
US-09-377-155-g
: Sequence 9, Application US/09377155
: Patent No. 6197312
: GENERAL INFORMATION:
: APPLICANT: PEAK, Ian Richard Anselm
: APPLICANT: JENNINGS, Michael Paul
: APPLICANT: MOXON, E. Richard
: TITLE OF INVENTION: NOVEL SURFACE ANTIGEN
: FILE REFERENCE: 065064/0128
: CURRENT APPLICATION NUMBER: US/09/377,155
: CURRENT FILING DATE: 1999-08-19
: PRIOR APPLICATION NUMBER: PCT/AU98/01031
: PRIOR FILING DATE: 1998-12-14
: PRIOR APPLICATION NUMBER: GB 9726398.2
: PRIOR FILING DATE: 1997-12-12
: NUMBER OF SEQ ID NOS: 33
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 9
: LENGTH: 594
: TYPE: PRT
: ORGANISM: Neisseria meningitidis
US-09-377-155-g

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Query Match      84.8%; Score 2533; DB 4; Length 594;
Best Local Similarity 86.4%; Pred. No. 2.8e-188;
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps

Qy      1 MNKYRIIWNSSALANAWAVSELTRNHTKRASATVKTAVLATLFLLFATVOANATDEDEBEL 60
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MNKYRIIWNSSALANAWAVSELTRNHTKRASATVATVATLFLLFATVOASTD-DDDLYL 59
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      61 ESVOR -SVVGIGIQASMEGSGELETSLSMINDS-----KEFVDPYIVTIVLKAGDNLKI 112
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      60 EPVQRTAVVLSRDSKEGTGEKE-----VTEDSNWGVYFDKKGVLTAGTITLKGADNLKI 114
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      113 KONTNENTNASSFTYSLKKDLTLGLINVEKLSFGANGKKYNIISDTKGLNFAKETAGTN 172
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      115 KONTNENTNASSFTYSLKKDLTDLTSVGTKEKLSFSANSKYNITSDTKGLNFAKKTAEFN 174
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      173 GDTTVHLNGIGSTLTDTLTLAGSSASVHDAGNOST--HYTPRAASIKDVLNAGNNIKGVKTGS 230
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      175 GDTTVHLNGIGSTLTDTLTLCATNTVNDNVNTDDEKKRAASVKDVLNAGNNIKGVKPGT 234
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      231 TTGQSENVDFVRTYDVFEEFLSADTKTTTVNVESKDNGKRTVEKLGAKTSVLEKDKGLVLT 290
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      235 TA--SDNVDFVRTYDVFEEFLSADTKTTTVNVESKDNGKRTVEKLGAKTSVLEKDKGLVLT 292
        | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

Qy      291 KGKKGSGSSDDBEGGLYTAKEVIDAVNKGWRMKTTTTANGOTGADKFEVTVTSGTNNVTF 350

```

Db 293 GKDKGENDSSTDKGEGLVTAKEVIDAVNKGWRMKTTTANGOTGQADKPEFVTSGTNVTF 352  
QY 351 ASKGGTATVSKDDQGNITVMYDGVNVDALNVNOLNSGWNLDKAVAGSSGKVISGNVS 410  
Db 353 ASKGGTATVSKDDQGNITVMYDGVNVDALNVNOLNSGWNLDKAVAGSSGKVISGNVS 412  
QY 411 PSKGKDETVNINAGNIEISRNGKNIDATSMAPQFSSVSLGAGADAPTLSVDDDEGALN 470  
Db 413 PSKGKDETVNINAGNIEISRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDDEGALN 472  
QY 471 VGSKDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNNRDNVDGNARAGIAQAATAG 530  
Db 473 VGSKDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNNRDNVDGNARAGIAQAATAG 532  
QY 531 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASVGY 590  
Db 533 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASVGY 592  
QY 591 QW 592  
Db 593 QW 594

RESULT 10  
US-09-669-974-9  
; Sequence 9, Application US/09669974  
; Patent No. 633173  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 9  
; LENGTH: 594  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-9

Query Match 84.8%; Score 2533; DB 4; Length 594;  
Best Local Similarity 86.4%; Pred. No. 2.8e-188;  
Matches 520; Conservative 20; Mismatches 44; Indels 18; Gaps 6;  
QY 1 MNKIYRIWNSALNANWAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIWNSALNANWAVAVSELTRNHTKRASATVKTAVLATLLFATVQASTTD-DDDLYL 59  
QY 61 ESVQR-SVSGIQASMEGSELETISLSMTNDS-----KEFVDPYIVVTLKAGDNLKI 112  
Db 60 EPVQRTAVLSFRSDKEGTGEKE-----VTEDSNWGVYFDKGVLTAGTITLKAGDNLKI 114  
QY 113 KONTNENTNASSFYSLKKDLTGLINVTETKLSFGANGKKNVNIISDTKGLNFAKTAGTN 172  
Db 115 KONTNENTNASSFYSLKKDLTGLTSDVTEKLSFGANSKNVNIISDTKGLNFAKKTAEIN 174  
QY 173 GDTTVHLNGIGSTLTDLAGSSASHVDAGNQST--HYTRAASIKDVLNAGNINIKGVKTGS 230  
Db 175 GDTTVHLNGIGSTLTDLLNTGATTNTVNDVDEKKRAASVKDVLNAGNINIKGVKPGT 234  
QY 231 TTGOSENVDVRYTDTVEFLSADTKTTTNNVESKDNKGRTEVKIGAKTSVKEKDGKLYT 290

Db 235 TA--SDNVDFVRYTDTVEFLSADTKTTTNNVESKDNKGRTEVKIGAKTSVKEKDGKLYT 292  
QY 291 GRKGENGSTDEGEGLVTAKEVIDAVNKGWRMKTTTANGOTGQADKPEFVTSGTNVTF 350  
Db 293 GKDKGENDSSTDKGEGLVTAKEVIDAVNKGWRMKTTTANGOTGQADKPEFVTSGTNVTF 352  
QY 351 ASKGGTATVSKDDQGNITVMYDGVNVDALNVNOLNSGWNLDKAVAGSSGKVISGNVS 410  
Db 353 ASKGGTATVSKDDQGNITVMYDGVNVDALNVNOLNSGWNLDKAVAGSSGKVISGNVS 412  
QY 411 PSKGKDETVNINAGNIEISRNGKNIDATSMAPQFSSVSLGAGADAPTLSVDDDEGALN 470  
Db 413 PSKGKDETVNINAGNIEISRNGKNIDATSMTPQFSSVSLGAGADAPTLSVDDDEGALN 472  
QY 471 VGSKDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNNRDNVDGNARAGIAQAATAG 530  
Db 473 VGSKDANKPVRITNVAPGVKEGDTVNVQALKGVAQNLNNRDNVDGNARAGIAQAATAG 532  
QY 531 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASVGY 590  
Db 533 LVQAYLPGKSMMAIGGGTYRGEAGYAIGYSSISDGGNWIILKGTASGNSRGHFGCASVGY 592  
QY 591 QW 592  
Db 593 QW 594

RESULT 11  
US-09-377-155-13  
; Sequence 13, Application US/09377155  
; Patent No. 6197312  
; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 13  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-13

Query Match 84.5%; Score 2524; DB 4; Length 598;  
Best Local Similarity 85.5%; Pred. No. 1.4e-187;  
Matches 520; Conservative 17; Mismatches 45; Indels 26; Gaps 8;  
QY 1 MNKIYRIWNSALNANWAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKIYRIWNSALNANWAVAVSELTRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59  
QY 61 ESVQR-SVSGIQASMEGSELETISLSMTNDSKEFVDPYI-----VVTLLKAGDNL 110  
Db 60 EPVQRTAVLSFRSDKEGTGEKE-----TEDSNWAV--YFDEKRVLKAGAITLKAGDNL 112  
QY 111 KONTNENTNAN-----SSFTYSLKKDLTGLINVTETKLSFGANGKKNVNIISDTKGLNFAK 166  
Db 113 KONTNENTNANSSFTYSLKKDLTGLTSDVTEKLSFGANGKKNVNIISDTKGLNFAK 172  
QY 167 ETAGTNGDTPVHLNGIGSTLTDLAGSSASHVDAGNQST--HYTRAASIKDVLNAGNINIK 224  
Db 173 ETAGTNGDTPVHLNGIGSTLTDLLNTGATTNTVNDVDEKKRAASVKDVLNAGNINIK 232  
QY 225 GVTGTTGGOSENVDVRYTDTVEFLSADTKTTTNNVESKDNKGRTEVKIGAKTSVKEK 284





Db 173 ETAGTNGDPTVHLNGIGSTLTDLTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGNNIK 232  
Qy 225 GVKTSSTGOSENVDVRYDYTVFELSADTKTTTNNVESKDNKRTVEVKIGAKTSVIKEK 284  
Db 233 GVKPGGTTA--SDNVDFVRYDYTVFELSADTKTTTNNVESKDNKRTVEVKIGAKTSVIKEK 290  
Qy 285 DGKLVTKGKGGSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFFETVTS 344  
Db 291 DGKLVTKGKGGSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFFETVTS 350  
Qy 345 GTNVTASGKGTTATVSKDDQGNITVMYDVGDLNVLNOLQNSGWNLDKSKAVAGSSGKV 404  
Db 351 GTRVTFASNGGTATVSKDDQGNITVMYDVGDLNVLNOLQNSGWNLDKSKAVAGSSGKV 410  
Qy 405 ISGNVSPSKGKMDETVNNAGNIEISRCKNIDTATSMAPOFSSVSLGAGADAPTLSDV 464  
Db 411 ISGNVSPSKGKMDETVNNAGNIEISRCKNIDTATSMAPOFSSVSLGAGADAPTLSDV 470  
Qy 465 DEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNVGNARAGIAQ 524  
Db 471 DEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNVGNARAGIAQ 530  
Qy 525 AIATAGLVQAYLPCKSMATGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGA 584  
Db 531 AIATAGLVQAYLPCKSMATGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGT 590  
Qy 585 SASVGYQW 592  
Db 591 SASVGYQW 598

## RESULT 14

US-09-669-974-5  
; Sequence 5, Application US/09669974  
; Patent No. 6333173

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/669,974  
; CURRENT FILING DATE: 2000-09-26  
; PRIOR APPLICATION NUMBER: US 09/377,155  
; PRIOR FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 5  
; LENGTH: 598  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-669-974-5

Query Match 84.4%; Score 2521; DB 4; Length 598;  
Best Local Similarity 85.5%; Pred. No. 2.4e-187;  
Matches 520; Conservative 16; Mismatches 46; Indels 26; Gaps 8;

Qy 1 MNKYRIIWNLSALNNAVAVSELNRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 1 MNKYRIIWNLSALNNAVAVSELNRNHTKRASATVKTAVLATLLFATVQANATD-DDDLYL 59  
Qy 61 ESVOR-SVWGSIQASMEGSGELETISLSMTNDSKEFVDPYI-----VTLKAGDNL 110  
Db 60 EPVORTAVLVSFRSDKEGTGKEG-----TEDSNWAV--YFDEKRVLKAGAILKAGDNL 112  
Qy 111 KIKONTNENTNA-----SSFTYSLSKKDLTGLINVTETEKLSFGANGKKVNIISDTKGLNFAK 166

Db 113 KIKONTNENTNENTSSFTYSLSKKDLTGLTGLINVTETEKLSFGANGKKVNIISDTKGLNFAK 172  
Qy 167 ETAGTNGDPTVHLNGIGSTLTDLTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGNNIK 224  
Db 173 ETAGTNGDPTVHLNGIGSTLTDLTLLNTGATNTVNDNVTDDEKKRAASVKDVLNAGNNIK 232  
Qy 225 GVKTSSTGOSENVDVRYDYTVFELSADTKTTTNNVESKDNKRTVEVKIGAKTSVIKEK 284  
Db 233 GVKPGGTTA--SDNVDFVRYDYTVFELSADTKTTTNNVESKDNKRTVEVKIGAKTSVIKEK 290  
Qy 285 DGKLVTKGKGGSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFFETVTS 344  
Db 291 DGKLVTKGKGGSGSTDEGEGLVTAKEVIDAVNKGAWRMKTTTANGQTQADKFFETVTS 350  
Qy 345 GTNVTASGKGTTATVSKDDQGNITVMYDVGDLNVLNOLQNSGWNLDKSKAVAGSSGKV 404  
Db 351 GTRVTFASNGGTATVSKDDQGNITVMYDVGDLNVLNOLQNSGWNLDKSKAVAGSSGKV 410  
Qy 405 ISGNVSPSKGKMDETVNNAGNIEISRCKNIDTATSMAPOFSSVSLGAGADAPTLSDV 464  
Db 411 ISGNVSPSKGKMDETVNNAGNIEISRCKNIDTATSMAPOFSSVSLGAGADAPTLSDV 470  
Qy 465 DEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNVGNARAGIAQ 524  
Db 471 DEGALNVGSKDANKPVRIITNVAPGVKEGDTNVAQLKGVAQNLNRRIDNVGNARAGIAQ 530  
Qy 525 AIATAGLVQAYLPCKSMATGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGA 584  
Db 531 AIATAGLVQAYLPCKSMATGGTYRGEAGYAGYSSISDGGNWIIGKTASGNSRGHFGT 590  
Qy 585 SASVGYQW 592  
Db 591 SASVGYQW 598

## RESULT 15

US-09-377-155-21  
; Sequence 21, Application US/09377155  
; Patent No. 6197312

; GENERAL INFORMATION:  
; APPLICANT: PEAK, Ian Richard Anselm  
; APPLICANT: JENNINGS, Michael Paul  
; APPLICANT: MOXON, E. Richard  
; TITLE OF INVENTION: NOVEL SURFACE ANTIGEN  
; FILE REFERENCE: 065064/0128  
; CURRENT APPLICATION NUMBER: US/09/377,155  
; CURRENT FILING DATE: 1999-08-19  
; PRIOR APPLICATION NUMBER: PCT/AU98/01031  
; PRIOR FILING DATE: 1998-12-14  
; PRIOR APPLICATION NUMBER: GB 9726398.2  
; PRIOR FILING DATE: 1997-12-12  
; NUMBER OF SEQ ID NOS: 33  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 21  
; LENGTH: 591  
; TYPE: PRT  
; ORGANISM: Neisseria meningitidis  
US-09-377-155-21

Query Match 82.5%; Score 2464.5; DB 4; Length 591;  
Best Local Similarity 84.2%; Pred. No. 5.7e-183;  
Matches 506; Conservative 30; Mismatches 46; Indels 19; Gaps 8;

Qy 1 MNKYRIIWNLSALNNAVAVSELNRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL- 59  
Db 1 MNKYRIIWNLSALNNAVAVSELNRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Qy 60 -LSVORSV-VGSIQASMEGSGELETISLSMTNDSKEFVDPYIV---VTLKAGDNLKIK 113  
Db 61 YLDPVORTAVLVSFRSDKEGTGKEGVE-ENSDWAVYFNEKGVLTAREITLKAGDNLKIK 119  
Qy 114 QNTNENTNASSFTYSLSKKDLTGLINVTETEKLSFGANGKKVNIISDTKGLNFAKETAGTNG 173



120	Q	-----NGNFYTSUKKDDTDTSVGTSEKLSFSAANGKNVNTSDTKGLNFAKETAGTNG	173
174	QY	DTTVHLNGIGSTLTDTLAGSSASHVDAGNQST--HYTRAASIKDVLNAGWNIIKGVKGTST	231
174	Db	DTTVHLNGIGSTLTDTLNTGATTNTVNDNDVDEKKRAASKVDVLNAGWNIIKGVKPGTT	233
232	QY	TGQSENVDFVRTYDVTVEFLSADTKTTTVNVVESKDNQKRTVEVIGAKTSSVIKEKDGKLVTG	291
234	A	--SDNVDFVRTYDVTVEFLSADTKTTTVNVVESKDNQKKTVEVIGAKTSSVIKEKDGKLVTG	291
292	QY	KKGKENGSSYDEGEGLVTAKEVTDVANKAGWRMKTITANGQTQADKPEFVTSCTNVTFPA	351
292	Db	KDKGENGSSYDEGEGLVTAKEVTDVANKAGWRMKTITANGQTQADKPEFVTSCTNVTFPA	351
352	QY	SGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGWNLDKAVAGSSGRVVISGNVSP	411
352	Db	SGKGTATVSKDDQGNITVMYDYNVGDALNVQLNSGWNLDKAVAGSSGRVVISGNVSP	411
412	QY	SKGMDETVINAGNITETSRNKNIDTATSMAPQSFSSVSLGAGADAPPLSVDDREGALNV	471
412	Db	SKGMDETVINAGNITETIRNGKNIDTATSMTPQSFSSVSLGAGADAPPLSVVDGD--ALNV	470
472	QY	GSKDANKPVRIITNVAPCVKEGDTVNAQLKGVQAQLNNRIDNVGDNARAGIAQAATATAGL	531
471	Db	GSKDANKPVRIITNVAPCVKEGDTVNAQLKGVQAQLNNRIDNVGDNARAGIAQAATATAGL	530
532	QY	VQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFCASASVGYQ	591
531	Db	VQAYLPCKSMMAIGGGTYRGEAGYATGYSSISDGGNWIILKGTASGNSRGHFCASASVGYQ	590
592	W	592	
591	Db	591	

Search completed: July 3, 2002, 08:37:13  
Job time: 339 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: July 3, 2002, 08:38:32 ; Search time 58.79 Seconds  
(without alignments)  
967.595 Million cell updates/sec

Title: US-09-771-382-10  
Perfect score: 2988  
Sequence: 1 MNKIYRIIWSALNAWAVS.....TASGNSRGHFGASASVGYOW 592

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 seqs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR\_71: \*  
1: pir1: \*  
2: pir2: \*  
3: pir3: \*  
4: pir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2988	100.0	592	2 A81888	probable surface f
2	2464.5	82.5	591	2 G81133	adhesin NMR0992 (i
3	561	18.8	298	2 G64138	adhesin homolog Hi
4	410.5	13.7	2059	2 D82671	surface protein XF
5	394.5	13.2	1190	2 A82615	surface protein XF
6	375.5	12.6	1107	2 AC0976	probable autotrans
7	373.5	12.5	1588	2 A86036	probable adhesin Z
8	373.5	12.5	1588	2 H91188	probable adhesin E
9	341.5	11.4	658	2 AH0110	probable surface p
10	252	8.4	1004	2 C82672	surface-exposed ou
11	248.5	8.3	1325	2 A64905	ydek protein - Esc
12	231.5	7.7	1343	2 E90893	hypothetical prote
13	227.5	7.6	1343	2 D85724	hypothetical prote
14	220.5	7.4	1238	2 AH0038	probable exported
15	219.5	7.3	949	2 D90803	Aida-1 adhesin-lik
16	219.5	7.3	1005	2 H85611	probable adhesin Z
17	219.5	7.3	1910	2 AF0394	probable adhesin h
18	219	7.3	1018	2 H83135	probable adhesin P
19	212	7.1	1417	2 A83080	hypothetical prote
20	210.5	7.0	1275	2 T33369	hypothetical prote
21	210.5	7.0	4919	2 T31105	hypothetical prote
22	210	7.0	1286	2 S28634	adhesin AIDA-1 pre
23	209.5	7.0	5188	2 B85547	probable RTX famil
24	209	7.0	1428	2 AC2224	hypothetical prote
25	209	7.0	4936	2 AH2515	hypothetical prote
26	208.5	7.0	936	2 I40711	sapB protein - Cam
27	207.5 /	6.9	1477	2 B43855	high-molecular-we
28	207.5	6.9	5291	2 F90696	hypothetical prote
29	205	6.9	1109	2 A56143	surface-array prot

ALIGNMENTS

RESULT 1

AB1888  
probable surface fibril protein NMA1200 [imported] - Neisseria meningitidis (strain 2  
C:Species: Neisseria meningitidis  
C:Date: 05-May-2000 #sequence\_revision 05-May-2000 #text\_change 02-Feb-2001  
C:Accession: AB1888  
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Mo  
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandre  
Nature 404, 502-506, 2000  
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491  
A:Reference number: AB1775; MUID:20222556  
A:Accession: AB1888  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-592 <PAR>  
A:Cross-references: GB:AL162755; GB:AL157959; NID:g7379742; PIDN:CAB84461.1; PID:g737  
A:Experimental source: serogroup A, strain Z2491  
C:Genetics:  
A:Gene: NMA1200

Query Match	Score	DB 2	Length	592
Best Local Similarity	100.0%			
Matches	592	Conservative	0	Mismatches
Indels	0	Gaps	0	
QY	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLLFATVQANATDEDEEEL	60	
DB	1	MNKIYRIIWSALNAWAVSELTRNHTKRASATVKTAVLATLLLFATVQANATDEDEEEL	60	
QY	61	ESVORSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVTVLKAGDNLKIKQNTNENT	120	
DB	61	ESVORSVVGSIQASMEGSGELETISLSMTNDSKEFVDPYIVTVLKAGDNLKIKQNTNENT	120	
QY	121	NASSFTYSLKDLTLGLINVEYTEKLSFGANGKKNIIISDTKGLNFAKETAGTNGDTTVHLN	180	
DB	121	NASSFTYSLKDLTLGLINVEYTEKLSFGANGKKNIIISDTKGLNFAKETAGTNGDTTVHLN	180	
QY	181	GIGSTLTDLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKGVKTGTTGQSENVD	240	
DB	181	GIGSTLTDLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKGVKTGTTGQSENVD	240	
QY	241	VRDYDVEFLSADTKTTVNVESKDKGRTEVKIGARTSVIKEKDKLVTGKKGNGSS	300	
DB	241	VRDYDVEFLSADTKTTVNVESKDKGRTEVKIGARTSVIKEKDKLVTGKKGNGSS	300	
QY	301	TDEGEGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFEFTVTSNTVTFASGKGTATV	360	
DB	301	TDEGEGLVTAKEVIDAVNKAGWRMKTNTANGQTQADKFEFTVTSNTVTFASGKGTATV	360	
QY	361	SKDDQGNITVYDVNVGDALNVNQLNSKAVAGSSGKVISGNVSPSKGMDETV	420	
DB	361	SKDDQGNITVYDVNVGDALNVNQLNSKAVAGSSGKVISGNVSPSKGMDETV	420	



A:Accession: D82671  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-2059 <SIM>  
A:Cross-references: GB:AE003982; GB:AE003849; NID:g9106554; PIDN:AAF84338.1; GSPDB:GN001  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier, R. as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A.; Rodrigues, V.; Nunez, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.Y.; F.G.; Nunez, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Miyaki, C.Y.; Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak M.; Tshako, M.H.; Vallada, H.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1529

Query Match 13.7%; Score 410.5; DB 2; Length 2059;  
Best Local Similarity 24.5%; Pred. No. 4e-13;  
Matches 170; Conservative 103; Mismatches 226; Indels 195; Gaps 30;  
QY 58 EELESVQSVSGSIOASMEGGSELETISLSMTNDSKEFVDPYIVVTLKAGD-NLKIKONT 116  
DB 1402 EETDAVNFSQLKSISTAVDQGW---TLTASGANGSK--VASGGTVDLKNTDGNLTISKSG 1456  
QY 117 NENTNASFTYSLKDLGLINVEKLSFGANGKV--NIISDTKGLNFAKETAGT--- 171  
DB 1457 DSNVDFVNLSEDLKESKSTVGTQDLK-----DGVKVSNNLLDSNELVITSHSSTSVK 1511  
QY 172 ---NGDTTVH---LNGIGSTLTD-----TLAGSSA-----SHVDAGNQ 203  
DB 1512 TLANGESVVRNVVNGDGVNIDVVVNDLGLSIVGASLTLGSLINAGSHKITNTAGTE 1571  
QY 204 ST---HYTRAASIKDVLNAGNWKV-KTGSTTGOSENVDVFR-----YDTV 247  
DB 1572 DTDVNFSQLKSIVSAPDKGWTLTASGANGSKVWSGGTVDLKNTDGNLAIKSGSDNDV 1631  
QY 248 EFLSADTK-----TTTVNESKDKRTEVKIGAKTSVKEKDKLVTKGKGEN--- 297  
DB 1632 FNLKDFKVDVETAGTNTVNTDGVKVG--SDVSLGAMGLFIANGPSVTASGPNAGDKVIS 1689  
QY 298 ---GSSTDEGEGLVTAKEVIDAVNKAQWRMKTIT-----ANGOTGO---ADKPE 340  
DB 1690 HVAVGMAUTDAVNVSQLKQAVQSVTVKATRYYSTNDGGTGGYDGDGATGSKAAGVG 1749  
QY 341 TVTSGTNV-----TFASGKGTTA----- 358  
DB 1750 TOASGEGAAVSGGAAASGKSTAGRNAIASADGSVALGDCAKDGGRGAEYSYTKYSGV 1809  
QY 359 -----TVS-----KDDQGNITVMYDVNG-DALNVNL-----QNSGNLDS----- 394  
DB 1810 QNNTVGTVSGVDAAGETRSISNADAKEMDVLNQLDVAQKNSLQTDMDRHEINNI 1869  
QY 395 ----KAVAGSSGKVTSGNVSPSKGMDVTNINA---GNNEISRN-----CKNIDIATS 442  
DB 1870 EDVFKITKDSASSVKG-----MGVNAIAGTNAAYSGTESVALGKNTNVNSD 1917  
QY 443 MAPQFSSVSLGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPCVKREGDVTNVAQLKG 502  
DB 1918 ----NAVAIGNSVA-----DRANSVSVSGGSSER--QVTNVAAGTADTDVAVNSQLNQ 1965  
QY 503 VAQNLNRINDVDGNAR-----AGIAQATATAGLVAOYLPKGSMAAIGGTYRGEAGYAG 558  
DB 1966 GLITAKQYTDGMVGNRLRRETSGVAAAATATANLPQAVQGRGMTSVGVSSYQGSIAIAGV 2025  
QY 559 YSSISDGGNWIKGTASGNSRGHFCASASVGYQW 592

DB 2026 VSAVESGHWVFKSGSANTRSHRVGVGAGVGYQW 2059  
RESULT 5  
A82615  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: A82615  
R:Anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: A82615  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1190 <SIM>  
A:Cross-references: GB:AE004017; GB:AE003849; NID:g9107083; PIDN:AAF84783.1; GSPDB:GN  
A:Experimental source: strain 9a5c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R. Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrier as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C. F.G.; Nunez, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, R. Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Saw M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L. A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1981

Query Match 13.2%; Score 394.5; DB 2; Length 1190;  
Best Local Similarity 25.4%; Pred. No. 1.3e-12;  
Matches 158; Conservative 90; Mismatches 249; Indels 125; Gaps 24;  
QY 19 VSELRNRHTKRASATVKTAVLATL---LFATVQANATDEEEESVORSVVGSIQAS 74  
DB 646 VDSLITGNTAMTIDGTVGSGNVTLGSLVITDGSVTSSSGISAGNOKITNVAAGTADTD 705  
QY 75 MBGSGELETIS-----LSMTNDSKEFVDPYIVVTLKAGD-NLKIKONTNENTNASSF 125  
DB 706 AVNFSOLQAVSSTASKGNWLLASGANSSNVAPGESVDLKNKTGDNIVISKESGSDNVLNL 765  
QY 126 TYSLKDLTLINVEKLSFGANGKKNIIISDTKGLNFAKETAGTNGTITVHLNGIGST 185  
DB 766 SSSLKLD-----KLTVG-----DTVMTTNGV-----TVGSG-----VTLGSMGLV 800  
QY 186 LDTLTAGSS--ASHVDAGNOS--THVTRAASIKDVLNAGNWKVTKTSTTGOSENVDVFR 242  
DB 801 ITD-----GPSVTSNGNAGSOKITNVAAGTADTDAV-----NLSQNTAMAGSAGKSVHYTS 853  
QY 243 TYDTVEFLSADTKTTTVNVNESKDNKRTEVKIGAKTSVKEKDKLVTKGKGENG-SST 301  
DB 854 TYD-----GGTQGGNYNGDGATGTRSIAGVGVTLASA---EGATAVSGGAAASGKGT 903  
QY 302 DEGEGLVTAKEVIDAVNKAQWRMKTITANGOTQADKFFETVTSNGTNTVTSAGKGTATVTS 361  
DB 904 AICRNAVASADGSVALGD--GAKDGARGAESYTKYSGLQNTVGTVSVGDASKGETRTVS 962  
QY 362 KDDQGNITVMYDVNGDALNVNL-----QNSGNLDSKAVAGSSKVISGNSVPSKGMKD 417  
DB 963 -----NVADAKEAT--DAVNLHOLDRVAODANKRYDNKLTESLSEGTTF----- 1003  
QY 418 ETVINAGNNIEISRNGKNIDIATSMAPQFSSVSLCAGADA-----PTLSVDDE 466

Db 1004 --VKVNSLNN-----SATPTAAGVDATAIGVGATASGADSIAMGNKASASADNA 1050  
QY 467 GAL-----NVGSKDANKPRVITNVAPGVKEGVDVTVNAQLKGVQAQLNNRIDNV 514  
Db 1051 VAIGNHVSADRANTVSVGSAGSER--QVTNVAAGTADTDVAVNSQLNOGLITAKQYTDGV 1108  
QY 515 DGNA-----AGIAQATATAGLVOAYLPKGSMAIGGTYRGEAGYAGYSSISDGGNWII 570  
Db 1109 VGSRLRDTGCGVAAATATANLPQAYIPGRGMTSVGVSSYRGQSAIAVGVSSVESGRWF 1168  
QY 571 KGTASGNSRGHFCASASVGYQW 592  
Db 1169 KFGSANTRSQVIGAGVGYQW 1190  
  
RESULT 6  
AC0976  
probable autotransporter sapB [imported] - Salmonella enterica subsp. enterica serovar  
C:Species: Salmonella enterica subsp. enterica serovar typhi  
A:Note: this species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 09-Nov-2001  
C:Accession: AC0976  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,  
S.; Moule, S.; O'Gaora, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov  
A:Reference number: AB0502; PMID:11677608  
A:Accession: AC0976  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1107 <PAR>  
A:Cross-references: GB:AL513382; PIDN:CAD03303.1; PID:g16504923; GSPDB:GN00176  
C:Genetics:  
A:Gene: sapB

Query Match 12.6%; Score 375.5; DB 2; Length 1107;  
Best Local Similarity 22.0%; Pred. No. 1.1e-11;  
Matches 184; Conservative 103; Mismatches 232; Indels 317; Gaps 36;  
  
QY 9 WNSALNNAW-----VAVSELTNRHHTKRASATVKTAVLATLLFATVQANATDEDEEEL 51  
Db 337 WNETTNSFSASHGSSITNKITNVAAGLSEEST-----DAVNSQLPETFNEKVDQNT 388  
  
QY 52 TD-----EDEEELESVQSV-----VGSIOASMEGS-GELE 82  
Db 389 TDIAANTNTQNTAIENTNLSVDINTSITGLTDNALLWDEDTGAFSANHGGSTSKIT 448  
  
QY 83 TISL-SMTNDSKEFVDPIVVTILKAGDNL-KIKQNTNENTNASSFTYSLKKDL-TGLINV 139  
Db 449 NVAAGALSEDSTAVN-----GSQLEYTNQKVDQNTSAIA-----DINTSITNL 492  
  
QY 140 ETEKLSFGANGKKNIIISDTKGLNFAKE-TAGTNGDPTVHLNGIGSLTDLTLGASSASHV 198  
Db 493 GTDALSW-----DDEGAFASSHGTSCTNKITNVAAGETASDSTDAINGSQLYET 542  
  
QY 199 D-----ACNQSTHYTRAASIKDVLNAGNIIKGVKTGSTGTQSENVDVFTYD 245  
Db 543 NMLISQYNESISOLAGDTSETI-----TENGTG-----VKYIRIND 579  
  
QY 246 T-----VEFLSADTKTTNVNYESKDNKRTEVKIGAKTSVIEKDKGLVTGKNGEN---- 297  
Db 580 NLEGQDAYATGATGATVAYDASVAGAC-LALQONS--SSIEGSLALGSGTSNRAIT 636  
  
QY 298 -----GSSTDEGEGL-----VTAKEVIDAVNKA-----GWRMKTITFANGOTQ----- 335  
Db 637 TGIRETSATSDGVIGYNTDRELGLALSIGTDSERYQITNVADGSEAQDAVTVROLQN 696  
  
QY 336 -----ADKFEVTSCTNVTASGKTTA-----TVSKDDOG-----NITVMYDVNVGD 378  
Db 697 AIGAVTTPTTKYHANSTEEDSLAVGDTSLAMGAKTIVNADAGIGIGLNTLVNADAINGI 756

QY 379 ALNVN-----OLQNSGWNLDK-----AVAGSSGKVISGNVS 410  
Db 757 AIGSNARANHANSIAMGNGSQTTTRGAQTDYATNMDTPONSVEGFSVSGEDGQRIQTNVA 816  
QY 411 PSKKGWDETVTNAG-----NNIEISRNGNI-----DIATSM 444  
Db 817 AGSADTDA-----VNVGOLKVTDAQVSRNTOSITNLNTQVSNLDTRVTNIENIGIDIVTGS 873  
QY 445 PQF-----SSVSLGAGADAP-----TSLVDDE-CALNVGSKDANKPV 480  
Db 874 TKYFKTNTDGADANAAGADSVAIGSGSIAAENSVALGTNSVADEANTVSVGSSTQOR-- 931  
QY 481 RITNVAPGVKEGVDTVNAQLK-----GVAQ----- 501  
Db 932 RITNVAAGVNTDVAVNAQLKASEAGSVRYETNADGSVNYSVLNLGDGSGGTTTRIGNVSA 991  
QY 502 -----GVAQ-----NLNRRIDNVGNRAGIAQATATAGLQAYL 536  
Db 992 AVNDTDAVNYAQLKRSVEEANTYTDQKMGEMNSKIKGIENKMGSGGIASANAMAGLPQAYA 1051  
QY 537 PGKSMMAIGGTYRGEAGYAGYSSISDGGNWIILKGTASGNSRGHFCASASVGYQW 592  
Db 1052 PGANMISIAGGTENGESAIVAIGVMSVSESGWYKLGTSNSOGDYSAALGAGFQW 1107  
  
RESULT 7  
A86036  
probable adhesin Z5029 [imported] - Escherichia coli (strain O157:H7, substrain EDL93  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 14-Sep-2001  
C:Accession: A86036  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
illier, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: A86036  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <STO>  
A:Cross-references: GB:AE005174; NID:g12518349; PIDN:AAG58749.1; GSPDB:GN00145; UWGP:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: Z5029

Query Match 12.5%; Score 373.5; DB 2; Length 1588;  
Best Local Similarity 23.1%; Pred. No. 2.2e-11;  
Matches 176; Conservative 95; Mismatches 261; Indels 231; Gaps 30;  
  
QY 7 IIV-----NSALNNAWVAVSELTRNHTKRASATVKTAVLATLLFATVQANATDEDEEEL 60  
Db 880 LLMADADAGENGAFSA-----AHGKOKTASVITNVAN-----GAISAASSDAINGSOL 926  
  
QY 61 ESYQRSVVGSI--QASMEGSGELETISLMTN-----DSKEFVDPIYIIVTLKAGDNLK 111  
Db 927 YTTNKYIADALGDAEVNADGTITAPTITIANAEYNNVNGDALDLD-----DNAL 976  
  
QY 112 IKONTNENTNASSFTYSLKKD-----LTGLINVE-TEKLSFGANGKKNV-----IISDTK 160  
Db 977 L--WDETANGGAGAYNASHDGRASITNVANGSISDSDTDAVNGSQLNATNMNIEQNTQ 1033  
  
QY 161 GLNFAKETACTNGDPTVHLNGIG-----STLUTDTLAGSSASHVDAGNQSTHYTRAASIKDV 216  
Db 1034 IIN--OLAGNTQATYIQENGAGINIVRTNDDGLAFNDASAQGVGATAYGNSVAKGDSS 1090  
  
QY 217 LNAG-WNIKGVKTGSTGTQSENVDVFTYDVEFLSADTKTTNVNYESKDNKRTEYKIG 275  
Db 1091 VAIGQGSYSDVDGTGIALGSSSVSRV-----IAKGRDTSIT-----ENG-----VVIG 1134  
  
QY 276 AKTSVIEKDKGLVTGKKGKENG-----SSTDEGGLVTAKEVIDAVNKAQWRM--- 324

Db 1135 YDIT-----DGLLGALSIGDGGKYRIINVADGSEAHDAVTVROLNAIGAIVATPTKY 1189  
QY 325 -----KTTTANGQTG-----QADKETVTSNTV----- 348  
Db 1190 PHANSTEEDSLAVGTDLSAMGAKTIVNGDKGIGIGYAYVDANALNGAIGNAQVIHVN 1249  
QY 349 TFASGKGTTAT-----VSXDDQGNITVMYDVNVG-----DAL 380  
Db 1250 STAIENGSTTTTGAQNTAYNMDAPQNSVGEFSVGSADGQRQIT--NVAAGSADTDAV 1306  
QY 381 NVNQLO-----NSGWNLSK----- 395  
Db 1307 NVGOLKVTDAQVSONTSITNLDNRVTNLDNRVTNIENGIGDIVTGTSTKFTKTDGVD 1366  
QY 396 -----AVAGSSGKVISGNVSPSKG-----KMDFTVINAGNIEISRN--GNKIDIA 440  
Db 1367 ASAQKDSVAIGSGSIAADNSVALGTGSVATEENTISVGSSTNORRTITNVAAGKNATDA 1426  
QY 441 TSMAPOQFSVSLGAGADAPTLISVDDDEGALNVGSKDANKPVRITINVPAGVYKGDVTVNAQL 500  
Db 1427 VNVQKLSSEAGGVRYDTKADGSIDYSNITLGGNGG--TTRISNVASGVNNNDVVNYAQL 1485  
QY 501 KGVAQ-----NLNRRIDNVGNARAGIAQIAIATAGLVQAYLPCKSMMAIGGTY 549  
Db 1486 KQSVQETQYTDORVMENDNKLSTESKLSGSIASAMAMTGLPQAYTPGASMASIGGTY 1545  
QY 550 RGEAGYATGYSSISDGGNWIKGTASGNSRGHFGASASVGYOW 592  
Db 1546 NGESAVALGVSVANGRWYKLGSTNSQGEYSALGAGIOW 1588

## RESULT 8

H91188  
Probable adhesin ECs4480 [similarity] - Escherichia coli (strain O157:H7, substrain RIMD)  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 02-Nov-2001  
C:Accession: H91188  
R:Hayashi, T.; Makino, K.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.  
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gen  
A:Reference number: A99629; PMID:21156231; PMID:11258796  
A:Accession: H91188  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1588 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA037903.1; PID:g13633955; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs4480

Query Match 12.5%; Score 373.5; DB 2; Length 1588;  
Best Local Similarity 23.1%; Pred. No. 2.2e-11;  
Matches 176; Conservative 95; Mismatches 261; Indels 231; Gaps 30;

QY 7 LIW-----NSALNAWAVSELTRNHTKRASATVYTAVALTLFATVQANATDEDEEEL 60  
Db 890 LLDADAGENGAFSA-----AHGKDKTASVTINVAN-----GAISAASDAINGSQL 926  
QY 61 ESVQSVVVGSI--QASMEGSGELETISLSMTN-----DSKEFVDPIYVTLKAGDNLK 111  
Db 927 YTNKYIADLGGDAEVNADGTITAPTITIANEYNNVGDALD-----DNAL 976  
QY 112 IKONTNENTNASSFTYSKKD-----LGLINVE--TEKLSFGANGKYN-----TISDT 160  
Db 977 L---WDETANGGAGAYNASHDCGASIIITNVANGSISEDSTDAVGSQNLNATNMIEQNTQ 1033  
QY 161 GLNFAKETAGTNGDITVHLNGIG-----STLDTLTLGSSASHVDAGNQSTHYTHRAASIKDV 216  
Db 1034 IIN---QLAGNTDARYIOENGAGINYVTRNDGDLAFNDASOAGVGTATAGYNSVAKGDS 1090  
QY 217 LNAG--WNIKGVKGTGTGSENVDFVRYDITVEFLSADTKITTVNVESKDNCKRTEVKIG 275

Db 1091 VAIGGYSYSDVTGIALGSSSVSSRV-----IAKSRDTSIT-----ENG---VVIG 1134  
QY 276 AKTSVIKEDKGLVTKGKGENG-----SSTDEGELVTAKEVIDAVNKAHRM--- 324  
Db 1135 YDIT-----DGLLGALSIGDGGKYRIINVADGSEAHDAVTVROLNAIGAIVATPTKY 1189  
QY 325 -----KTTTANGQTG-----QADKETVTSNTV----- 348  
Db 1190 PHANSTEEDSLAVGTDLSAMGAKTIVNGDKGIGIGYAYVDANALNGAIGNAQVIHVN 1249  
QY 349 TFASGKGTTAT-----VSXDDQGNITVMYDVNVG-----DAL 380  
Db 1250 STAIENGSTTTTGAQNTAYNMDAPQNSVGEFSVGSADGQRQIT--NVAAGSADTDAV 1306  
QY 381 NVNQLO-----NSGWNLSK----- 395  
Db 1307 NVGOLKVTDAQVSONTSITNLDNRVTNLDNRVTNIENGIGDIVTGTSTKFTKTDGVD 1366  
QY 396 -----AVAGSSGKVISGNVSPSKG-----KMDFTVINAGNIEISRN--GNKIDIA 440  
Db 1367 ASAQKDSVAIGSGSIAADNSVALGTGSVATEENTISVGSSTNORRTITNVAAGKNATDA 1426  
QY 441 TSMAPOQFSVSLGAGADAPTLISVDDDEGALNVGSKDANKPVRITINVPAGVYKGDVTVNAQL 500  
Db 1427 VNVQKLSSEAGGVRYDTKADGSIDYSNITLGGNGG--TTRISNVASGVNNNDVVNYAQL 1485  
QY 501 KGVAQ-----NLNRRIDNVGNARAGIAQIAIATAGLVQAYLPCKSMMAIGGTY 549  
Db 1486 KQSVQETQYTDORVMENDNKLSTESKLSGSIASAMAMTGLPQAYTPGASMASIGGTY 1545  
QY 550 RGEAGYATGYSSISDGGNWIKGTASGNSRGHFGASASVGYOW 592  
Db 1546 NGESAVALGVSVANGRWYKLGSTNSQGEYSALGAGIOW 1588

## RESULT 9

AH0110  
Probable surface protein (partial) YPO0902 [imported] - Yersinia pestis (strain CO92)  
C:Species: Yersinia pestis  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0110  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.  
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.  
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell  
Nature 413, 523-527, 2001  
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.  
A:Reference number: AB0001; PMID:21470413; PMID:11586360  
A:Accession: AH0110  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-658 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89747.1; PID:g15978974; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0902

Query Match 11.4%; Score 341.5; DB 2; Length 658;  
Best Local Similarity 24.5%; Pred. No. 3e-10;  
Matches 155; Conservative 74; Mismatches 235; Indels 169; Gaps 24;

QY 45 ATVOANATDEDEEELSVQSVVGS--IQASMEGSGELETISLSMTNDSKEFVDPIYV- 101  
Db 110 ATISSTSTD-----AVGSQLYNLVQDGTTRYPHANSVNPDTSLASGLETVAG 157  
QY 102 -VTLKAGDNKIKONTNENTNASSFTYSLSKDLTGLINIVETEKLSFG-----ANGKKVNI 155  
Db 158 PATVVYSGDNGVIGNT-----ALVGAATGGTGAIGTGTVTAAGATGCS 202  
QY 156 ISDTKGLNFAKETAGTNGDITVHLNGIGSTLDTLTLGSSASHVDAGNQSTHYTHRAASIKD 215  
Db 203 AAQAQG---AQSLALGAGAVTTSQANSI-----ALGAASINTVGAQSSYSAYALTAPQAS 253

QY 216 VLNAG-----WNIKVGKTGTGGSENV-----DFVRYDVTVEFLSADTKTTTV-- 259.  
Db 254 VGEIGTGTALGNRKITGVAAGSASSDAVNVAQLTAYGDQVQ-QNTANITSLGGRVTTIEG 312  
QY 260 NVESKONG-----KRTEVKIGAKT-----SVIK 282  
Db 313 SMASIANGGGVKYFHANSTQPDVSASGTSVAIGPASLASGNNAALASGAGAVNIGCAA 372  
QY 283 EKDKLVTKGKGKENGSSSTDEGGLVTAKEVIDAVNKAQWRMKTITTTTANGQTQGAQKFETV 342  
Db 373 SADGSAVIGGGSGDNGRVENYIG-----KYSNASNTSSG-----TV 409  
QY 343 TSGTNTVFASGKTTTATVSKDDOGNITVMYDVNVGDALNVNQLONGSWNLDSKAVAGSSG 402  
Db 410 SVGNAT-----CETRTSVNADG-----QAQDAVNLRQLDG-----TAASI 447  
QY 403 KVISGVNPSKGRMDEVTMINAGNNT-EISRNCKNIDI--ATSMAPQFSSVSLGAGADAP 459  
Db 448 VVYENVNVSGLQNTDGMFQVNNSSGLAKPSATGANSATGGAGSVASGNNSTAFGSGAKAT 507  
QY 460 TLS-----VDDGALNVSGDKANKPVRITNVAPGVKEGDVTVVAQLKGVAQN----- 506  
Db 508 AANSAALGANSVADRANSVSGVGNR--QITNVAPATQGTDAVNFQDLKSTSNQTNAY 565  
QY 507 LNNRIDNVGNAR-----AGIAQAIAVAGLVQALPGKSMMAIGGTVRGEGVAIGY 559  
Db 566 TNQYSELKODLRKQNSVLSAGIASMSASLTQPTYTSGSSMTTIGAASVYRGOSALSIGV 625  
QY 560 SSTSDGNNIIKGTASGNSRGFGASVGYQW 592  
Db 626 SSTSDGRRWYVKLQASNTQDGFVGIGVGYQW 658

RESULT 10  
C82672 surface-exposed outer membrane protein XF1516 [imported] - Xylella fastidiosa (strain 9a)  
C:Species: Xylella fastidiosa  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 20-Aug-2000  
C:Accession: C82672  
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequences  
Nature 406, 151-157, 2000  
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.  
A:Reference number: A82515; MUID:20365717  
A:Note: for a complete list of authors see reference number A59328 below  
A:Accession: C82672  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1004 <SIM>  
A:Cross-references: GB:AE003981; GB:AE003849; NID:g9106543; PIDN:AAF84325.1; GSPDB:GN001  
A:Experimental source: strain 9a3c  
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; B  
R:Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carre  
as-Neto, E.; Docena, C.; El-Dorriy, H.; Facincani, A.P.; Ferreira, A.J.S.  
submitted to GenBank, June 2000  
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm  
J.D.; Junqueira, M.L.; Kemper, E.B.; Kitzajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig  
chado, M.A.; Madeira, E.M.B.N.; Madeira, H.M.F.; Marino, C.D.; Marques, M.V.; Martins, E  
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y  
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, C.A  
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak  
A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir  
M.; Tshuhako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z  
A:Reference number: A59328  
A:Contents: annotation  
C:Genetics:  
A:Gene: XF1516

[illegible]

Query Match 8.4%; Score 252; DB 2; Length 1004;  
Best Local Similarity 22.0%; Pred. No. 2e-05;  
Matches 159; Conservative 102; Mismatches 279; Indels 184; Gaps 33;  
QV 2 NKIVRIWNSALNAWVAVSELTRNH-----TKRASATVKTVAVLATILFATVOANATDED 55





A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-1343 <STO>  
A:Cross-references: GB:AE005174; NID:g12515159; PIDN:AAG56256.1; GSPDB:GN00145; UWGP:Z21  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: ydek

```
Query Match          7.6%; Score 227.5; DB 2; Length 1343;
Best Local Similarity 22.7%; Pred. No. 0.00053;
Matches 147; Conservative 86; Mismatches 252; Indels 163; Gaps 27;

QY 1 MNKIYRIINWALNAWVSELTRNTHKRASATVKTAVLATLFLATVQANATDEDEEEL 60
   ||:||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 MNRIRYVWVWCTLQVQACSELTRVRGKTSTVNLKSSGLTKFS----- 45

QY 61 ESQVRSVGSIQASMEGSELETISLSMTNDSKEFDVPIVVTLKAGDNLKIKONTNEMT 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 46 -----RLTLGVLAL-----SGSVGASLEVDNG-----QITNIDT 76

QY 121 NASFTYSLKDLTLGLINVEKLSFGANGKKVNIISDTKGLNFAKETAGT----- 171
   : : : : : | | | | | : : : : : | | | | | : : : : : | | | | |
Db 77 DVAIDLVLGWTGTGVLNLA-----GGNASLTTITTSVIGGN--EDSEGTNNVLGTWR 129

QY 172 ---NGDPTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHY-----TRAASIKDVLNAGWNK 224
   : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 130 LYDSGNARPLN--VQSGGTGLNIKQKHGVDG-----YRLGCTAAGVGTV-----NVE 178

QY 225 GVKGTSGTSGSENVDFRYDYTFEFLSADTKTTTVMV-----ESKDNKRTVEKIGAKT 278
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 179 GEDSVLTTELFE-----IGSYGTGSLNITDKGYVTSSIVAILGYQANSKVVYKGG--E 232

QY 279 SVIKERDGLVTKGKGEGSSSTDEGEGLVTAKEVIDAVNKAQWKMKTITANGOTQADK 338
   : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 233 WLIKNDSSIEFOIGNOGTGEATIREGGLITAENTWIGGNATG-----VGLNVQ--DQDS 286

QY 339 FETVSGTNNVTFASG-----KGTATVSKDDQGNITVMYD----- 373
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 287 VIVRRLYNGYFCGAVNISNNGLINNKEYSLVGQDGHVGVNVTDKGHNFLGTGEAF 346

QY 374 --VNVGDA----LVNQQLNSGNLDSKAVAGSGKVISGNVSPSKGMDETVNIAGN 427
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 347 RYIYIGDAGXELNVR-----EGKVDSGIITAGMKETGTGNLTV---KDKNSVITLGTN 399

QY 428 IEISRNKG-NIDIATSMAPOFSSVSLCAGADAPTLSDDEGALNV-----GSKDANKPVR 481
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 400 LGYDGHGEMNI-----SNEGLVSVNGSSSLGTYGTVGKVSITTTGGIWEVKNVY 449

QY 482 ITNVAPGVKEGDTNVNAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYLP--GK 539
   | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 450 TTICVAGVGNLNSDGG--KFVSNQITFLGDKASGIGTLMDATSSFDVGINVGNFGS 507

QY 540 SMAIAGGTYRGAGYAI-----GYSSISDGGWNIKGTASGNSR 579
   : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 508 GIVNVSNGATLNTGTGFIGGNASGKGIIVNISTDSLWNLK-TSSTNAQ 554
```

RESULT 14  
AH0038  
Probable exported protein YPO0309 [imported] - *Yersinia pestis* (strain C092)  
C:Species: *Yersinia pestis*  
C:Date: 02-Nov-2001 #sequence\_revision 02-Nov-2001 #text\_change 02-Nov-2001  
C:Accession: AH0038  
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrrell, Nature 413, 523-527, 2001  
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.  
A:Reference number: AB0001; MUID:21470413; PMID:11586360  
A:Accession: AH0038  
A>Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-1238 <KUR>  
A:Cross-references: GB:AL590842; PIDN:CAC89171.1; PID:g15978410; GSPDB:GN00175  
C:Genetics:  
A:Gene: YPO0309

```
Query Match          7.4%; Score 220.5; DB 2; Length 1238;
Best Local Similarity 20.7%; Pred. No. 0.0011;
Matches 142; Conservative 123; Mismatches 239; Indels 183; Gaps 37;

QY 19 VSELTRNHT-----KRASATVKTAVLATLFLAT--VQANAT-----DEDEEELESVOR 65
   : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 78 ISYLTNSALDTSRYLYIKNDTLITEQSASINVQSGSISSGVYIDNQSSDDSTIRV 137

QY 66 SVVGSIQASMEGSELETISLSMTNDSKEFDVPIVVTLKAGDNLKIKONTNEMTNASSF 125
   : | : | : | | | | | | | | | | | | | | | | | | | | | | | |
Db 138 DLSGILSSLSGAPALSIFS--SAGNDST-----ILNTHAISGVTGIGQSDNNSQNGATI 190

QY 126 TYSCLKDLTLGLINVEKLSF--GANGKKVNIISDTKGLNFAKETAGT--NGDPTVHLNG 181
   | : | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 191 TH---VDVTCGINVSGSVSIRNAANG-----GTSIINFNSKSIINTYNSFYIONTY 240

QY 182 IGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGWNKGVKGTGTG----- 233
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 241 VGVVIIDI-----NID--GDISSANSQAARIYNYNGLASLRFRRANNVGTGLYIDN 292

QY 234 QSEN---VDFRTYDTPVEFLSADTKTTTVNVEKONGKRTVEKIGAKTSVK-----E 283
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 293 SSQNGAVTDIILTG---LTATSGSALQANASDEGNIETAKLNNVSYDALNLSDT 349

QY 284 KQKGL-----VTGKKGKENGSTDD---EGEGLVTAKEVIDAVNKAQWKMKTITANGQTG 334
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 350 RSGNILLHDLDISGTTITAEANGTGKIKVMAAGEGST---MLINVNNTSSQSOLDINNYF 406

QY 335 QADKEFTVSGTNTVFASGKGTATVSKDDQGNITVMYDQNVGDA---LVNQL--QNSG 389
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 407 LGSFAISATATGHLTAENGQGMQLQTHS-----SLGDATLHFNIDITAMSSG 454

QY 390 WNLDSKAVAGSSGK--VISGNVSPSKGMDETVNIAGNIEISRNGK---NIDIATSM 444
   : | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 455 ISLINEANGTSTADITVTGQINVSHG---EGITLNA-----LTTDGRTLVNVDV--NNIA 505

QY 445 POFSSVSL-----GAGADAPTLSVD--DEGAL-----NVGSKDANKP 479
   : : : : | | | | | | | | | | | | | | | | | | | | | |
Db 506 SEYDAIRLYNRYNDNYATGVDDGTGADNGTSTIDLITRGALVSOQGYGINIETNADTY 565

QY 480 VRTTNVAPGVKEGDTNVNAQLKGVAQNLRNIDNVGNARAGIAQAIATAGLVQAYL--- 536
   | : | : | | | | | | | | | | | | | | | | | | | | | | | | |
Db 566 VTVGGLVHG---GNGTAI---GI-----HRLDNIQTSATLELSQGVALEGVTVQALVFTG 613

QY 537 -----PKSMMAIGGTYRGAGYAI-----GYSSISDGG 566
   : : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 614 SYAEINDAALDLANSHLVLLGA---GDAAFDLTRIDNREAILDGNRITGTGTLTKTN 670

QY 567 N--WIITKGT--ASGNSRGHFGASASVG 589
   | : | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 671 NSITVLTGANMADGDANAFLSANIAG 697
```

RESULT 15  
D90803  
Aida-I adhesin-like protein [imported] - *Escherichia coli* (strain O157:H7, substrain C:Species: *Escherichia coli*  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 18-Jul-2001  
C:Accession: D90803  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C. gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H. DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic *Escherichia coli* O157:H7 and g A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: D90803  
A>Status: preliminary  
A:Molecule type: DNA

A:Residues: 1-949 <HAY>  
A:Cross-references: GB:BA000007; PIDN:BA034819.1; PID:ql3360856; GSPDB:GN00154  
A:Experimental source: strain 0157:H7, substrain RMD 0509952  
C:Genetics:  
A:Gene: ECs1396

```
Query Match          7.3%; Score 219.5; DB 2; Length 949;
Best Local Similarity 21.4%; Pred. No. 0.00087;
Matches 179; Conservative 97; Mismatches 253; Indels 307; Gaps 42;

QY 1 MNKIYRIIWNALNVAWVSELTRNHTKRASATVK-----TAVLATLLFATVQANATDE 54
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 5 LNTSYRLVWNHITGTLVAVSELARSGRKAGVAVALSAAVTSVPALAAADKVVQAGETVN 64
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 55 D-----EEEELESVORSVVVGS-----QASM 75
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 65 DGTLTNHDNQIVFGTANGMTISTGLELDPDSEENTGGQWQIONGGIAGNTVTTNNGRQVYL 124
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 76 EGSGELET-----ISLSMTNDSKEFVDPIYIVT-----LKAGDNL 110
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 125 EGTASDVTIRDDGGOSLAVNTILNRRGEQWHEGCVATGTIINRDGYQSVKSGG-- 182
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 111 KIKQNTNENTNA-----SFTYSLLKKDLJGLINVEFKLSFGANGKKVNIISDTKGLNFA 165
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 183 -LATGTIINTGAEGGPDSDNSVTGQK-----VQGTAEASTTINKNGRQIILFS-----GLA 231
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 166 KET---ACTNGDTTVHLNGIGSTLTDTLAGSSASHVDAGNQSTHYTRAASIKDVLN-AGW 221
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 232 RDTLIYAG--GDOSVH---GRALNTTLNG-----GYQYVHRDGLA-LNTVINNEGOW 276
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 222 NIKGVKGTSTGGOSENVDPVRTYDTVEFLSADTKTTNVNVEKDNKRTKVEKIGAKTSVI 281
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 277 QV--VKAGGAAG-----NFTIN-----QNGELRVHAGGEATV 308
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 282 KEKDKGLVT-----GKGKG-----ENGSTDEGEGLVTAKEVID----- 315
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 309 QNTGGALVTSTAATVIGTNRLGNFTVENGGKADGVVLESGGRDLVLESHSAQNTLVDDGGT 368
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 316 -AVNKAGWRMKTTTANGQTQADKPFETVTSCTNVTFASCK-----GTT 357
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 369 LAVSAGGRATSVTITSGGALIADSGATV-EGTN---ASGKFSIDGTSQASGLLLENGGS 424
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 358 ATVSKDDQ-GNITVMYD-----VNVGDALNVNOLQN 387
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 425 FTVNAGGQAGNTVGHRCGTTLTAAAGSLSGRTQLSKGASWVLNGDVVSTGDIVNAGEIRF 484
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 388 SGWNLD-----SKAVAGSSG-----KVISGNVSPSKGMDETVNI----- 422
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 485 DNQTTNPAALSRAVAKSNPSVTFHKLTTTLTGQGGTINMRVRLDGSNASDQDLVINGGQA 544
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 423 -----NAGN-NTEISRNGKNIDI-----ATSMAPQFS-SVSLGACADAPILSVDD 465
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 545 TGTWLAFTNVGNSNLGVATVGGIRVVDVAQNGATTEGAFALSRPLQAFNYTLNRDS 604
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 466 EGALNVGSKDANK---PVRITNVAPG-----VKEGDVTNVAOLKGVAAOINNNRI----- 511
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 605 DEDWYLRSENAYRAEVPLTYSMLTQMDYDRILAGSRSHQTGVNGENNVRLSIQGGHLG 664
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 512 -DNVDGNARAGIAQAIATAG-----LVQAYLPKSKMM-----AIG----- 545
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 665 HDNNGGIARGATPESGSGYGFVRLEGDLRLTEVAGMSLTGTVYGAAGHSSVDVKDDGDSR 724
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 546 GGTYRGEAGYATGYSSI---SDGGNW---IIKGT-----ASGNSRGHFGASASVGYQW 592
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

Db 725 ACTVRDAGSLGGYLLNVLVHTSSGLWADIVAQGTRHSMKASSDNDNDRAR---GWGW 777
   :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
```

Search completed: July 3, 2002, 08:38:38  
Job time: 309 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM prtein - protein search, using sw model

Run on: July 3, 2002, 08:49:07 ; Search time 29.79 Seconds  
(without alignments)  
769.452 million cell updates/sec

Title: US-09-771-382-10  
Perfect score: 2988  
Sequence: 1 MNKIYRIIWNALNAWAVS.....TASGNSRGHGASASVGYQW 592

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	248.5	8.3	1325	1 YDEK_ECOLI	P32051 escherichia
2	210	7.0	1286	1 AIDA_ECOLI	Q03155 escherichia
3	197	6.6	1608	1 HLYA_SERMA	P15320 serratia ma
4	197	6.6	1655	1 OMPB_RICCN	Q9kka3 r outer mem
5	196.5	6.6	1039	1 AG43_ECOLI	P39180 escherichia
6	194.5	6.5	1654	1 OMPB_RICRI	Q53047 r outer mem
7	189	6.3	1567	1 ICEN_XANCT	P18127 xanthomonas
8	189	6.3	1953	1 BIGA_SALTY	P25927 salmonella
9	188.5	6.3	2249	1 OMPA_RICRI	P15921 rickettsia
10	187	6.3	1025	1 SLAP_CAUCR	P35828 caulobacter
11	186	6.2	1645	1 OMPB_RICTY	P96989 r outer mem
12	185.5	6.2	1656	1 OMPB_RICJA	Q06653 r outer mem
13	181.5	6.1	1861	1 APU_THETU	P38536 t amylopull
14	180	6.0	2003	1 YDBA_ECOLI	P33666 escherichia
15	180	6.0	2021	1 OMPA_RICCN	Q52657 rickettsia
16	179	6.0	933	1 SLAP_CAMFE	P35827 campylobact
17	179	6.0	1577	1 HLYA_PROMI	P16466 proteus mir
18	173	5.8	2329	1 YS99_CAEEL	Q06624 caenorhabdi
19	172.5	5.8	959	1 N100_YEAST	Q02629 saccharomyc
20	172	5.8	918	1 YMBJ_CAEEL	P34487 caenorhabdi
21	171.5	5.7	1196	1 ICEN_PSESX	Q33479 pseudomonas
22	170.5	5.7	2334	1 WAPA_BACSU	Q07833 bacillus su
23	168	5.6	1300	1 120K_RICRI	P14914 rickettsia
24	167.5	5.6	1034	1 ICEN_PANAN	Q47879 pantoea ana
25	167.5	5.6	1322	1 ICEA_PANAN	P20469 pantoea ana
26	167	5.6	1569	1 YPJA_ECOLI	P52143 escherichia
27	165.5	5.5	1210	1 ICEN_PSEFL	P09815 pseudomonas
28	164.5	5.5	1258	1 ICEN_ERWHE	P16239 erwinia her
29	164	5.5	814	1 SLAI_BACAN	P49051 bacillus an
30	164	5.5	1200	1 ICEN_PSESY	P06620 pseudomonas
31	164	5.5	1643	1 OMPB_RICPR	Q53020 r outer mem
32	163.5	5.5	574	1 FLA3_CAMJE	Q46113 campylobact
33	162	5.4	1694	1 IGA0_HAEIN	P44969 haemophilus

## ALIGNMENTS

## RESULT 1

ID	YDEK_ECOLI	STANDARD;	PRT: 1325 AA.
AC	P32051: P76140; P77168;		
DT	01-OCT-1993 (Rel. 27, Created)		
DT	01-NOV-1997 (Rel. 35, Last sequence update)		
DE	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Hypothetical lipoprotein ydek precursor (ORET).		
GN	YDEK OR ORET OR B1510.		
OS	Escherichia coli		
OC	Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;		
OC	Escherichia.		
OX	NCBI_TaxID=562;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=K12 / MG1655;		
RX	MEDLINE=97426617; PubMed=9278503;		
RA	Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,		
RA	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,		
RA	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,		
RA	Mau B., Shao Y.;		
RT	"The complete genome sequence of Escherichia coli K-12.";		
RL	Science 277:1453-1474(1997).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=K12;		
RX	MEDLINE=97251357; PubMed=9097039;		
RA	Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,		
RA	Kasai H., Kashimoto K., Kimura S., Kitakawa M., Kitagawa M.,		
RA	Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,		
RA	Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,		
RA	Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,		
RA	Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horuchi T.;		
RT	"A 570-kb DNA sequence of the Escherichia coli K-12 genome		
RT	corresponding to the 28.0-40.1 min region on the linkage map.";		
RL	DNA Res. 3:363-377(1996).		
RN	[3]		
RP	SEQUENCE OF 595-1325 FROM N.A.		
RX	MEDLINE=94100243; PubMed=8274505;		
RA	Cartwright P.J., Timms M.W., Lithgow T., Hoeg P.B., Hoogenraad N.J.;		
RT	"An Escherichia coli gene showing a potential ancestral relationship		
RT	to the genes for the mitochondrial import site proteins ISP42 and		
RT	MOM38.";		
RL	Biochim. Biophys. Acta 1153:345-347(1993).		
CC	-!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor		
CC	(Potential).		
CC	-!- SIMILARITY: TO E.COLI YFAL.		
CC	-!- SIMILARITY: SOME, TO FUNGAL MITOCHONDRIAL IMPORT SITE PROTEINS		
CC	ISP42 AND MOM38.		
CC	-!- CAUTION: REF.3 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A		
CC	FRAMESHIFT IN POSITION 653.		
CC	-----		
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CC	use by non-profit institutions as long as its content is in no way		

P45384 haemophilus  
Q08860 shigella fl  
P22251 campylobact  
O84419 chlamydia t  
O30611 pseudomonas  
Q46114 campylobact  
P12021 sus scrofa  
P22252 campylobact  
P50493 plasmodium  
P04949 escherichia  
P35825 bacillus st  
Q92812 chlamydia p

34 162 5.4 1702 1 IGA2\_HAEIN  
35 161 5.4 550 1 FLIC\_SHIFL  
36 161 5.4 575 1 FLA2\_CAMJE  
37 161 5.4 1770 1 PMPC\_CHLPR  
38 160 5.4 1148 1 ICBK\_PSESX  
39 159.5 5.3 574 1 FLB3\_CAMJE  
40 159 5.3 1150 1 APMU\_PIG  
41 158 5.3 575 1 FLB2\_CAMJE  
42 157.5 5.3 1153 1 PVDB\_PLAKN  
43 156 5.2 497 1 FLIC\_ECOLI  
44 156 5.2 1228 1 SLAP\_BACST  
45 155 5.2 1723 1 PM20\_CHLPN



```
QY 350 PASGKGTATVSKDDQGNITVMYDVNVDALNVNOLONGWNL-----DSKAVAGSSG 402
DB 390 LSDGARGITILNSRENVS-----NGGVSYNMINITGGNQYIYSDGEATAAIWNTSG 442
QY 403 --KVISGNVSPSKGMDETVNTNAGN---NIEISRNGKNI-----DIATSMAPQF 447
DB 443 FQRINSGGTAPVONSVVVTRTVSSAAKPDABEYSGGKQTVYLWRGIWYSNFLTAVWSMF 502
QY 448 SSVSLGAGADATPLSDVDEGALN-----VGSKDANKP 479
DB 503 PCTASGA-----NVNLSGRILNAPAGNVVGTILNQEGRQYIYSGATAITVYGNREGREY 555
QY 480 VRITNVAPGVKGGDVNTVAOLKGVQAQNLNRINDVNGNAR-----GIAQAATATAGLVQA 534
DB 556 V-----LSGGITDGTVLNSGGLQAVSSG-----GRASATVINEGGAQFYVDGGQV-- 600
QY 535 YLPGRSMAAGGTYRGEAGYAGYSSISDGN 567
DB 601 --TGTNIK--NGGTIRVDGASALNIALSSGN 629

RESULT 3
HLIA_SERMA
ID HLIA_SERMA STANDARD; PRT: 1608 AA.
AC P15320;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 01-NOV-1990 (Rel. 16, Last annotation update)
DE Hemolysin precursor.
GN SHLA.
OS Serratia marcescens.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Serratia.
OX NCBI_TaxID=615;
RN [1]
RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-40.
RC STRAIN=SN8;
RX MEDLINE=88257037; PubMed=3290200;
RA Poole K., Schiebel E., Braun V.;
RT "Molecular characterization of the hemolysin determinant of Serratia marcescens.";
RL J. Bacteriol. 170:3177-3188(1988).
CC -!- FUNCTION: BACTERIAL HEMOLYSINS ARE EXOTOXINS THAT ATTACK BLOOD CELL MEMBRANES AND CAUSE CELL RUPTURE BY MECHANISMS NOT CLEARLY DEFINED.
CC -!- FUNCTION: CELL-BOUND HEMOLYSIN, WHICH RELEASES HEME-IRON FROM ERYTHROCYTES BY INTERACTION WITH THE ERYTHROCYTE MEMBRANE. SHLA REQUIRES SHLB FUNCTION.
CC -!- SUBCELLULAR LOCATION: Outer membrane.
CC -!- SIMILARITY: TO P.MIRABILIS HEMOLYSIN (HPMA).
CC -----
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CC -----
DR EMBL; M22618; AAA50323.1; -
DR PIR; A28182; A28182.
KW Hemolysin; Toxin; Outer membrane; Signal.
FT SIGNAL 1 30
FT CHAIN 31 1608 HEMOLYSIN.
SQ SEQUENCE 1608 AA; 165078 MW; D669B476FE7DAD51 CRC64;

Query Match 6.6%; Score 197; DB 1; Length 1608;
Best Local Similarity 21.8%; Pred. No. 0.013;
Matches 161; Conservative 82; Mismatches 255; Indels 240; Gaps 35;
QY 24 RNHTKRASATVKTA-----VLAT-----LLFATVQAN-----ATD-----EDEEEL 60
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```
DB 396 REQLQAGSTVAASGSAKLISQEDVKKLGANVSADRALSVKAAARDVHLAGLVEKDKSE 455
QY 61 ESQVQSVVGSIOAS--MEGSGELETISLMTNDSKEFVDPIYIVTLKAGDNL----- 110
DB 456 RGYORNTSSTLGRWSNDESELSKASELSEGE-----LTLKAGRNVTQCGAKVHA 508
QY 111 -----KIKQNTNENTNASSFTYSLKDLITGLINIVETEKLSFGANG---KKNIIIS 157
DB 509 QRDLIDADNQIQGVQKATANAKA-----VRDDKTSWGGIGGGDKNN--S 552
QY 158 DTKGLNFAKETAGTNGDTVTYHLNG-IGSTLTDTLA--GSSASHVDAGNQSTHTYTRAASIK- 214
DB 553 NRREISHASEL--TSGG-TLRNGQGGVITGSKARGQKGEVTAHGLRLIDNALSTTV 609
QY 215 DVLNAGWNILKVKTGST---TGQSENVDFVRYDVTVEFLSADTKTTTVNVESKD--NGKRT 270
DB 610 DKIDA-----RTGTAFNITSSSHKADNSYOSSTASELSKSDTNLTLVSHKDAVDIGSOV 662
QY 271 ----EVKIGAKTSVIEKDKLVTKGKGSGSSTDEGEGLVT----AKEVIDAVNKAGW 322
DB 663 ASGGELSVESKGTGNVVK-----AAERQONIDEQKALTALTVNGYAKEAGDKQYRAGL 713
QY 323 RM-----KTT-----TANGOTGOADKPEFVTVTSGTNVTFASG 353
DB 714 RIEHTRDSEKTTTENSASSLSGGSVKKAEDVTFSGSKLVADKGDASVSGNKVSFLAA 773
QY 354 KGTTA-----TVSKDDQGNITVM 371
DB 774 DDKTASNTBQTKIGGFFYTGIDKLGSGVEAGYENKTKQAOSSKAITSGSDVKGNLT-- 831
QY 372 YDVNVGDALNVNOLONGWNLDSKAVAGSSGKVISGNVSPSKGMDETVINAGNNIETS 431
DB 832 --INARDKLTQOGAHSVCGAYQENAGVYDHLAAADTASTTTTKTD--VGVNIGANVDYS 887
QY 432 RNGKNIDIATSMAPQFSVSL-----GAGADAPTILSVDDG-----ALNV 471
DB 888 AVTRPVERAVGKAALKDATGTVINDIGGIGAPNVGLDIGAGGSSSEKRSSSQAVVSSVOA 947
QY 472 GSKDANKPRTINVPAGVKEGVDVNTVAOLKGVQAQNLN-----NRIDNVGDNARAG 521
DB 948 GSIDIN-----AKGEVRODGTQYQASKG--AVNLTADSHRSEAAANKQDEOSRDR-- 996
QY 522 IAQAATATAGLVQALPGKSMMAIG---GGTYRGEAGYAGYSSISDGNW----- 568
DB 997 ----GSAG--VRVYTTTGSDLITVDAKEGGTQORSNSASQAQVTSIDAANGINNVKKDA 1050
QY 569 IIKGTASGNSRGHFGASA 586
DB 1051 IYQGTALNGGRGKTAVNA 1068

RESULT 4
OMPBL_RICCN
ID OMPBL_RICCN STANDARD; PRT: 1655 AA.
AC O9KKA3; O9KK98; O9XC45;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR RC1085.
OS Rickettsia conorii.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsieae; Rickettsia.
OX NCBI_TaxID=781;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Malish 7;
RX MEDLINE=21442074; PubMed=11557893;
RA Ogata H., Audic S., Renesto-Audiffren P., Fournier P.-E., Barbe V.,
```





DNA Res. 3:379-392(1996).

[3] SEQUENCE FROM N.A.  
RN STRAIN-ML 308-225;  
RC Henderson I.R., Owen P.;  
RA Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.  
[4] PRELIMINARY SEQUENCE OF 53-78.  
RN STRAIN-ML 308-225;  
RC MEDLINE=89291704; PubMed=2661530;  
RA Caffrey P., Owen P.;  
RT "Purification and N-terminal sequence of the alpha subunit of antigen  
43, a unique protein complex associated with the outer membrane of  
Escherichia coli.";  
RL J. Bacteriol. 171:3634-3640(1989).  
RN SEQUENCE OF 53-63.  
RC STRAIN-K12 / EMG2;  
RX MEDLINE=97443975; PubMed=9298646;  
RA Link A.J., Robison K., Church G.M.;  
RT "Comparing the predicted and observed properties of proteins encoded  
in the genome of Escherichia coli K-12.";  
RL Electrophoresis 18:1259-1313(1997).  
RN GENE NAME.  
RX MEDLINE=97257509; PubMed=9103983;  
RA Henderson I.R., Meehan M., Owen P.;  
RT "Antigen 43, a phase-variable bipartite outer membrane protein,  
determines colony morphology and autoaggregation in Escherichia coli  
K-12.";  
RN FEMS Microbiol. Lett. 149:115-120(1997).  
CC -!- FUNCTION: CONTROLS COLONY FORM VARIATION AND AUTOAGGREGATION. MAY  
FUNCTION AS AN ADHESIN.  
CC -!- SUBUNIT: HETERODIMER OF THE PERIPHERAL MEMBRANE PROTEIN (ALPHA  
CHAIN) ANCHORED TO THE INTEGRAL OUTER MEMBRANE PROTEIN (BETA  
CHAIN).  
CC -!- SUBCELLULAR LOCATION: OUTER MEMBRANE ASSOCIATED.  
CC -!- SIMILARITY: TO ADHESIN AID-I AND TO BORDETELLA PERTACTIN.  
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EMBL; AE000291; AAC75061.1; ALT\_INIT.  
DR EMBL; D90838; BAA15825.1; ALT\_INIT.  
DR EMBL; D90839; BAA15832.1; ALT\_INIT.  
DR EMBL; U24429; AAB47869.1; -  
DR Ecogene; EGI2686; flu.  
KW Outer membrane; Signal; Complete proteome.  
FT SIGNAL 1 52  
FT CHAIN 53 551 ANTIGEN 43 ALPHA CHAIN.  
FT CHAIN 552 1039 ANTIGEN 43 BETA CHAIN.  
FT VARIANT 2 2 K -> N (IN STRAIN ML 308-225).  
FT VARIANT 41 42 SL -> FF (IN STRAIN ML 308-225).  
FT VARIANT 46 46 T -> K (IN STRAIN ML 308-225).  
FT VARIANT 157 157 W -> L (IN STRAIN ML 308-225).  
FT VARIANT 188 188 V -> F (IN STRAIN ML 308-225).  
FT VARIANT 303 305 ATN -> STI (IN STRAIN ML 308-225).  
FT VARIANT 320 320 A -> T (IN STRAIN ML 308-225).  
FT VARIANT 372 372 N -> Q (IN STRAIN ML 308-225).  
FT VARIANT 493 493 E -> V (IN STRAIN ML 308-225).  
FT VARIANT 497 497 S -> N (IN STRAIN ML 308-225).  
FT VARIANT 585 585 H -> Y (IN STRAIN ML 308-225).  
FT VARIANT 709 709 E -> K (IN STRAIN ML 308-225).  
FT VARIANT 721 721 M -> T (IN STRAIN ML 308-225).  
FT VARIANT 751 753 GHL -> SHF (IN STRAIN ML 308-225).  
FT VARIANT 803 803 S -> P (IN STRAIN ML 308-225).  
FT VARIANT 815 815 A -> V (IN STRAIN ML 308-225).  
FT VARIANT 824 824 C -> S (IN STRAIN ML 308-225).

FT VARIANT 829 835 LNLVHTS -> MNLIYNA (IN STRAIN ML 308-  
225).  
FT VARIANT 845 847 QGT -> LGA (IN STRAIN ML 308-225).  
FT VARIANT 855 855 S -> T (IN STRAIN ML 308-225).  
FT VARIANT 888 888 O -> L (IN STRAIN ML 308-225).  
FT VARIANT 1025 1025 S -> I (IN STRAIN ML 308-225).  
FT CONFLICT 61 63 ETV -> TTT (IN REF. 5).  
SQ SEQUENCE 1039 AA; 106841 MW; 5170D647C8DEEB0 CRC64;

Query Match 6.68; Score 196.5; DB 1; Length 1039;  
Best Local Similarity 20.18; Pred. No. 0.0083;  
Matches 134; Conservative 79; Mismatches 268; Indels 185; Gaps 27;

QY 1 MNKIYRIIWSALNAWAVASELTRNHTKRASATVKTAVALTATLLFATVQANATDEDEEEL 60  
Db 5 LNTCYRLVWHTMGAFVASELARARGKGVAVALSAAVTSLPVLAADIVHPGE--- 61  
QY 61 ESVQSVVSGSIQASMEGSGELETISLSMTNDSKEFVDPYIVVTLKAGDNLIKIKONTNENT 120  
Db 62 -----TWNGG-----TLANHDNQIVFGTTNGMT 84  
QY 121 NASFTYSLKLDLTGLINVEKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLN 180  
Db 85 ISTGLEYPDNEA-----NTGGQWV-----QDGGTANKTTVTSG 118  
QY 181 GI-----GSTLTDTL--AGSSAS-----HVDAGNOSTHYTRAASIKDVLNAGNIKG 225  
Db 119 GLQVRNPGSVSDVISAGGOSQGRVAVTTLNGGEQWHEGATATGTVINDKQWV-- 176  
QY 226 VKTGS-----TTQGSENVDFVRYDTVEFLSADTKTTTVN-----VESKDNKRREV 272  
Db 177 VKPGTVAITVVNTGAEQGPD-AENGDTGQFVRGDAVRTTNKNGRQIVRAEGTANTTV 235  
QY 273 KIGAKTSV-----IKEKDGKLVTKGKGKNGSGSSTDEGSL 307  
Db 236 YAGGDTVHGHALDTTLNGGYQYVHNGGTASDTVVNSDQWQIVKNG-GVAGNTTVNQGR 294  
QY 308 VTAKEVIDAVN---KAGRMKTTTANGOTG--QADKFEFVT-SGTNVTFASG-----KG 355  
Db 295 LQVDAGGTATVTLKQGGALVTSTAATVGINLGAFSVEGKADNVLENGRDLVLTG 354  
QY 356 TTATSKDDQGNITVYDYNVGDALNVQLNSGNLWLSKAVAGSSGKVISGNVSPSK-- 413  
Db 355 HTATNTRVDDGG---TLDVRNGGTATTVSMNGG-----VLLADSGAAVSTRSDGRA 405  
QY 414 ---GKMDTVNINAGNNIEISRNGKNIDIAISMARQFSSVSLGACADAPTLSDDEGALN 470  
Db 406 STGGQADALMLEKGSFTLNAG-----DTATDTTVNGGLFTARGGTLAGTTTLNNGAILT 461  
QY 471 VGSKDANKPVRTNVAPGVKEGDTNVNQLKGVAQNLRNIDNVGNARAGIAQAIAATAG 530  
Db 462 LSGKTVN-----NDTLTIREG-----ALLQGGSLTGNGSVEK-SGSGTLTVSNTTLTQK 510  
QY 531 LVQAYLPKGSMAAGGTT-----YRGEAGYAIQYS-----SISDGGNMIKG 572  
Db 511 AVNL---NEGTLTNDSTVTTDVIAQRGTALKLTGSTVLNGAIDPTNVTNLASGATWNIPD 567  
QY 573 TASGNS 578  
Db 568 NATVQS 573

RESULT 6  
ID OMPB\_RICRI STANDARD; PRT; 1654 AA.  
AC Q53047;  
DC 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DE Outer membrane protein B precursor (168 kDa surface-layer protein)  
DE (Surface protein antigen) (cell surface antigen 5) (Sca5) (rOmpB)  
DE (Contains: 120 kDa surface-exposed protein (surface protein





Db 341 I---ADNTTIVISGDDQAHNSDRGMDISGDRGTGVIISGDRVTWLTGDSVVDGATGMV 397  
QY 153 V-----NIISD-----TKGL-----NEAKETAGTNGDTTVHLNAGIGSTLIDT-- 199  
Db 398 ISGDTNTISGHSTVDNATGALISGNGTTFNAGDIAVSGGTAIIIDGDNATIKTGT 457  
QY 190 ----LAGSSASHVDAGNQSTHYTRAASIKDVLNAGW-----NIRKGVKTGSTTQSGSENVDFV 241  
Db 458 SDISGAGSTGTVIDGNARNYNDGDMTITDGGTGGHTGDTGDNVDNAGSTTVSGADA--- 514  
QY 242 RTVDYTFEELSADTKTTVNVNVEKNDKRTVEKTAKTSTVKEKDKLVTGK-----KG 295  
Db 515 ----TALYIEGDNALVINEGNTISGAVGTRIDGDDAHTTNTGDIADVAGAGAAVING 570  
QY 296 ENGSSDDEGLVT--AKEVI--DAVNKAGWRMKTITANGOTQADKFEVTGNTVTF- 350  
Db 571 DNGSLTQAGDLLVTDGAWGIIITGTGNEA-----KNTGNATVRDADSFGVFAKEKNTFK 625  
QY 351 -----ASRGKTATYSKDDQGNITVMYDYNVGDALNVNQLNSGWNLDKSAVAGSGKV 404  
Db 626 NKGIDVSLNGTALVSGD-----MSQVTLDDGINVSVQ-----DSEGVFSSATGV 672  
QY 405 ISGNVSPSKMDETVINAGNIEISRNKNIDIAFMAPQSSVSLGAGADAPTLSVD 464  
Db 673 ---SVSGDSNAVDITGNV-----ISADYGQDDLAAG-APPLTGVVVGNGNTVTILN-- 720  
QY 465 DEGALNVGSKD---ANKPVRTNVPVKEGV-----TNV-----AQLKGVA 504  
Db 721 --GALNIDDDLSATGQYLDVGLVSGTGDNDNDEIDGGINITHSEDPDGTADITGIS 778  
QY 505 QNLNNRI-----DNVDGNARAG---IAQAIATAGLV-----QAYLP-----GK 539  
Db 779 VSGNSTVTLNGHSTIDNTTVGGHVLARNVNGSLILGDDSVVDVNVISPIPTGYTYNA 838  
QY 540 SMAIGGTGVRGAG-----YAI-----GYSSISDGNWIIKGTASGNSRGHFGASV 588  
Db 839 LLMADGEGTSIENKGDITSHGVSVIRADNGSEVNSGDLIVATSSNSEDRAAITRAS 898  
QY 589 G 589  
Db 899 G 899  
RESULT 9  
OMPA\_RICRI  
ID OMPA\_RICRI STANDARD; PRT: 2249 AA.  
AC PI5921;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Outer membrane protein A precursor (190 kDa antigen) (Cell surface  
DE antigen) (rOmpA) (rOmpA).  
GN OMPA.  
OS Rickettsia rickettsii.  
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;  
OC Rickettsiaceae; Rickettsiidae; Rickettsia.  
OX NCBI\_TaxID=783;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=R;  
RX MEDLINE=90354033; PubMed=2117568;  
RA Anderson B.E., McDonald G.A., Jones D.C., Regnery R.L.;  
RT "A protective protein antigen of Rickettsia rickettsii has tandemly  
RT repeated, near-identical sequences.";  
RL Infect. Immun. 58:2760-2769(1990).  
CC -I- FUNCTION: ELICITS PROTECTIVE IMMUNITY.  
CC -I- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A  
CC S-LAYER WITH HEXAGONAL SYMMETRY.  
CC -I- PTM: GLYCOSYLATED (PROBABLE).  
CC -I- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.  
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CC  
DR EMBL; M31227; AAA26380.1; -.  
DR PIR; A41477; A41477.  
DR InterPro; IPR003858; rOmpA\_rOmpB.  
DR Pfam; PF02708; rOmpA\_rOmpB; 1.  
KW Antigen; Repeat; Signal; Cell wall; S-layer; Glycoprotein.  
FT SIGNAL 1 28  
FT CHAIN 1 28  
FT DOMAIN 29 2249  
FT REPEAT 212 1180  
FT REPEAT 212 386  
FT REPEAT 287 358  
FT REPEAT 339 430  
FT REPEAT 431 505  
FT REPEAT 506 577  
FT REPEAT 578 652  
FT REPEAT 653 724  
FT REPEAT 725 799  
FT REPEAT 800 874  
FT REPEAT 875 949  
FT REPEAT 950 1021  
FT REPEAT 1022 1093  
FT REPEAT 1094 1165  
FT REPEAT 1166 1180  
FT TYPE I (INCOMPLETE).  
FT SEQUENCE 2249 AA; 224333 MW; A9D6646C089DF087 CRC64;  
SQ  
Query Match 6.3%; Score 188.5; DB 1; Length 2249;  
Best Local Similarity 22.5%; Pred No 0.052;  
Matches 155; Conservative 79; Mismatches 273; Indels 181; Gaps 38;  
QY 10 NSALNAWAVAVSELTRNHT-----KRASATVKT-AVLATLFLATVOANATDEDEEE-- 59  
Db 703 DSTGNANGIVTFTGNTSTVGTGDTGNTNATLVNAGTAGTATLGAVIKATTTKLTNAASVL 762  
QY 60 -LESQSVVSGISQASMEG-----SCELETISLSMTNDSKEFVDPIVTVLTKAG-- 107  
Db 763 TLTNANAVLTGAIDNTTGGDNVGLNGLSQTGIDGNTNS-----LATISVGAGT 815  
QY 108 ---DNLKIKONTNENTNASSFTYSLKDK--LTGLINVEKTEKLSFGANGKKVNIISDTKGL 162  
Db 816 ATLGGAIVKATTTKLTNAASVLTLTNANAVLTGAVDNTT-----GGDNVGLNGLAL 868  
QY 163 N-FAKETAGTNGDTTVHLNIGIGSTLTDTLTLAGSSASHVDAGNQSTHYTRAASIKDVLNAGW 221  
Db 869 SQVTGDTGNTNSLATISV-GAG--TATLGGAIVKAT-----TTKLTNAASVLTLTNA-- 917  
QY 222 NIKGVKTG---STTQSENVDFVRYTDTVEFLSADTKTT---TVNVEKDK---NG---K 268  
Db 918 --NAVLTGAIDNTTG-GDNVGLNGLNGLSQTGIDGNTNSLATISVGAGTATLGGAIVK 974  
QY 269 RTEVKIGAKTSVIKEDGKLVGT---KRGKENGSSSTDEGEGLVTAK---EVIDAVNKA 320  
Db 975 ATTTKLTDAASAVKFTNPVVVTVGAIDNTGNANGIVTFTGNTSVTGNVGNATLVNAG 1034  
QY 321 -----GWRMKTITAN-----GOTGQADKFEVTGNTVTFASGKGTAT 359  
Db 1035 AGLLQVQGGVVKANTINLTNDSAVTFTNPVVVTVGAIDNTGNANGI-VTFTGNTSTVGN 1093  
QY 360 VSKDDGNTVVMYDVNVGDAL-----NVN-----QLQNSGW 390  
Db 1094 V-----GNTNATLVNAGLLOVQGGVVKANTINLTNDSAVTFTNPVVVTVGAIDNTG- 1147  
QY 391 NLDKSAVAGSGKGVISGNVSPSKGMDVTVINAGNIEISRNK-----KNIDIAFMAPQ 446  
Db 1148 NANGIVTFTGNTSTVGTGI-----GNTNATLVNAGGAGITLQAGSSLAANNIDFGARSTLE 1203  
QY 447 FSSVSLGAGADAP-----TLSDDEGALNVGSKDANK-----PVRTNVAPG-----V 489

Db 1204 FNGPLDGGKALPYFKAINGNAILNVTNKLITASHLTGTVAEINIGAGNLTIDA 1263  
QY 490 KEGDVTNVAQLKGVQNLNLR-----IDNVGHNARAGIAQAIATAGLVQVYLPG--KS 540  
Db 1264 SVGDVTILN-----AQNINFRARDSVLVLSNLTG---VGVNILLAADLV---AFGADEG 1312  
QY 541 MVAIGGTVRGEAGYAGYGS--SISDGG 566  
Db 1313 TVVFNCGVNLNNGSVNAGTARNIGDGG 1340

RESULT 10  
SLAP\_CAUCR  
ID SLAP\_CAUCR STANDARD; PRT; 1025 AA.  
AC P35928; Q46015;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE S-layer protein (Paracrystalline surface layer protein).  
GN RSAA OR CC1007.  
OS Caulobacter crescentus.  
OC Bacteria; Proteobacteria; alpha subdivision; Caulobacter group;  
OC Caulobacter.  
OX NCBI\_TaxID=69394;  
RN [1]  
RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-21; 646-660 AND 1021-1025.  
RC STRAIN=ATCC 19089 / CB15; PubMed=1393820;  
RX MEDLINE=93007489; PubMed=1393820;  
RA Gilchrist A., Fisher J.A., Smit J.K.;  
RT "Nucleotide sequence analysis of the gene encoding the Caulobacter  
crescentus paracrystalline surface layer protein.";  
RL Can. J. Microbiol. 38:193-202(1992).  
RN [2]  
RP REVISIONS TO 376; 636 AND 842-843.  
RA Awram P.;  
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 19089 / CB15;  
RX MEDLINE=21173698; PubMed=11259647;  
RA Nierman W.C., Feidblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
RA DeBoy R.J., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
RA Atterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
RT "Complete genome sequence of Caulobacter crescentus.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
RN [4]  
RP SEQUENCE OF 1-313 FROM N.A., AND SEQUENCE OF 1-20.  
RC STRAIN=ATCC 19089 / CB15;  
RX MEDLINE=89008089; PubMed=3049545;  
RA Fisher J.A., Smit J.K., Agabian N.;  
RT "Transcriptional analysis of the major surface array gene of  
Caulobacter crescentus.";  
RL J. Bacteriol. 170:4706-4713(1988).  
RN [5]  
RP CHARACTERIZATION.  
RC STRAIN=CB15;  
RX MEDLINE=98292737; PubMed=9620954;  
RA Awram P., Smit J.K.;  
RT "The Caulobacter crescentus paracrystalline S-layer protein is  
secreted by an ABC transporter (type I) secretion apparatus.";  
RL J. Bacteriol. 180:3062-3069(1998).  
CC -!- FUNCTION: THE S-LAYER IS A PARACRYSTALLINE MONO-LAYERED ASSEMBLY  
OF PROTEINS WHICH COAT THE SURFACE OF BACTERIA. PROBABLY ACTS AS A  
PHYSICAL BARRIER TO PARASITES AND LYTIC ENZYMES.  
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-  
LAYER WITH HEXAGONAL SYMMETRY. SECRETED BY AN ABC TRANSPORTER  
(TYPE I) SECRETION APPARATUS.  
CC -!- MISCELLANEOUS: THE CALCIUM BINDING OF THIS PROTEIN MAY MEDIATE

CC SURFACE ATTACHMENT BY IONIC BRIDGING BETWEEN THE S-LAYER AND A  
CC SPECIFIC MEMBRANE-ASSOCIATED OLIGOSACCHARIDE.  
CC -----  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC -----  
DR EMBL; AF062345; AAC38665.2; -;  
DR EMBL; AE005779; AAK22991.1; ALT\_INIT.  
DR HSSP; P01549; 2MCM.  
DR TIGR; CC1007; -;  
DR InterPro; IPR001343; Hemlysn\_Ca\_bind.  
DR Pfam; PF00353; hemolysinCbind; 1.  
DR PRINTS; PR00313; CABNDNGRPT.  
KW Cell wall; S-layer; Calcium-binding; Complete proteome.  
FT INIT\_MET 0  
SQ SEQUENCE 1025 AA; 98001 MW; AD7A326E1363D8AC CRC64;  
-----  
Query Match 6.3%; Score 187; DB 1; Length 1025;  
Best Local Similarity 24.1%; Pred. No. 0.024;  
Matches 160; Conservative 73; Mismatches 274; Indels 156; Gaps 29;  
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QY 18 AVSELRNHTKRASATVKTAVLATL-----LFAFVQAN-----ATDEDEEEELSVQ 64  
Db 138 AYDKIGNAVAATAAGVDVAAAFSLRQANIDYLTAFVRANTPFTAAADID-----LAVK 192  
QY 65 RSVVSGI--QASMEGSGELETISLSMTNDSKEFVDPIVVTILKAGDNLIKIKONTNENTNA 122  
Db 193 AALIGTILNAATVSGIGGYATATAAMIND---LSDGALSTDNAAGVNL---FTAYSSGV 246  
QY 123 SSFTYSL---KKDLTGLINVT-----EKLSPGANGKKVNIISDTKGLNF 164  
Db 247 SGTSLSLTTGTDTLTGTANNDTFVAGEVAGAAATLVGDTLGGAG-----TDVLNW 297  
QY 165 AKETAGTNGDTVHLNGI-----GSTLDTLAGSSASHVDAG-NQ 203  
Db 298 VQAAAVTALPTGVTISGIIETNMVTSAAITLNTSGVTLTALTNTSGAAQTVTAGAG 357  
QY 204 STHYTRAASIKD--VLNAGNMIKGVKTGTTGSENVDFVRYDTVEFLSADTKTTTVNV 261  
Db 358 NLTATTAQAANNAVVDGGAANTVASTGVTSGTTTGVGANSASCTVSVSVANSSTTTTGA 417  
QY 262 ESKDNGKRTVEKIGAKTSVIKEKDKGLVTGKKGKNGSSTDEGEGLVTA-KEYIDAVNKA 320  
Db 418 IAVTGGTAVTVAQTAGNAVNNTLTQADVTVTGNSSTTAVTQTAAATAGATVAGRVNGA 477  
QY 321 GHRMKTTHANGOTGOADKFETVTS-----TNVTFASGKGTTATVSKDDQGN 368  
Db 478 VTITDSAAAAT--AGKIATVTLGSGAATIDSSALTTVNL-SGTGTSLGIGR---GAL 531  
QY 369 TVMYDVNVGDALNVNOLQNSGNLDSKAVAGS-----SGKVISQNVSPSKMDETVN 421  
Db 532 TATPTANT-LTLNVNGLTTTGATIDSEAAADGFTTINAGSTASSTIASLVAADATTLN 590  
QY 422 INAGNNIEISRN-----GKNI--DIATSMAPQFSSVSLGAGADAPTLSVDD 465  
Db 591 ISGDARVTITSHATAALTGITVNSVGATLGAEATGLV--FTG---GAGADSLIGATT 645  
QY 466 EGALNVGSKDANKPVRIITNVAPG--VKEGDVTVNAOLKGAQNLLNRIDNVD----- 515  
Db 646 K-AIVMGAGDDTTVSSATLGAGGSYNGDGTDV-----LVANVNGSSFSADPAFGFET 699  
QY 516 ----GNARAG-----IAQATATAGLVQ----AVLPCKSMMAIGGGYRGEAGYAGY 559  
Db 700 LRVAGAAAGSHNANGFTALQLGATAGATFTTNVAVNVGLTVLAAPTGTITVTLANATGT 759  
QY 560 SSI 562  
| :

Db 760 SDV 762

## RESULT 11

```
OMPBRICITY STANDARD; PRT; 1645 AA.
AC P96989;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB OR SLP.
OS Rickettsia typhi.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
OX NCBI_TaxID=785;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WILMINGTON;
RX MEDLINE=94040787; PubMed=8224896;
RA Hahn W.-J., Kim K.-K., Kim I., Chang W.-H.;
RT "Cloning and sequence analysis of the gene encoding the crystalline
RT surface layer protein of Rickettsia typhi.";
RL Gene 133:129-133(1993).
RN [2]
RP PARTIAL SEQUENCE.
RC STRAIN=WILMINGTON;
RX MEDLINE=92114896; PubMed=1370573;
RA Ching W.M., Carl M., Dasch G.A.;
RT "Mapping of monoclonal antibody binding sites on CNBR fragments of
RT the S-layer protein antigens of Rickettsia typhi and Rickettsia
RT prowazekii.";
RL Mol. Immunol. 29:95-105(1992).
RN [3]
RP IDENTIFICATION OF CLEAVAGE SITE.
RC MEDLINE=92104668; PubMed=1729180;
RA Hackstadt T., Messer R., Cieplak W., Peacock M.G.;
RT "Evidence for proteolytic cleavage of the 120-kilodalton outer
RT membrane protein of rickettsiae: identification of an avirulent
RT mutant deficient in processing.";
RL Infect. Immun. 60:159-165(1992).
CC -1- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION.
CC -1- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR.
CC -1- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A
CC S-LAYER WITH HEXAGONAL SYMMETRY.
CC -1- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMP FAMILY.
CC
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CC
CC EMBL; L04661; AAB48987.1; -.
CC InterPro; IPR003858; rOmpA_rOmpB.
CC Pfam; PF02708; rOmpA_rOmpB; 1.
CC Antigen; S-layer; Transmembrane; Cell wall.
CC CHAIN 1 1353 120 KDA SURFACE-EXPOSED PROTEIN.
CC FT CHAIN 1354 1645 32 KDA BETA PEPTIDE.
CC TRANSNEM 1415 1429 MEMBRANE ANCHOR (POTENTIAL).
CC CONFLICT 657 657 H -> N (IN REF. 2).
CC CONFLICT 842 842 V -> I (IN REF. 2).
CC CONFLICT 1071 1071 G -> A (IN REF. 2).
CC CONFLICT 1306 1306 G -> S (IN REF. 2).
CC SEQUENCE 1645 AA; 169698 MW; 0CB5641C7EB185EE CRC64;
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Query Match 6.2%; Score 186; DB 1; Length 1645;

Best Local Similarity 21.1%; Pred. No. 0.048; Mismatches 251; Indels 266; Gaps 37;

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QY 28 KRASATVKTAVLATL-----LFATVQANATDEDEEELESVQRVSVGSIQASMEGSG 79
DB 10 KIISAGLVTAATVIVAGSGVAMGAVMYNRT-----TNAATTVDDGAG 54
QY 80 ELET-----ISLSMTNDSKEFVDPYIVVTLKAGDNKLTQKNTNENTNASSFTYSUKDLTGL 136
DB 55 FDOTGAGVNLPVATNS-----VIT--ANSNNAITFT-PNGNLSLFLDTANTLAVT 103
QY 137 INVETKLSFGANGKKVNIISDTKGLNFAKETAGTNGDTTVHLNGIGS--TLTDTLAGSS 194
DB 104 IN-ENTTLGF-----VTNVTKGNFFFTIGAGKSUTITGHGTAOAAATTKSAQNV 154
QY 195 ASHVDAGNQ-----STHVTRAASIKDV-----LNAGWNK----- 224
DB 155 VSKVNAAGAINNDLSGVGSIDFTAAPSVEFLNINPTTQEAPLTLGDNAKIYVNGANGIL 214
QY 225 -----GVKTGSTTGQSENVDFVRYDTVEFLSADTKTTTVNVESKD----- 265
DB 215 NITNGFVKVSDKTFAGIKT-INIGDNQGLMFTTTPDAANALNLQGGNTINFNRGDTGK 273
QY 266 -----NGKRTVEKI-----GAKTSVIKED-----GKLVTKGKG-----ENGSG 299
DB 274 LVLVSKNGNATEPNVTGSLGGLKGVIEFTTAAAGKLIANGGAANAIVGTDTNGAGRAAG 333
QY 300 ---STDEG-----EGLVTAKEVIDAVNKGWRMKTITANGOT-----GOADKFT 341
DB 334 FIVSDVNGNAATISGQVYAKDIV-----IQSANAGQVTFEHLVDVGLGKTNFKT 384
QY 342 VTSCTNVTASGKGTATVSKDQGNITVMYDVN-----VGDALNVNQLNSGNWL 392
DB 385 ADSKVIITENASEGST-----DFGNLAVQIVVPNNKILTNFGIDA-----KNNG-NT 431
QY 393 DSKAVAGSGKVISGNVSPS-----KGKMDTVNI-----NAGNNTEISR 432
DB 432 AGVITFNANGTLVSGNTDPIVVTNIKAIEVGAGIVQLSGIHGAELRLGNAGSIFKLA- 490
QY 433 NGKNIDIATSWAPQFSVSLGAGA---DAPTLSDVD--EGALNVGSKD---ANKPVRIITN 484
DB 491 DGVINGPVNQNLVNNALAAAGSIQLDGSAIITGIDIGNAVNAALODITLANDASKILT 550
QY 485 VAP-----GVKEG-----DVTNVAQLKQVAQN--- 506
DB 551 LSGANIIGANAGGAIHFQANGGIQTLSTONNILLDFDLDTTDDQGVVDASSLTNNQTL 610
QY 507 -LNNRIDNVGNAR-----AGTAQAIATAGLV-----QAYLPKGSMM 542
DB 611 TINGSIGTIGANTKTLGRFNVGSSKTLINAGDVAINELVMENDGSHLTHNTYLTITNTIN 670
QY 543 AIGGTYRGAGYAGYSSISDGNWLIKTAGSNRSGHFSGASVYG 589
DB 671 AANOGKIIVAADPINTDATALDGTN--LGSAESPLSNIHFAKRAAG 715
```

## RESULT 12

```
OMPBRICITY STANDARD; PRT; 1656 AA.
AC O06653;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Outer membrane protein B precursor (168 kDa surface-layer protein)
DE (Surface protein antigen) (Cell surface antigen 5) (Sca5) (rOmpB)
DE (rOmp B) [Contains: 120 kDa surface-exposed protein (Surface protein
DE antigen) (120 kDa outer membrane protein ompB); 32 kDa beta peptide].
GN OMPB.
OS Rickettsia japonica.
OC Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
OC Rickettsiaceae; Rickettsiae; Rickettsia.
```

```
OX NCBI_TaxID=35790;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YH;
RA Uchiyama T.;
RT "Sequencing of the gene encoding the protein rOmp B of Rickettsia japonica.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: THE 120 KDA SURFACE-EXPOSED PROTEIN IS A MAJOR
CC STRUCTURAL PROTEIN WHICH MAY PLAY A ROLE AS A RICKETTSIAL
CC VIRULENCE FACTOR AND/OR IMMUNOGEN DURING INFECTION (BY
CC SIMILARITY).
CC -!- FUNCTION: THE 32 KDA BETA PEPTIDE MAY SERVE AS A MEMBRANE ANCHOR
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELL WALL. THIS BACTERIUM IS COVERED BY A S-
CC LAYER WITH HEXAGONAL SYMMETRY.
CC -!- SIMILARITY: BELONGS TO THE RICKETTSIAE OMPA/OMPB FAMILY.
CC
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CC
DR EMBL: AB003681; BAA20138.1; -.
DR InterPro: IPR003858; rOmpA_rOmpB.
DR Pfam: PF02708; rOmpA_rOmpB; 1.
KW Antigen; S-layer; Cell wall.
FT CHAIN 1 1338 120 KDA SURFACE-EXPOSED PROTEIN.
FT CHAIN 1339 1656 32 KDA BETA PEPTIDE.
FT DOMAIN 528 533 POLY-GLY.
FT SEQUENCE 1656 AA; 168097 MW; 3132A69C9DD5999F CRC64;
SQ
Query Match 6.2%; Score 185.5; DB 1; Length 1656;
Best Local Similarity 22.0%; Pred. No. 0.051;
Matches 140; Conservative 81; Mismatches 229; Indels 187; Gaps 34;
QY 46 TVQANATDEDEEELS-----VORSVVGSIQASMEGSELETTISLWMTNDSKEFVDPYI 100
DB 262 TIFNGTGTGRLVLLSKNGAATDFNVTSGLGNLKGIIELNVAINGQ----- 310
QY 101 VYTLKAGDNLKONTNENTNASSFTYSLKDLTGLINVETELKSLFGANGKKVNIISDTK 160
DB 311 -LIANAGPANAVIGTWNGAGRAAGFVVSD-----NGKAATIDGQVY 351
QY 161 GLNFAKETAGTGTTV-HLNGIGSTLTDTLAGSSASHVDAGNQSTHY-----TRAA 211
DB 352 AKDMVIOANANGOVNFRHIVDVG--IDGTTAFKTAASIVAITQNSNFGTTDFGNLAAQV 409
QY 212 SKDVLNAGNWKGVVTGTGTGSENN-----VDFVRVYDVVEFLSADTKTTTVN---- 260
DB 410 TVPDTMTL-----TGNFTGDANNPGNTAGVITPAAN-GTLASASADANAVTNNITA 460
QY 261 VESKDG-----KTEVKIGAKTSVIREKDKLVTKG-----GKGECSSTDEGE 305
DB 461 IEASGVGVOLSTHFAELRLGNAGSVFKLADGTGVINGKVNQTVLVGGVLAAGAITLDGS 520
QY 306 GLVTAKEVIDAVNKAGWR--MKTTTANGOTGOADKPEVT-----SGTNVTFASGK 354
DB 521 ATITG---DIGNNGGGAALQSITLAN-----DATKTLTLGANIISANGGTINQANG 570
QY 355 GTTATVSKDDQGNITWYDV-----NVGDALNVNOLQNSGNLDSKAVAGSGKVISG 407
DB 571 GTIKLTS--TQNNIVVDCDLAIATDQTVGVVDASSL-----NAOTLTISGTIGIIGAN 621
QY 408 NVSPSK---GKMDETV-----IN--AGNN--IETSRNGKNIDIATSWAPQ-----FSSV 450
DB 622 NTLTGQFNIGSSKTTLNGGNVAINELVIGNNGSVQFAHNTYLTITRTNAGQGKIIFNPV 681
QY 451 -----SILGAGADAPTLSDVDEGALNVGSKDANKPVRITNVAPGVKEGDVTNVAQLKGVAG 505
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DB 682 VNNNTTLAAGT-----:||| || | :||| || | :||| || | :||| || |
QY 506 NLNNRIDNVGNARAGIAQAIATAGLVQAYLPKSKMMAIGGTYGCGEAGYATGYSSISDG 565
DB 726 YATN-ITTTDAN-----VGSFVFNAG-----GKNTVS---GTVGQOQGNKFNVTALDNG 770
QY 566 -----GNWIIKGT-----SGNSRGHFGASA 586
DB 771 TTVKFLGNATFNGNTTIANSTLOISGNTADFIASA 807
RESULT 13
APU_THETU STANDARD; PRT; 1861 AA.
AC P38536;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Alpha-pullulanase precursor (Alpha-amylase/pullulanase) (Pullulanase
DE type II) [includes: Alpha-amylase (EC 3.2.1.1) (1.4-alpha-D-glucan
DE glucanohydrolase); Pullulanase (EC 3.2.1.41) (1.4-alpha-D-glucan
DE glucanohydrolase) (Alpha-dextrin endo-1,6-alpha-glucosidase)].
GN AMYB.
OS Thermoanaerobacter thermosulfurogenes (Clostridium
OS thermosulfurogenes).
OC Bacteria; Firmicutes; Bacillus/Clostridium group;
OC Thermoanaerobacter group; Thermoanaerobacterium.
OX NCBI_TaxID=33950;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DSM 3896 / EM1;
RX MEDLINE=94252998; PubMed=8195085;
RA Matuschek M., Burchhardt G., Sahn K., Bahl H.;
RT "Pullulanase of Thermoanaerobacterium thermosulfurogenes EM1
RT (Clostridium thermosulfurogenes): molecular analysis of the gene,
RT composite structure of the enzyme, and a common model for its
RT attachment to the cell surface.";
RL J. Bacteriol. 176:3295-3302(1994).
CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-alpha-glucosidic
CC linkages in oligosaccharides and polysaccharides.
CC -!- CATALYTIC ACTIVITY: Hydrolysis of (1->6)-alpha-D-glucosidic
CC linkages in pullulan and in amylopectin and glycogen, and the
CC alpha- and beta-limit dextrins of amylopectin and glycogen.
CC -!- SUBCELLULAR LOCATION: CELL-BOUND. IT C-TERMINUS MAY SERVE AS AN
CC S-LAYER ANCHOR.
CC -!- PTM: GLYCOSYLATED.
CC -!- SIMILARITY: BELONGS TO FAMILY 13 OF GLYCOSYL HYDROLASES, ALSO
CC KNOWN AS THE ALPHA-AMYLASE FAMILY.
CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -!- SIMILARITY: CONTAINS 3 S-LAYER HOMOLGY (SLH) DOMAINS.
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CC
DR EMBL: M57692; AAB00841.1; -.
DR HSP: Q08751; 1BVZ.
DR InterPro: IPR000461; Alpha.amylase.
DR InterPro: IPR003961; FN_III.
DR InterPro: IPR001119; SLH.
DR InterPro: IPR004185; alpha.amylase_N.
DR InterPro: IPR004193; isoamylase_N.
DR Pfam: PF00128; alpha.amylase; 1.
DR Pfam: PF02806; alpha.amylase_C; 1.
DR Pfam: PF02903; alpha.amylase_N; 1.
DR Pfam: PF00041; fn3; 2.
DR Pfam: PF02922; isoamylase_N; 1.
DR Pfam: PF00395; SLH; 3.
```



DR SMART; SM00060; FN3; 1.  
DR PROSITE; PS01072; SLH\_DOMAIN; 3.  
KW Hydrolase; Glycosidase; Carbohydrate metabolism; Signal; Repeat;  
KW Multifunctional enzyme; Glycoprotein.  
FT SIGNAL 1 35 POTENTIAL.  
FT CHAIN 36 1861 AMYLOPULLULANASE.  
FT DOMAIN 928 1018 FIBRONECTIN TYPE-III 1.  
FT DOMAIN 1157 1248 FIBRONECTIN TYPE-III 2.  
FT ACT\_SITE 628 628 BY SIMILARITY.  
FT ACT\_SITE 657 657 BY SIMILARITY.  
FT ACT\_SITE 734 734 BY SIMILARITY.  
FT DOMAIN 1681 1739 SLH 1.  
FT DOMAIN 1740 1803 SLH 2.  
FT DOMAIN 1804 1861 SLH 3.  
FT CONFLICT 1734 1734 D -> E (IN REF. 1; AAB00841).  
SQ SEQUENCE 1861 AA; 206104 MW; 06C23070E453B574 CRC64;

Query Match 6.1%; Score 181.5; DB 1; Length 1861;  
Best Local Similarity 19.5%; Pred. No. 0.093;  
Matches 128; Conservative 98; Mismatches 226; Indels 205; Gaps 29;

QY 2 NKIVRIIWSALNA---WVAVSELTNRHTKRASATVKTAVLATLLFATVQA----- 49  
DB 1208 NEVINYIDTSVINGVTYNYKVAVDLSFNRTESNVVTPKIPVNFVTPDTPDA 1267  
QY 50 -----NATDEEELESVQSVVSGSIQASMEGSELE-----TISLMTNDSKE 94  
DB 1268 VNLGATPFPNATPSAQOMTKIDNTY-SITLTLDEGTQIEYKVGWDBKDEYVNE 1326  
QY 95 FVDPYIVVTLKAGDN-LIKIKONTNENTNASSFTYSLKKDLTGLINVTETKLSFGA-NGKK 152  
DB 1327 FASNRKVTIVNOGNEMTINDTVYWRWDIPFIYSPSNNTVDSNTSMVEVNGTYKGA 1386  
QY 153 VNI-----ISDTGLNFAKETA---GPN-----GDTTVHLNGIG--STLT-----DT 189  
DB 1387 VTINGDSFVQKNGV-FTKDSLVNYGVNKKIKHVPNDGSGVYNDQGRITELKDEIDV 1445  
QY 190 LAGSASHVDAGNQSTHYTRAASIKDVLNAGNIKVGKTSTTGQSNVDVFRTYDFVEF 249  
DB 1446 IROENSSGSGTGNNTS-----TSGNSSTSGSGTSGTSTITSNTSNTSNT 1494  
QY 250 LSADTKTTTVNVEKNGKTEVIGKAKTSVIEKDGKLV---TGKKGNGSGSTDEGEG 306  
DB 1495 IGVITKNGNVTITLTDAGK-----AKDLIVNSKDKKVVFDITIGEGQQ-----KV 1540  
QY 307 LVTAKEVIDAVNAGWRMKTITANGOTGQADKPTVTSCTNVTFASGKGTATVSKDDQG 366  
DB 1541 VQISKDILD-----TSAANGKD-----IVIKSDNA 1565  
QY 367 NITVMYDVNVDALNVOLQNSGNLDSKAVAGSGKVISGNVSPSKGMDVTNINAGN 426  
DB 1566 SIAL-----TKDALNQIQN-GVNVSIK-----DNGKPNVTNYVSLSN 1603  
QY 427 NIELSRGNKIDITASMAPOFSSVSLGAGADAPTLVSDDDEGALNVGSKDANKPVRI----- 482  
DB 1604 VVDITISGISGNV-----TLAKPVEVTLNISK--ANDPKVAVYY 1641  
QY 483 -----TNVAPGVKEGDTVNAQLKGVAQNLRNIDVNDGNARAGIAQAIAT 528  
DB 1642 YNPITNWEYVGGKVDASSGTITFNATHFSQY--AAFEYDKTFNDIKDNKAKDVIEVLAS 1699  
QY 529 AGLVQA-----YLPKKS-----MMAIGGGTYRGEAGYAGYSSISDGGNW 568  
DB 1700 RHIVEGMDTQYEPNKTVTTRAFTAMILRLNLNIKDETYSGE-----FSDVK-SGDW 1749

RESULT 14  
YDAA\_ECOLI STANDARD; PRT; 2003 AA.  
AC P33666; P76087; P76088; P76856; P76857; P76859;  
DT 01-FEB-1994 (Rel. 28, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Hypothetical protein ydba.  
GN YDAA OR B1401/B1405.  
OS Escherichia coli.  
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
OC Escherichia.  
OX NCBI\_Taxid=562;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12 / MG1655;  
RX MEDLINE=97426617; PubMed=9278503;  
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,  
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
RA Mau B., Shao Y.;  
RT "The complete genome sequence of Escherichia coli K-12.";  
RL Science 277:1453-1474(1997).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=97251357; PubMed=9097039;  
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isono K., Itoh T.,  
RA Kasai H., Kashimoto K., Kimura S., Kitagawa M., Kitagawa M.,  
RA Makino K., Miki T., Mizobuchi K., Mori H., Mori T., Motomura K.,  
RA Nakade S., Nakamura Y., Nashimoto H., Nishio Y., Oshima T., Saito N.,  
RA Sampei G., Seki Y., Sivasubram S., Tagami H., Takeda J.,  
RA Takemoto K., Takeuchi Y., Wada C., Yamamoto Y., Horiuchi T.;  
RT "A 570-kb DNA sequence of the Escherichia coli K-12 genome  
corresponding to the 28.0-40.1 min region on the linkage map.";  
RL DNA Res. 3:363-377(1996).  
RN [3]  
RP SEQUENCE OF 464-2003 FROM N.A.  
RC STRAIN=K12;  
RX MEDLINE=92190338; PubMed=1665988;  
RA Moszer I., Glaser P., Danchin A.;  
RT "Multiple IS insertion sequences near the replication terminus in  
Escherichia coli K-12.";  
RL Biochimie 73:1361-1374(1991).  
CC -!- SIMILARITY: TO S-TYPHIMURIUM ORF NEAR CYSG (AC P25928).  
CC -!- CAUTION: THIS IS A CONCEPTUAL TRANSLATION; THE GENE CODING FOR  
THIS PROTEIN IS INTERRUPTED BY A HYBRID IS2D/IS30C ELEMENT  
BETWEEN AMINO ACIDS 839 AND 840.  
CC -----  
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or send an email to license@isb-sib.ch).  
CC -----  
CC EMBL; AE000237; AAC74483.1; ALT\_SEQ.  
DR EMBL; AE000237; AAC74487.1; ALT\_SEQ.  
DR EMBL; D90778; BAA15009.1; ALT\_SEQ.  
DR EMBL; D90778; BAA18880.1; ALT\_SEQ.  
DR EMBL; D90779; BAA18881.1; ALT\_SEQ.  
DR EMBL; X62680; -; NOT\_ANNOTATED\_CDS.  
DR EcoGene; EGI1307; ydba.  
KW Hypothetical protein; Complete proteome.  
FT CONFLICT 489 489 I -> V (IN REF. 2).  
FT CONFLICT 495 495 I -> V (IN REF. 2).  
SQ SEQUENCE 2003 AA; 205949 MW; B83A12C8B53220EE CRC64;

Query Match 6.0%; Score 180; DB 1; Length 2003;  
Best Local Similarity 23.0%; Pred. No. 0.12;  
Matches 160; Conservative 89; Mismatches 224; Indels 222; Gaps 43;

QY 55 DEEELESVQSVV-----GSTQASMEGSELETISLMTNDSKEFV----- 96  
DB 149 DKTEKTLTIRDSVFTYENADGTI-SLQDSNGRKATINLWQIDENNTVALEGSADGAT 207  
QY 97 -----DPYIVVTLKAGDNLIKQNTNENTNASSFTYSLKKDLTGL-IN-----VETEK 143





Search completed: July 3, 2002, 08:49:15  
Job time: 721 sec

FT	CONFLICT	809	823	LLRVQGVVKSNTIN -> KATLGGAIKATTTK (IN REF. 1).
FT	CONFLICT	898	898	D -> Y (IN REF. 1).
FT	CONFLICT	908	908	P -> N (IN REF. 1).
FT	CONFLICT	985	985	N -> K (IN REF. 1).
FT	CONFLICT	1009	1009	L -> S (IN REF. 1).
FT	CONFLICT	1013	1013	Y -> S (IN REF. 1).
FT	CONFLICT	1182	1182	K -> Q (IN REF. 1).
FT	CONFLICT	1314	1314	N -> Y (IN REF. 1).
FT	CONFLICT	1451	1451	H -> N (IN REF. 1).
FT	CONFLICT	1624	1624	G -> D (IN REF. 1).
FT	CONFLICT	1628	1628	E -> G (IN REF. 1).
FT	CONFLICT	1872	1872	A -> V (IN REF. 1).
FT	CONFLICT	1875	1875	T -> P (IN REF. 1).
FT	CONFLICT	1878	1879	MS -> LP (IN REF. 1).
FT	CONFLICT	1936	1936	E -> A (IN REF. 1).
FT	CONFLICT	1965	1970	MTAPLP -> ITPPLS (IN REF. 1).
FT	CONFLICT	1997	1997	G -> R (IN REF. 1).
SQ	SEQUENCE	2021 AA;	203328 MW;	327FC42D7CB24668 CRC64;
Query Match 6.0%; Score 180; DB 1; Length 2021;				
Best Local Similarity 20.5%; Pred. No. 0.12;				
Matches 138; Conservative 94; Mismatches 277; Indels 164; Gaps 30;				
Qy	13	LNAWVAVSELTRN-HTKRASATYKT-AVLATLLFATVQANATDEDEEELESQORSVVG	70	
Db	274	LNLGALSQVGTGNIGTGNATATISVGAGKATLGGAVIKATTTKLTDNASAVTFNPNV	331	
Qy	71	IQASMEGSGELETISLWNTDSK---EFVDPYIVVTLKAG-----DNLKIKONTNENT-	120	
Db	332	VTGAIDNTGNANNIGVTFGTGSTVTGNTGNATATISVGAGKATLGGAIKATTTKLT	391	
Qy	121	NASFTYSLKDLTGLINVTETKLSFCGANGKYNIIISDTKGLNFAKETAGTNGDTTVHLN	180	
Db	392	NASAVTFNPNVVTGAI-----DNTGNANG-----IVTFGTGSTVTGNTGNATATISVG	443	
Qy	181	GIGSTLTDTLAGSSASHVDAGNOSTHYTRAASIKDVL-NAGWNIKGVKT---GSTTQS	235	
Db	444	AGKATLGGAIKATTTKLTDNASAVTFNPNVVTGAI DNTGNANNIGVTFGTGSTVTGNI	503	
Qy	236	ENVDFVITYDTVEFLSADTKTTTVNVEKONG---KTEVKIGAKTSVIREKDKLVTG-	291	
Db	504	GNTNALAT-----ISVGAGKATL-----GGAIKATTTKLTDNASAVTFNPNVVTGA	551	
Qy	292	---KGCGENGSTDEGBELVTAKEVIDAVNKAGWRMKTITANGOTGOADKFEVTSCTNV	348	
Db	552	IDVTGNANNIGVTFGTGSTVT-----GNIGNATATISVGAGK	590	
Qy	349	TFASGKGTATVSK--DDOGNITVMYDVNVGDALNVNQLNSGNWNLDSKAVAGSSGKVIS	406	
Db	591	ATLGGAIKATTTKLTDNASAVTFNPNVVTGAI-----NTG-NANNIGVTFGTGSTVT	644	
Qy	407	GNVSPSKGKMDETVMNAGNNEISRNKNIDITATSMAPOFSSV-----SLGAGADAP	459	
Db	645	GNIGNTAL--ATVNVGAG---IATLEGAVIKATTTKLTNAASVLTLTNTVNAVLTGAIDN	699	
Qy	460	TLSDVDDGAL-----NYGSKDANKPVRI-----TNVAPGVKEG	492	
Db	700	TTGVDNVGVNLNGALSQVGTGNIGNTGNATATISVGAGKATLGGAVIKATTTKLTDNASAV	759	
Qy	493	DVTNVAQLKGVAQNLRNNDVNDGNRAGIA-----QAIATAGLVQAYLP	537	
Db	760	TFTNPNVVTGA-----IDNT-GNANNIGVTFGTGSTVTGNTGNATATVNV-----	805	
Qy	538	GKSMMAIGGTYRG-----EAGYATGYS-----SISDGNWIIKGTASGNSRGH	581	
Db	806	GAGLLRVQGVVKSNTINLTNDNASAVTFNPNVVTGAI DNTGNANNIGVTFGTGSTVTGN	865	
Qy	582	FG-----ASASVG	589	
Db	866	IGNTGNATATISVG	878	



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